

9th International Conference on Polar and Alpine Microbiology



9-14 October 2022
GFZ German Research Centre for Geosciences,
Potsdam, Germany

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Welcome by the Conference Chairs

Dear polar and alpine microbiology enthusiasts,

It is our pleasure to welcome you to the 9th International Conference on Polar and Alpine Microbiology in Potsdam, Germany.

Since the first conference on Polar and Alpine Microbiology (PAM) in Rovaniemi, Finland, the world's microbial society which is interested in polar and alpine environments has been meeting regularly every second year until SARS-CoV-2 appeared on the world stage. Therefore, it is our special honour and a great privilege to host the first PAM conference after the world-wide Covid lock-down in person.

Potsdam, in particular the German Research Centre for Geosciences, Helmholtz Centre Potsdam (GFZ) and the Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research (AWI) on the Albert Einstein Campus, are known for their research in the Arctic (including Siberia, Svalbard, Greenland, Canada and Alaska) and Antarctica. Our work addresses, among other topics, the microbiological processes of greenhouse gas release in permafrost regions, the albedo effect of microalgae on ice sheets, the diversity of microbial communities in initial cold deserts, and the general response of microorganisms to climate change. With the commissioning of the new GeoBioLab at the GFZ, which gives our two sections, Interface Geochemistry and Geomicrobiology, a new modern home, research in polar regions and alpine areas will be further advancing and, in particular, the interaction of microbiological and geological processes will become a stronger focus of our research.

The PAM conferences in the past have been very successful in bringing together the diverse research strands in the polar and alpine areas and have allowed an intensive exchange of scientists on the different aspects of microbiological research in these areas. We feel committed to this tradition and are therefore looking forward to the numerous scientific presentations, lively scientific exchanges on new aspects in our research field, the establishment of new collaborations and last but not least to meet old and new friends after more than two years under pandemic conditions.

We cordially welcome you to Germany and to Potsdam, the capital of Brandenburg (which *someone* called a museum). We hope that you will enjoy the location and the 9th International Conference on Polar and Alpine Microbiology as well as the various social events.

Chairs of the Conference



Dirk Wagner



Liane G. Benning

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9th International Conference on Polar and Alpine Microbiology

Abstract Volume

Edited by
**Dirk Wagner, Liane G. Benning, Susanne Liebner, and
Sizhong Yang**

9-14 October 2022
GFZ German Research Centre for Geosciences
Potsdam, Germany

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Program overview

Venue: GFZ German Research Centre for Geosciences

Address: Haus H, Albert Einstein Science Park, Telegrafenberg, 14473 Potsdam (Germany)

Sunday October 9, 2022	
17:00-21:00	Registration and Ice breaker
Monday October 10, 2022	
09:00-09:15	Opening / Welcome notes by conference chairs and GFZ officials
09:15-12:40	Session 1: Microbial communities and global change (Part1) Chairs: Robin Kodner, Tyler Kohler
09:15	Trinity Hamilton (keynote) Geomicrobiology of mid-latitude glaciers
09:55	Jade Brandani A 'common garden' to understand and predict effects of glacier shrinkage of microbial life in high-mountain streams
10:15	Aritri Sanyal Contrasting patterns of bacterial metabolic potentials in coastal Antarctic melt-water environments during the summer
10:35-11:00 Coffee break	
11:00	Concepcion Sanchez-Cid Environmental and anthropogenic factors shape the snow microbiome and Antibiotic resistome
11:20	Eva L. Doting Diurnal oscillations in the Greenland Ice Sheet supraglacial exometabolome
11:40	Ian T. Stevens Where do they come from, where do they go? Viability of microbes in the melting spring snowpack of Midtre Lovénbreen, Svalbard
12:00	Susanne Liebner Microbial methane sources and sinks in sediments of Arctic thermokarst lagoons
12:20	Rey Mouro Biogeography of glacier microbial communities
12:40-14:00 Lunch break	
14:00-16:20	Session 2: Microbial gene pool and biotechnology of cold environments (Part1) Chairs: Beat Frey, Bellas Christopher
14:00	Lukasz Dziewit (keynote) Insights into plasmidome and resistome of polar regions
14:40	August Steigmeyer Oxidative sulfur cycling by a novel subglacial bacterium
15:00	Matthias Wietz Seasonal, interannual and spatial patterns of bacterial taxonomy and genetic functions in the Arctic Ocean
15:20	Amedea Perfumo Ancient DNA preserved in cryo-environments: what can we learn from past gene pools?

15:40	Margarita Smirnova Antarctic bacteria as a potential source of keratinase for degrading poultry feathers waste
16:00-19:00	Poster Session I with drinks and snacks (presenting authors only until 18:00)
Tuesday October 11, 2022	
08:40-10:40	Session 1: Microbial communities and global change (Part2) Chairs: Trinity Hamilton, James Bradley
08:40	Birgit Sattler (keynote II) Ethics in glacier protection under the pressure of climate change
09:20	Maria Monteiro (online) Predicting and validating the impact of warming on terrestrial microbial systems in Antarctic Polar deserts using laboratory and field space for time approaches
09:40	Taylor Priest Atlantification drives taxonomic and functional shifts in the Arctic Ocean microbiome
10:00	Leïla Ezzat Global biogeography of the sediment biofilm microbiome in glacier-fed streams
10:20	Lasse Z. Jensen Seasonal variation of the atmospheric bacterial community in the Greenlandic High Arctic is influenced by weather events and local and distant sources
10:40-11:10 Coffee break	
11:10-12:30	Session 2: Microbial gene pool and biotechnology of cold environments (Part2) Chairs: Beat Frey, Amedea Perfumo
11:10	Ate H. Jaarsma Microbial diversity on the Greenland Ice Sheet
11:30	Anja Černoša Population genomics and biocontrol potential of the Arctic black yeast <i>Aureobasidium subglaciale</i>
11:50	Christopher Bellas Polintoviruses in high alpine lakes and beyond
12:10	Rafael Gonzalez-Serrano Metagenomics uncovers differential viral diversity of an alpine lake and glacial stream in the Pyrenees
12:30-14:00 Lunch break	
14:00-16:20	Session 1: Microbial communities and global change (Part3) Chairs: Tyler Kohler, Trinity Hamilton
14:00	Alexandre M. Anesio Microbial dynamics drive enhanced melting of the Greenland ice sheet
14:20	Emily LM Broadwell Investigating the photophysiology of supraglacial microalgae
14:40	Athanasios Zervas TotalRNA metatranscriptomics: genome evolution, community succession and predation in complex cold-adapted microbiomes in Greenlandic permafrost and ice

15:00	Jan Kollár Preliminary results on the investigation of microbial communities inhabiting the diverse lakes of James Ross Island, Antarctica
15:20	Christian DF Castenschiold Linking microbial taxa to ice-nucleation protein production in Arctic marine environments
15:40	David Pearce Aerobiology over the Southern Ocean – implications for bacterial colonization of Antarctica
16:00	David Touchette Response of alpine stream biofilms to climate change induced stressors
16:30-19:30	Poster Session 2 with drinks and snacks (presenting authors only until 18:30)
Wednesday October 12, 2022	
08:40-11:40	Session 3, Open session on cryosphere microbiology Chairs: Tatiana Vishnivetskaya, Laura Selbmann
08:40	Tom J. Battin (keynote) Cruising our planet's roof towards the unlocking of microbial life in glacier-fed streams
09:20	Max Häggblom Acidobacteriota diversity in Arctic tundra soils
09:40	Jean-Piere de Vera Life beyond Earth: where and how should we look for it? - Permafrost as a key player to solve the task
10:00	James A. Bradley Active and dormant microorganisms on glacier surfaces
10:20	Laura Selbmann Genome-assembled metagenomics to untangle bacterial diversity and functionality in Antarctic microbial endolithic communities
10:40-11:00 Coffee break	
11:00	Valentina Savaglia Disentangling terrestrial microbial community composition in the Sør Rondane Mountains, East Antarctica
11:20	Sizhong Yang Influence of short term warming on microbial communities and functions in Arctic peat soil
12:00	Cultural Excursion (with lunch pack)
Thursday October 13, 2022	
09:00-12:00	Session 4, Eukaryotic microbial diversity Charis: Anne Jungblut, Athanasios Zervas
09:00	Jun Uetake (keynote I) High-resolution seasonal change of Chlorophyta ASVs in the snow in the Japanese beech forest

09:40	Patrick M. Hooper Changes in microbial diversity and ecology in Arctic freshwater biofilms across a broad latitudinal gradient (56-83 °N)
10:00	Federico Biagioli Ecological networks of Antarctic cryptoendolithic communities
10:20	Jasmin L Millar Novel instrumentation for the in situ measurement of glacier algae physiology within ice
10:40-11:00 Coffee break	
11:00	Alexander M.C. Bowles (keynote II) Cryogenian origins of multicellularity in algae
11:40	Steven Hanes Co-evolution of the Ess1-CTD axis in polar fungi suggests a role for phase separation in cold tolerance
12:00	Robin Kodner Patchy and pink: Dynamics of a <i>Chlainomonas</i> sp. (Chalmydomonadales, Chlorophyta) algal bloom on Bagley Lake, North Cascades, WA
12:20-14:00 Lunch break	
14:00-18:00	Session 5, Adaptation, survival and subzero activity Chairs: Jean-Piere de Vera, Ianina Altshuler
14:00	Anne D. Jungblut (keynote) Genomic and amino acid traits of cold adaptation in Antarctic cyanobacteria
14:40	Kari Green Genomic characterization and identification of cold-adaptation signatures in metagenomic assembled genomes of Archaea from Arctic seawater
15:00	Elisa K. Peter Intracellular metabolic signatures of pigmented algal blooms from the Greenland Ice Sheet
15:20	Ianina Altshuler Novel Antarctic yeast adapts to cold by switching energy metabolism and increasing small RNA synthesis
15:40	Volha Akulava Profiling pigments in the psychrotrophic Antarctic bacteria by FT-Raman spectroscopy
16:00-16:20 Coffee break	
16:20	Alexander Tveit (keynote III "Microbial communities and global change") Microbial physiological responses to global warming
17:00	Catherine Larose Microbial community selection and adaptation in snow
18:30	Conference banquet, Restaurant Meierei, Potsdam (with bus shuttle)
Friday October 14, 2022	
08:40-10:40	Session 6, Carbon and nitrogen turnover, Chairs: Runa Antony, Taylor Priest
08:40	Jenni Hultman (keynote) Illuminating microbial communities in the Finnish subarctic soils using omics approaches
09:20	Laura Halbach Nutrient requirements of microalgae on the Greenland Ice sheet revealed by single-cell analyses

09:40	Laura Helene Rasmussen Do Arctic extreme winter warming events lead to microbial N immobilization and plant N limitation?
10:00	Pamela E. Rossel Microbial carbon dynamics in cryogenic environments of the western Greenland ice sheet
10:20	Quincy Faber Environmental conditions and biogeochemical cycling in supraglacial weathering crust habitats
10:40-11:00 Coffee break	
11:00-12:20	Session 7, Plant-Microbe Interaction, Chairs: Riitta Nissinen, Robyn Barbato
11:00	Riitta Nissinen Aerobic anoxygenic photosynthetic bacteria are common in endosphere and phyllosphere microbiomes of arctic and boreal plants
11:20	Barbara von Hippel Temporal rhizobiome changes inferred from ancient DNA shotgun sequencing
11:40	Malek Marian Exploring the functional potential of plant-associated microbiomes in alpine region to enhance cold stress tolerance in plants
12:00	Robyn Barbato Simulated snow drives rhizosphere recruitment in subarctic soils
12:20-12:50	Closing remarks and Poster prize
12:50	Lunch break and departure

Geomicrobiology of mid-latitude glaciers

Trinity Hamilton, Jeff Havig

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Abstract

Glaciers and snow are key components of the terrestrial landscape and regional climate as well as the hydroelectric industry and municipal and agricultural water supplies to large population centers. In the Pacific Northwest Region (PNW) of the United States, recent global warming predictions suggest as many as 77 % of the glaciers will cease to exist in the coming 100 years. Here we examine snow microbe activity and composition on PNW supraglacial snow to better constrain the role of supraglacial ecosystems in local and global biogeochemical cycles and subglacial weathering. We have conducted integrative studies of geochemistry, microbial community composition, and primary productivity in supra- and peri-glacial systems at Mt. Adams (WA), Mt. Hood (OR), and North Sister (OR) in Cascade Range of the PNW. Our work has demonstrated: 1) snow algae communities drive primary productivity across a range of supra- and peri-glacial regions; 2) snow algae biomass contributes to subglacial weathering; 3) snow algae communities incorporate fixed nitrogen from anthropogenic sources; and 4) increasing dissolved inorganic carbon concentration correlates with increase algal activity. These results have implications for improving modern global climate models, understanding past snowball Earth events, and searching for evidence of life on Mars.

A 'common garden' to understand and predict effects of glacier shrinkage on microbial life in high-mountain streams

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Abstract

In alpine regions worldwide, climate change has induced unprecedented glacier shrinkage, and various stream ecosystems draining glacierized catchments are experiencing profound environmental changes. However, how microbial life in these streams will be affected remains poorly understood. We conducted a field-based, common garden experiment to study how glacier shrinkage may affect biofilm's microbiome in glacier-fed and groundwater-fed streams' sediment. This is relevant as melt waters may dominate runoff during glacier peak flow, while groundwater becomes more important beyond peak flow. We started biofilm growth in 30 flumes initially fed from a glacier-fed and groundwater-fed stream, mixing these waters (i.e., 0:100, 25:50, 50:50, 50:75 glacier: groundwater) along a source gradient once nascent biofilms had formed. We let biofilm develop in these treatments and compared their biomass (as chlorophyll-a, bacterial abundance) and community structure (16S rRNA and 18S rRNA genes) to the control (either 100% glacier- or groundwater-stream fed). We found that biofilm biomass increased with the influence of the groundwater-fed stream and that microbial diversity and turnover showed a gradual change along the source gradient. Our findings shed new light on the potential ecological trajectory of microbial life in rapidly changing alpine stream networks and provide a more unified understanding of the resilience potential of bacterial communities considering this transition.

Contrasting patterns of bacterial metabolic potentials in coastal Antarctic melt-water environments during the summer

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Abstract

Supraglacial ecosystems such as cryoconite holes (CH, melt-water depressions with nutrients and debris) respond to seasonal variability in surface hydrology during the summer season and are likely to influence supraglacial and downstream glaciomarine microbial community and functioning. We used high-throughput amplicon sequencing and predictive functional metagenomic tools to study the bacterial diversity and functioning in supraglacial CH and hydrologically connected adjoining fjord water during a summer meltseason. The CH debris community shifted from autotrophic Cyanobacterial lineages at the beginning to heterotrophic Bacteroidota-related lineages over the melt season. A corresponding shift from predicted carbon fixing and photosynthetic protein-related functions to the energy-related carbohydrate, amino acid, and glycan metabolic pathways were seen in the debris community. The bacterial community in the CH water comprised heterotrophic Proteobacteria-related lineages. Predicted functions of bacteria in the water contrasted with that of the debris, wherein most energy-related metabolic pathways declined, while carbon fixing and sulphur metabolic pathways increased over the summer season. The transient fjord waters, comprising heterotrophic bacteria, showed an increased incidence of predicted energy-related metabolic pathways. Thus, changes in microbial communities throughout the meltseason could potentially influence supraglacial and downstream biogeochemical cycles.

Environmental and anthropogenic factors shape the snow microbiome and Antibiotic resistome

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Abstract

Winter tourism can generate environmental pollution and affect microbial ecology in mountain ecosystems. This could stimulate the development of antibiotic resistance in snow and its dissemination through the atmosphere and through snow melting. Despite these potential impacts, the effect of winter tourism on the snow antibiotic resistome remains to be elucidated. In this study, snow samples subjected to different levels of anthropogenic activities and surrounding forest were obtained from the Sudety Mountains in Poland to evaluate the impact of winter tourism on snow bacteria using a metagenomic approach. Bacterial community composition was determined by the sequencing of the V3-V4 hypervariable region of the 16S rRNA gene and the composition of the antibiotic resistome was explored by metagenomic sequencing. Whereas environmental factors were the main drivers of bacterial community and antibiotic resistome composition in snow, winter tourism affected resistome composition in sites with similar environmental conditions. Several antibiotic resistance genes (ARGs) showed a higher abundance in sites subjected to human activities. This is the first study to show that anthropogenic activities may influence the antibiotic resistome in alpine snow. Our results highlight the need to survey antibiotic resistance development in anthropogenically polluted sites.

Diurnal oscillations in the Greenland Ice Sheet supraglacial exometabolome

Eva L. Doting¹, Marie B. Jensen¹, Elisa K. Peter², Martyn Tranter¹, Liane G. Benning²,
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Abstract

During the ablation season, microbial blooms colonize the Greenland Ice Sheet bare ice surface. These blooms, dominated by the pigmented glacier ice algae *Ancylonema alaskanum* and *Ancylonema nordenskiöldii*, darken the ice surface, significantly reducing its albedo and enhancing ice sheet melt. Net productivity of primary producers is an order of magnitude higher than consumption by ice surface heterotrophs, leading to an accumulation of supraglacial dissolved organic carbon (DOC). However, little is known about the ecological role of, as well as diurnal or seasonal variation in, this microbially-derived supraglacial DOC. We used a high-resolution mass spectrometry-based untargeted metabolomics workflow to identify metabolites in the supraglacial DOC pool. We putatively annotated 17 metabolites, including riboflavin, lumichrome, the auxin indole acrylic acid and tryptophan, which have previously been associated with microbial interactions such as controls on growth. This suggests that, in addition to its role as an energy source for ice sheet heterotrophs, the supraglacial DOC pool may play an important role in microbe-microbe interactions, likely providing a control on supraglacial community composition. Diurnal sampling revealed a highly dynamic stress response in the algal community as well as the exometabolome, with significant changes over the timescale of several hours. Future studies should address the role of the exometabolome in microbial interactions as well as the implications of variations in the exometabolome over diurnal and seasonal timescales with respect to the export of microbially-derived DOC from the Greenland Ice Sheet surface.

Where do they come from, where do they go? Viability of Microbes in the Melting Spring Snowpack of Midtre Lovénbreen, Svalbard

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Abstract

Mass loss from glaciers and ice sheets is accelerating, driven by climate warming, and is expected to peak within the next 50 years. Higher air temperatures will extend both the areal extent and duration of the summer melt season, amplifying glacier melt. These increasingly exposed bare-ice surfaces are darkening globally, driving a positive feedback loop of reduced albedo, increased radiative energy receipt, and further enhanced melt rates. Surface darkening is driven, in part, by “biologically active impurities” comprised of surface algae, cryoconites and water-borne bacteria. To date, there remains limited knowledge of the controls upon this microbial biomass. One proposed control is the seeding of the glacier surface by the winter snowpack, delivering microbes to the bare-ice surface as it melts during the spring transition period.

We report the first assessment of microbial glacier surface seeding from the snowpack, using samples collected from the melting spring snowpack and ice near-subsurface at Midtre Lovénbreen, Svalbard, in June 2022. The viability of microbial cells in these habitats was assessed in the field by analysing membrane permeability using a BD Accuri C6+ flow cytometer and a live/dead staining protocol. We report total and viable microbial counts and distinguish between microbe communities at the domain level, allowing us to establish and differentiate between the contribution of viable microbes to the bare-ice surface from the winter snowpack, and those which “melt-out” from near sub-surface ice. Our work provides a first understanding of how glacier micro-ecology may respond to the up-glacier retreat of snowlines and lengthened ablation seasons that climate warming will cause.

Microbial methane sources and sinks in sediments of Arctic thermokarst lagoons

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Abstract

Arctic thermokarst lagoons form at the terrestrial-marine interface when thermokarst lakes erode and connect to the Ocean. They are dynamic environments with potential alternations between freshwater and marine conditions and harbor unknown microbiomes and carbon cycling processes. We investigated sources and sinks of microbial methane in sediment cores from Polar Fox lagoon, a semi-closed thermokarst lagoon in north-eastern Siberia, and of two adjacent thermokarst lakes by analyzing sediment geochemistry, microbial traits and microbial taxa. In-situ methane concentrations, methane-carbon isotopic signatures, analysis of amplicon sequencing variants (ASVs), metagenomics, and pore-water profiles point towards active methane oxidizing microbial communities. These communities are mainly composed of ANME2 a/b organisms, common in marine sediments, and perform anaerobic oxidation of methane (AOM) in a sulfate-methane transition zone 2-3 meters below the sediment surface of the lagoon. Additionally, we observed co-occurrence of known freshwater AOM taxa, specifically of *Candidatus Methanoperedens*, with ANME2 a/b. Based on metagenomic analyses, we suggest that *Ca. Methanoperedens* is not involved in dissimilatory nitrate reduction which can act as the electron sink for AOM. In the sulfate zone of the lagoon's sediment, in-situ methane concentration was only 0.4-5% of deeper sediment and of adjacent thermokarst lakes without connection to the Arctic Ocean, which further supports efficient sulfate-driven AOM. In lagoon sediments below the sulfate-zone and in sediments of the adjacent thermokarst lakes, methane concentrations reached values up to 2.2 $\mu\text{mol g}^{-1}$. This means an oversaturation with methane. Non-competitive methylotrophic methanogens dominate the methanogenic

community of the lakes and the lagoon, independent of porewater chemistry. This abundance of methanogens likely caused the high methane concentrations observed in all sulfate-poor sediments. In conclusion, our study shows that Arctic thermokarst lagoons can host efficient methane-filtering AOM communities and that transitions from thermokarst lake to lagoon can mitigate methane fluxes in Arctic coastal environments.

Biogeography of glacier microbial communities

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Abstract

The cryosphere, which harbours endangered polar ecosystems, is a climatically sensitive refugia for life. The present-day climate change gives an imperative to investigate glacier biodiversity, which remains largely understudied. It was thought for a long time that glaciers were largely devoid of life, yet supraglacial environments are in fact dynamic microbially driven habitats. Glaciers host diverse communities which regulate key biogeochemical elements, and their response to seasonal and environmental variations influences glacier melting and nutrient inputs to downstream ecosystems. While the structure of these communities has been studied extensively on local levels, little is known about the global biogeographical patterns across the glacial biome. To fill this gap, we analysed 16S and 18S rRNA amplicon sequencing data from more than six hundred supraglacial snow, ice and cryoconite samples that were either produced by our team or were retrieved from public repositories. We investigated the microbial composition and diversity of glaciers and snowfields all over the world, including the Arctic, Antarctic as well as temperate glaciers. We evaluated the global biogeography of these microbial communities and will discuss how they are structured based on environmental characteristics.

We found a core microbiome present in all samples, composed not only of polar dominant taxa such as the *Polaromonas* or the *Flavobacterium* genera, but also of rarer taxa. We identified key factors in determining microbial community diversity and composition, including geographical location and nutrient availability. Amplicon-based co-occurrence networks revealed clear ecological patterns of intra and inter-kingdom interactions, yet the role of the rare biosphere on the ecology and adaptation at the community scale remain unknown. Complementary multi-omic-based approaches will help widen our findings with respect to mutualistic and antagonistic relationships. Our results highlight the clear need for further investigation into the factors influencing dissemination and nutrient import/export onto/from glaciers and ice sheets worldwide.

Ethics in glacier protection under the pressure of climate change

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Abstract

With climate change, cryospheric habitats are under severe pressure. Especially Alpine tourism areas relying on snow reliability suffer severely under the scarcity thereof. Countermeasures to guarantee the quality of glacial skiing are connected with extreme effort in manpower and investments. Glacier ski operators in Austria, Italy, Switzerland, Slovenia and France are hence in the mode of covering neuralgic spots on industrial glaciers with geotextiles to increase albedo. In the county of Tyrol, ca. 100 hectares with increasing trend are covered with white blankets made of polypropylene (PP). By covering large areas of ski slopes over the summer months ca. 1.80m in height of snow and ice can be retained from melting verifying the mechanical success story of this method. However, geotextiles made of polypropylene fleece are severely altering conditions in the cryobiota such as nutrient concentrations, light conditions, the cut-off of atmospheric input, etc. On top of it, those geotextiles release substantial amounts of plastic fibers (up to 3.000 accumulated meters of fibers m⁻²). In high altitude conditions, PP fibers show a tendency to degrade to smaller particles which are to be categorized as microplastics. These particles are incorporated into the sensitive high alpine food chains such as aquatic insect larvae in glacial rivers. Additionally, it has been proven that the presence of microplastics can foster antibiotic resistance genes of bacteria dwelling in snow and ice. The dilemma is obvious: The enormous economic pressure from touristic areas has to compete with ecological concerns. The evident microplastic pollution of high-altitude regions is still not quantified sufficiently, however, the question about the ethics to conserve glacial structures “by all means” is meanwhile asked by numerous ecologists and NGOs. As a final consequence, scientists, politicians, stakeholders and economists must cooperate to ensure the usage of sustainable and economically friendly materials.

Predicting and validating the impact of warming on terrestrial microbial systems in Antarctic Polar deserts using laboratory and field space for time approaches

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Abstract

The McMurdo Dry Valleys (MDV) contain unique and sensitive ecosystems increasingly responsive to the changing global climate. However, unlike the more temperate terrestrial ecosystems, monitoring and predicting biological responses to environmental change remains a significant challenge due to the limited time frame allocated to field access, the requirement for permits, and substantial financial and logistic support. Here, we present two complementary approaches developed to help assess and validate the capacity of the MDV terrestrial microbiome to respond to future impacts of climate change. Firstly, we demonstrate how geochemically defined space-for-time gradients can help predict compositional and diversity changes across space by replicating gradients across systems with different historical legacies of water availability. Secondly, using a custom-designed environmental chamber capable of emulating polar desert conditions of MDV, we validate the use of laboratory experiments as monitoring tools for the microbial response to natural wetting events in a polar desert. We demonstrate a fast and asynchronous response from dominant taxa during wetting and re-drying disturbances, which offers insights into the diversity of metabolic traits and strategies inherent in polar desert communities. We further explore the ecological consequences of these responses for the stability and resilience of this ecosystem. Lastly, we strongly advocate that laboratory-based Antarctic research can complement field studies with adequate and controlled infrastructure. Such studies would allow more complex disturbances and activity measurements to be examined without the temporal, logistic and permit constraints, nor the environmental and anthropogenic impacts associated with Antarctic fieldwork.

Atlantification drives taxonomic and functional shifts in the Arctic Ocean microbiome

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Abstract

The Arctic Ocean is experiencing unprecedented changes as a result of climate warming, necessitating detailed analyses of the ecology and dynamics of biological communities to understand ecosystem shifts. The Fram Strait, the only deep-water gateway connecting the Arctic and subarctic Atlantic, acts as a primary exit point for polar water masses and sea-ice and entry point for Atlantic water, thus providing a unique opportunity to study present trends and predict future changes. Combining autonomous, on-site sampling with ship expeditions, we generated 67 long-read and 11 short-read metagenomes of microbial communities from across the Fram strait over four years. Using the >120 million genes recovered, we identified that distinct shifts in community taxonomy and functionality were primarily driven by water mass, and secondarily by ice-cover and seasonal conditions. Comparing the distribution of genes across different ecosystem states further revealed functional signatures, such as an enrichment of genes involved in amino acid, protein and ketone compound degradation under high-ice compared to phytoplankton-derived organic matter degradation genes under low-ice. We further used the metagenomic data to recover >200 species-representative metagenome-assembled genomes and compared the distribution dynamics at the population- and species-level. Population and species-specific signatures of different ecosystem states were evident, including a species of BD2-11 terrestrial group in polar waters and Formosa in Atlantic waters, as well as species that were universally present. These population and species signatures also harbour distinct metabolic capacities. Using this extensive dataset, we predict that the expanding influence of Atlantic water in the Arctic Ocean is likely to lead to a “Biological Atlantification” of microbial communities, with shrinking ecological niche space for current Arctic populations, with further implications for ecosystem functioning.

Global biogeography of the sediment biofilm microbiome in glacier-fed streams

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Abstract

Glacier-fed streams serve as headwaters to many of the world's largest river catchments. These ecosystems are often characterized by low water temperatures and oligotrophic conditions, elevated turbidity, sediment loads, and high discharge variability resulting from diel and seasonal melt dynamics. Despite these harsh conditions, glacier-fed streams harbor an underappreciated biodiversity, especially within sediment biofilms, which play pivotal roles in downstream biogeochemical cycles. However, we still miss an adequate overview of the diversity of bacterial biofilm communities in glacier-fed streams, particularly at the global scale. In addition, little is known about how bacterial diversity relates to environmental characteristics, and how these relationships in turn drive global distribution patterns. Using 16S rRNA gene sequencing data from the Vanishing Glaciers project, we conducted a detailed and comprehensive survey of sediment biofilm bacterial diversity spanning more than 130 glacier-fed streams across five continents. Next, we assessed the scale of biogeographic organization and the potential key taxa contributing to community spatial patterns across geographic regions. Finally, we used an array of physico-chemical and glaciological metrics to identify the roles of environmental and spatial patterns in driving bacterial biofilm community composition. Preliminary results revealed strong biogeographic patterns in the glacier-fed stream sediment microbiome, particularly among remote mountain ranges, such as the Ecuadorian Andes and the Southern Alps (New Zealand). Furthermore, primary production and glaciology were important predictors structuring biofilm community composition at regional scales. Our findings shed light on the previously unresolved global diversity of glacier-fed streams, and are particularly relevant given the unprecedented rate of glacier shrinkage worldwide.

Seasonal variation of the atmospheric bacterial community in the Greenlandic High Arctic is influenced by weather events and local and distant sources

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Abstract

The Arctic is a hot spot for climate change with potentially large consequences on a global scale. Bioaerosols are important in regulating the heat balance through direct interaction with sunlight and indirectly, through inducing cloud formation. Airborne bacteria are the major bioaerosols with some species producing the most potent ice nucleating compounds known, which are implicated in formation of ice in clouds. Little is known about the numbers and dynamics of airborne bacteria in the Arctic and even less about their seasonal variability. We collected aerosol samples and wet deposition samples in spring 2015 and summer 2016, in Northeast Greenland. We used amplicon sequencing and qPCR targeting the 16S rRNA genes to assess the quantities and composition of the DNA and cDNA-level bacterial community. We found a seasonal variation in the atmospheric bacterial community, which is likely due to variable sources and meteorology. In early spring, the atmospheric community was dominated by taxa originating from temperate and Subarctic regions and arriving at the sampling site through long-range transport. We observed an efficient washout of the aerosolized bacteria during a snowstorm, which was followed by low concentrations of bacteria in the atmosphere during the consecutive 4 weeks. We suggest that this is because in late spring, the long-range transport ceased, and the local sources which comprised only ice and snow surfaces were weak resulting in low bacterial concentrations. This was supported by observed changes in the chemical composition of aerosols. In summer, the air community was confined to local sources such as soil, plant material and melting sea-ice. Overall, we show how the composition of bacterial aerosols in the high Arctic varies on a seasonal scale, identify their potential sources, demonstrate how their community sizes varies in time, investigate their diversity and determine their activity potential during and post Arctic haze.

Microbial dynamics drive enhanced melting of the Greenland Ice Sheet

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Abstract

Glaciers and ice sheets were long believed to be sterile environments, but just like other large ecosystems (e.g., tropical forests, tundra), they are now widely recognized as one of the Earth's biomes, teeming with life. On the ice surface, microbes have been shown to alter physical and chemical characteristics of snow and ice with direct consequences for snow/ice solar-heating and amplified melt. The bare ice is increasingly darkening during the summer ablation, as it becomes more and more colonized by deep purple-pigmented glacier ice algae. Here, we present an overview of the most recent results of the ERC-Synergy project Deep Purple, through which we investigate the physical, chemical and microbial processes that darken the Greenland Ice Sheet and accelerate sea level rise. We present an overview of bottom-up and top-down controls of glacier ice algae growth, in addition to their impact on the physical and chemical characteristics of the ice. Biological growth of ice-bound algal cells can accumulate biomass high enough to cause albedo reduction between 12% and 21%, depending on the algal cell abundances. Furthermore, microbial metabolism and linked dissolved and particulate carbon dynamics on ice surfaces affects the cycling, accumulation and export of labile dissolved organic matter to downstream ecosystems, including the production of volatile organic carbon. Fungi and giant viruses could potentially be major top-down controllers of algal biomass on ice surfaces. We demonstrate that nutrient requirements for glacier ice algae are generally low and we also predict that the impact of microbially-mediated albedo reduction will increase further with climate change, as in a warming climate melt areas on the Greenland Ice Sheet will further extend.

Investigating the photophysiology of supraglacial microalgae

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Abstract

The supraglacial region on the surface of glaciers and ice sheets is a high-light, low-temperature, and oligotrophic environment that is home to a diverse assembly of microorganisms. Of these, Chlorophyte snow algae and Streptophyte glacial algae represent the major primary producers within this cryospheric landscape. Both groups form widespread algal blooms during summer melt seasons. These blooms have been highlighted to have far-reaching consequences for both the physical and chemical characteristics of the supraglacial environment, e.g., through impacts to ice surface albedo, and large-scale nutrient cycling. Despite their potential importance, however, our understanding of the diversity of adaptive capabilities within the snow and glacier algae to dominate their dynamic supraglacial environments remains diminutive.

Here we first report on recent efforts to examine the photophysiology across the snow algae phylogeny (*Microglena* sp. and *Chloronomas* sp.,) relative to different light, temperature, and nutrient regimes. PAM fluorimetry was used to constrain the photophysiology, and cells were preserved to quantify the cellular stoichiometry and pigmentation during growth. Preliminary results indicate a diverse and dynamic photophysiological system that allows these snow algal species to adapt their light adaptation mechanisms to the light to which they are incubated. There also appears to be a correlation between the availability of nitrogen and the capacity at which the algal species can adapt themselves to the increased exposure to light. Our lab incubations gave us a strong starting point to try and constrain the amount of dynamism these species have relative to light, nutrients, and temperature in situ. These investigations have begun by investigating the photophysiological adaptations of snow algal bloom growth in early June 2022, with a corresponding trip to focus on glacier algal bloom growth in August 2022. Here we will present how these findings compare with the trends uncovered during the original laboratory incubations.

TotalRNA metatranscriptomics: genome evolution, community succession and predation in complex cold-adapted microbiomes in Greenlandic permafrost and ice

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Abstract

Glaciers and ice sheet surfaces, some of the most recent additions to the catalogue of biomes on Earth, harbour surprisingly high biomass and diverse microbial communities. High biomass and diverse microbial communities are also found in permafrost soils, which contain over half of the global soil carbon inventory. These soils are host to many unknown microbial communities, some of which are stable for millennia, despite being frozen. Both niches are present in Greenland, where global warming is impacting on their physico-chemical characteristics. Current microbiological studies in permafrost and glacial habitats primarily include DNA-based amplicon sequencing, which may introduce biases when aiming to decipher shifts in microbial communities and their functions. We have used TotalRNA sequencing of diverse samples originating from the ice sheet surface and from permafrost soils across Greenland, and with this approach eliminated amplification biases related to the primers and enzymes used during library preparation. We also captured the diversity of prokaryotes and eukaryotes simultaneously, and gained a greater taxonomic resolution due to the coverage of all variable regions of the rRNA gene, and supplemented this analysis to look at differentially regulated genes the Comparative Metatranscriptomics Workflow (CoMW) pipeline. TotalRNA sequencing requires considerably a shallower sequencing depth, compared to shotgun metagenomics, is simpler to implement and is not affected by the community composition. We successfully extracted RNA from low biomass ice samples and ancient permafrost environments and derived a new understanding of these rarely accessed microbiomes. We have assembled full length rRNA genes covering all domains of life and used the data to study genome evolution, succession of the active microbial communities, as well as predation patterns of predatory bacteria and microeukaryotes.

Preliminary results on the investigation of microbial communities inhabiting the diverse lakes of James Ross Island, Antarctica

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Abstract

James Ross Island, located close to the northern tip of the Antarctic Peninsula, hosts a diverse ensemble of lakes recently divided into six types based on their origin, bedrock geology, geomorphology, hydrological stability, and physical and chemical characteristics. However, the influence of the defined lake types (and associated parameters) on the assembly of microbial communities remains largely unexplored. In this study, we have used V4 16S rDNA metabarcoding to explore the diversity of prokaryotic communities inhabiting 22 lakes belonging to the six lake types on James Ross Island. In addition, we have tested potential associations of the computed Alpha (Observed Features, Faith's Phylogenetic Diversity, Shannon Diversity Index, Pielou's Evenness) and Beta (Jaccard Distance, Bray-Curtis Dissimilarity, Unweighted and Weighted Unifrac) diversity metrics with spatiotemporal, geological, hydrological, and chemical characteristics of the lakes. Our preliminary results suggest that the lake types divide into two groups based on both the richness and phylogenetic diversity of hosted prokaryotic communities. The two groups differ in the age and stability of the lakes. While the stable old lakes (originating thousands of years ago) host diverse prokaryotic communities, the less-stable young lakes (originating a century or even decades ago) are significantly less diverse (in terms of both observed ASVs and their phylogenetic diversity). In addition, other significant relationships between diversity metrics and individual environmental parameters were observed. These results improve our understanding of the drivers of microbial diversity and community structure in freshwater Antarctic ecosystems, and help us to predict how the microbial landscape may shift with the creation of new habitats and in the context of a changing environment.

Linking microbial taxa to ice-nucleation protein production in Arctic marine environments

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Abstract

Clouds have one of the most profound effects on Earth's climate, yet they are still responsible for some of the biggest uncertainties in climate models. Cloud formation, radiative properties, thickness and lifetime are tightly interlinked with the presence of atmospheric particles (aerosols) and the formation of ice. Biological aerosols (bioaerosols) such as ice-nucleation proteins (INpro) produced by microorganisms are most efficient catalysts in the formation of ice and can trigger heterogenous freezing between -1°C and -15°C. Several studies have demonstrated that Arctic environments are a source of airborne INpro. Sea spray is one of the major sources of aerosols, which aside of the sea salt contain large amounts of organic material. These are ejected into the atmosphere through the process of wave breaking and bubble bursting of small bubbles, which eject drops from the sea surface microlayer (SML) to the atmosphere. Here, we present preliminary results derived from droplet freezing assays and amplicon sequencing combined with quantitative PCR, targeting the 16S rRNA gene from sea and aerosol samples collected along a transect from sub- to high Arctic Greenland (Baffin Bay). We demonstrate a positive correlation between INpro concentration and higher latitudes in sea bulk water (SBW) and SML. Additionally, we try to link specific taxonomic groups from the microbial communities to INpro production. Last, we aim to investigate if partitioning of specific taxonomic groups can be observed from SBW to SML and from SML to the atmosphere. Finally, we performed laboratorial sea-spray experiments simulating turbulent sea conditions. This study has the potential to help closing the current knowledge gap in understanding the partitioning of microorganisms from the sea to the atmosphere and unravel which microbes are the major contributors to atmospheric INpro and hence cloud formation.

Aerobiology over the Southern Ocean – implications for bacterial colonization of Antarctica

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Abstract

The Antarctic is experiencing drastic ecosystem change due to rapid and record warming. Understanding dispersal processes is paramount to assess the risks of microbiological invasions. Here, we analyze bacterial biodiversity in the circumpolar air above the Southern Ocean. This diversity had both local and global origins and presented from very low to very high Shannon biodiversity indices with consistent low richness, compatible with a scenario whereby samples are composed of a suite of different species in very low abundances. However, only 4% of ASVs were identified in both Polar and non-Polar air masses, suggesting that the air mass over the Southern Ocean can act as a selective dispersal filter. Furthermore, air microbial diversity varied significantly with meteorological data, suggesting that regional bacterial biodiversity could be sensitive to changes in weather patterns. Future changes in weather patterns could, therefore, potentially alter the existing pattern of microbial deposition in the Antarctic.

Response of alpine stream biofilms to climate change induced stressors

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Abstract

Alpine streams are expected to face an intensification of environmental stressors due to climate change. At the vanishing cryosphere interface, alpine streams are particularly susceptible to increasing temperatures and to changing hydrology. As biofilms are the dominant form of microbial life in alpine streams, monitoring their microbial composition changes due to environmental stressors would inform on how alpine streams respond to climate change. In this study, we designed a flume set-up using water from an alpine stream to directly grow biofilms under hydrological and temperature stressors. Biofilms were grown on clay coupons in flumes under four different flow regimes and two temperatures, as follow: a natural flow reproducing the natural flow events of the alpine stream, a constant flow, a purely stochastic flow, and an intermittent flow with zero-flow days and peak flows, all at the *in-situ* stream temperature or at 2°C warmer. This represented eight different flow/temperature conditions, each in triplicate. This setup was repeated over two summers, where biofilms were harvested from the coupons for DNA extraction, for bacterial abundance and chlorophyll A quantification, to evaluate the community composition of each flow/temperature conditions over time. Preliminary results suggest that time is the main driver of changes in the microbial community, and is responsible for an increase in bacterial abundance, chlorophyll A concentration and alpha diversity. However, the intermittent flow regime had a significant impact on the microbial composition, while the other flows did not induce changes: drought decreased the bacterial and algal abundance and the alpha diversity, promoted the colonization by members of the *Hymenobacter* and *Massilia* genus, while decreased the representation of the *Luteolibacter* genus. Further analyses will be used to identify the sentinel taxa, i.e. taxa driving the phylogenetic turnover in communities, using the “community assembly” and the “phyloscore analysis” frameworks.

Microbial physiological responses to global warming

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Abstract

How microorganisms respond to temperature change is a key question in microbial ecology. Soils and other ecosystems are exposed to both short-term (daily, weekly, monthly) and long-term (interannual variation) temperature changes. Due to global warming temperatures are increasing and changes are becoming more extreme. Despite being a key factor that affects most microorganisms, much of our knowledge of how temperature change affects microbial physiology stems from studies on *E. coli*. At the same time, numerous studies have addressed temperature effects on microbial communities and environmental processes like methane production, methane oxidation and soil respiration. This has left a knowledge-gap: temperature effects on the physiology of non-model microorganisms with important roles in global biogeochemical cycles. Here we present new knowledge about temperature effects on the physiology of important microorganisms in the global carbon and methane cycle. We show that physiological adjustments, and in particular regulatory adjustments of the protein biosynthesis machinery are central to long-term and short-term microbial responses to temperature change. Our findings have implications for our understanding of how carbon is cycled and stored by microorganisms.

Insights into plasmidome and resistome of polar regions

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Abstract

Plasmidome defined as a sum of plasmids in a given bacterial taxon or environment and resistome, i.e. pool of antibiotic and metal resistance genes in analyzed microbiome, are structurally and functionally connected, since plasmids are frequently vectors carrying the resistance genes. The genomic and functional analyses of plasmidomes and resistomes in human-impacted environments are common and well documented, while the knowledge about plasmids and resistance genes of cold-active bacteria, and especially these inhabiting polar regions, is still scarce.

In our studies, over 300 plasmids originating from psychrotolerant bacteria, as well as various plasmid contigs retrieved from metagenomic data were characterized. Detailed analysis of plasmids and plasmid contigs revealed the presence of numerous genes, that may impact bacterial adaptation to extreme environmental conditions. Amongst identified genes of adaptive value were these involved in: (i) protection of bacteria against reactive oxygen species and UV, (ii) enabling utilization of hardly-degradable carbon sources, (iii) conferring resistances, and (iv) increasing biofilm formation. Interestingly, as shown in the similarity network analysis, closely related genes were found within plasmids of bacteria belonging to various taxonomic groups, which exemplify the possible directions and range of horizontal gene transfer in polar regions. Parallely, the resistome of polar regions was investigated. For this purpose, novel bioinformatic tools were developed, including the database of PCR primers for the detection of the resistance genes and the novel system for semi-automatic annotation of bacterial genomes. Resistome analyses comprised culture-dependent and culture-independent approaches. They revealed the presence of various resistance genes in Arctic and Antarctic bacteria, including these conferring resistances to drugs of the last resort, e.g., *mcr* (resistance to colistin).

Oxidative sulfur cycling by a novel subglacial bacterium

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Abstract

Subglacial environments have likely acted as refugia for microorganisms during times in Earth's history with significant terrestrial ice cover, including the present day. These subglacial environments have relatively stable temperatures, and where liquid water is present, the flowing ice generates fine grained sediments from abrasion and crushing of the bedrock. Microbes are active in these cold, dark subglacial environments and can be the primary producers in these systems coupling energy generation to the fixation of inorganic carbon into biomass. In the absence of photosynthesis, the energy that drives CO₂ fixation is derived from oxidation-reduction reactions involving inorganic substrates.

The presence of redox active minerals in bedrock underlying glaciers has been suggested to be a key factor in supporting microbial activity in those subglacial environments. This is particularly true for bedrock that contains pyrite (FeS₂). The abiotic oxidation of pyrite at a circumneutral pH produces the metastable intermediate thiosulfate, which can be used as an electron donor by sulfur-oxidizing microorganisms. Only one organism capable of thiosulfate oxidation at close to in situ temperatures (5°C) has previously been isolated from a subglacial system, a species of *Thiobacillus* from pyritic sediments of Robertson Glacier, Canadian Rockies.

Here we describe a novel bacterium isolated from subglacial sediments from Bench Glacier, Alaska, that is capable of oxidizing thiosulfate to generate energy and fixing inorganic carbon into biomass at low temperatures similar to those at the glacier bed. The organism is most closely related to the bacterial genus *Polaromonas*. Analysis of the organism's genome has identified the pathways that allow for thiosulfate oxidation and CO₂ fixation, confirming our physiological data. Since pyrite is common in subglacial environments, as are circumneutral pH conditions, organisms capable of using thiosulfate as an electron donor may be widespread beneath glaciers/ice masses on Earth today and in the geologic past.

Seasonal, interannual and spatial patterns of bacterial taxonomy and genetic functions in the Arctic Ocean

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Abstract

Bacterial diversity and function across time and space in the Arctic Ocean, including the Polar Night, remain virtually unknown. In the FRAM Observatory, we study microbial composition and genetic potential in ice-covered and ice-free regions of the Fram Strait, the major gateway between the Arctic and Atlantic Oceans. A continuous amplicon time-series, derived from moored autonomous samplers, revealed marked taxonomic and functional seasonality among bacterial communities in the ice-free West Spitsbergen Current, with distinct succession of taxonomic modules. PacBio long-read metagenomes showed peaks of proteorhodopsin- and DMSP-utilizing genes in late summer, whereas winter mixing of the water column covaried with ammonia- and nitrite-metabolizing bacterial genes. In the ice-covered East Greenland Current, taxonomic and functional diversity varied less with seasons, with prominent influence of ice cover and polar water masses. For instance, high-ice conditions coincided with a higher number of peptidoglycan-utilizing genes. Continuous observations were contextualized with five-year amplicon and biogeochemical data from summertime samples collected across Fram Strait, integrating seasonal and interannual patterns of bacterial community dynamics. This fundamental baseline information helps understanding ecological and biogeochemical processes in a marine region severely affected by climate change.

Ancient DNA preserved in cryo-environments: what can we learn from past gene pools?

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Abstract

Cryo-environments provide ideal conditions for the long-term preservation of DNA molecules. Despite of the inherent degraded nature of ancient DNA (aDNA), it is possible to obtain meaningful information over geological timescales of up to hundreds of thousands of years into the past. This paleo-ecological perspective has far-reaching implications for our understanding of microbial ecosystems evolution and interaction with their environment. Pools of aDNA genes stored in ice and permafrost for millennia carry the genetic fingerprint of microbial biodiversity and population dynamics through time, adaptive traits to environmental change, microbially-driven biogeochemical cycles and their impact on ecosystem functioning. Not less importantly, they also hold the code for extinct biomolecules that may have been lost over time and that can inspire today's new biotechnological products and solutions. Stemming from our work in microbial paleo-genomics, we will present key-findings on ancient gene pools that we have recovered from ice and permafrost that are up to 600,000 years old. Based on the analysis of aDNA metagenomic chrono-sequences at different locations of the Arctic such as the Batagay megaslump and Muostakh island (two emblematic examples of human-impacted nature), we will demonstrate the valuable contribution of microbial aDNA pools to paleo-ecosystem reconstruction and discuss the implications for climate change biology. Since functional gene pools are not only drivers of the adaptation to environmental extremes but are also a source of biomolecules with novel/enhanced properties (e.g. enzymes for biocatalysis), we will also present our preliminary work aimed at exploring the biotechnological potential of ancient microbial genes. Overall, our study cases demonstrate that research into ancient DNA holds great promise to advance our understanding of life in the cold, how it was and how it might be in the future, and how it can help us building a more sustainable society.

Antarctic bacteria as a potential source of keratinase for degrading poultry feathers waste

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Abstract

According to the EU reports poultry industry generates about 3.5 million tons of feather waste annually. Only 25% of this waste is used for animal feed or fertilizers, while the rest is being disposed of in landfills or incinerated, causing environmental and health hazards. Therefore, development of bioprocesses that degrade and utilize feather waste is of high interest. Microorganisms from polar regions are known producers of cold-adapted enzymes with biotechnological applications. In this study, we performed a screening of Antarctic green snow bacteria for ability to produce keratin degrading enzymes and degrade poultry feather waste. The bacteria were isolated during the Belarussian Antarctic Expedition (2014-2015), from two sites in the Vecherniy district of the Tala Hills oasis, located in the Western part of Enderby Land (East Antarctica). All isolated bacteria were characterized by genotypic and phenotypic techniques, and those possessing a high proteolytic activity was included in the screening study. Poultry feather waste was turned into feather meal by grinding, and the screening was performed at different temperatures. After 7 days of cultivation at 25°C, isolate *Arthrobacter oryzae* GS26 was able to degrade more than 50% of feather meal, and up to 67% after 12 days of cultivation. In comparison, the control strain *Bacillus licheniformis* CCM 2145 was able to degrade about 70% of feather meal after 48h of cultivation at 35°C, and up to 88% after 12 days of cultivation. Isolate *Arthrobacter oryzae* GS26 can be especially useful to perform degradation of feather meal at low temperature.

Microbial diversity on the Greenland Ice Sheet

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Abstract

This is an exploratory study into the microbial diversity and biosynthetic potential of different habitats on the Greenland Ice Sheet (GrIS) i.e., surface ice, cryoconite, and a biofilm from cryoconite holes. Various sequencing methods are applied in parallel to investigate how powerful each method is in resolving the microbial diversity and phylogeny of dominant organisms. Amplicon sequencing, both short and long reads, was compared to metagenome sequencing, on the same DNA extracts from field samples. A novel culturing method was used to complement the sequencing approach. After identification of the cultures, 88 bacterial isolates were whole-genome sequenced, and a comparison of the communities represented by the isolates with amplicons and MAGs was done. The isolates belong to 14 genera, predominantly *Pseudomonas*. Pseudomonadota also make up the most abundant taxa in all environments according to 16S rRNA amplicon sequencing. Among eukaryotes, Phragmoplastophyta and Chytridiomycota were the dominant taxa. Amplicon sequencing revealed that cryoconite had the highest alpha diversity of prokaryotes, followed by the biofilm and surface ice. Of eukaryotes, the alpha diversity in biofilm and cryoconite was comparable and higher than that of ice surface. Both the genomic data, and access to the cultured microbes, will help illuminate the diversity, cultivability, and biotechnological potential of these microbes from spatially close, but distinct habitats of the GrIS.

Population genomics and biocontrol potential of the Arctic black yeast *Aureobasidium subglaciale*

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Abstract

Aureobasidium subglaciale is a black, yeast-like fungus that has been isolated from various cold environments. Like its close relative, *Aureobasidium pullulans*, *A. subglaciale* shows antagonistic activity against phytopathogenic fungi. The use of microorganisms as biological control agents is increasingly coming to the fore in the search for more environmentally friendly solutions as the synthetic fungicides used in agriculture become more problematic. In our study, we investigated the potential of *A. subglaciale* for postharvest rot control in apples. Apples are attacked by numerous fungi known as storage rots, which cause significant losses before and after harvest. First, we sequenced the genomes of 15 strains previously identified as *A. subglaciale*. Then we examined the different phenotypic characteristics of the sequenced strains. Finally, we tested their biocontrol potential against the important phytopathogenic fungi *Botrytis cinerea*, *Colletotrichum acutatum*, and *Penicillium expansum* in the dual culture test and in vivo on apples. Genome analysis showed that only seven of the strains tested were actually *A. subglaciale* s. str. and the other strains likely belong to other or unknown species. The strains of *A. subglaciale* grew at low temperatures, were tolerant to high temperatures and elevated solute concentrations, and produced various extracellular enzymes and siderophores. All these phenotypic characteristics could contribute to the biocontrol ability of the species. Our results showed that the tested strains significantly reduced postharvest rot of apples at low temperatures caused by *B. cinerea* (over 60%), *C. acutatum* (over 60%), and *P. expansum* (about 40%). Overall, these data suggest *A. subglaciale* is a promising biological agent for disease control during cold storage of produce.

Polintoviruses in high alpine lakes and beyond

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Abstract

Metagenomics has recently revealed highly abundant and diverse polintoviruses present in alpine lakes. These enigmatic new viruses, which are related to virophages, infect unicellular eukaryotes in an unknown life cycle. Despite their high abundance, a comprehensive analysis of polintovirus diversity and hosts is lacking, which will guide future isolation efforts. Here we show that polintoviruses are integrated into the genomes of over one third of all sequenced protists, accounting for a significant fraction of eukaryotic genomes. The implications of this integration are discussed, along with probable life strategies of these new virus groups.

Metagenomics uncovers differential viral diversity of an alpine lake and glacial stream in the Pyrenees

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Abstract

Viruses are the most abundant biological entities in the biosphere and represent one of the biggest reservoirs of undetected genetic diversity on Earth. They play a critical role in regulating the microbial composition of ecosystems and the diversity of the host they infect. Metaviromics shows that most of the viruses have not been previously identified, indicating the enormous diversity of these microorganisms and the lack of knowledge we have about them, especially in extreme and remote environments such as alpine ecosystems. The viral composition in these ecosystems may be used as a sensor of early changes caused by climate change. Here we present a comprehensive study of the viral community present in the water systems of the Ordesa and Monte Perdido National Park (Pyrenees), including DNA and RNA viruses. We analyzed samples from the water column of Lake Marboré and the stream that drains from the front of the Monte Perdido glacier. Our sequencing data showed a higher number of contigs in the glacial stream, despite having a lower number of generated sequences, suggesting that the diversity of viruses in this sample is much higher than that found in Lake Marboré. These results may reflect that the ecosystem of Lake Marboré is more homogeneous, and suggest that the glacial stream may collect viruses from more ecological niches and may also contain viruses that had been trapped in the glacier ice for a long time. The vast majority of these viral sequences are unrelated to known viruses, highlighting the enormous diversity of unknown alpine viruses. We have also purified viruses from other locations in the park and have identified by electron microscopy a high diversity of bacteriophages and eukaryotic viruses.

Cruising our planet's roof towards the unlocking of microbial life in glacier-fed streams

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Abstract

Today, we understand microbial life in the deepest ocean better than in the rivers that drain the roof of our planet. This appears surprising given that these rivers, mostly fed by glacier meltwaters, figure among the ecosystems that are most vulnerable to climate change. Here, we present results from the 'Vanishing Glaciers' project supported by The NOMIS Foundation and cruising the world's mountain ranges towards unlocking the biofilm mode of life across more than 150 glacier-fed rivers. Leveraging 16S rRNA, 18S rRNA amplicon sequencing and metagenomics, we found an unexpectedly diverse microbiome associated with the river sediments including representatives spanning all three domains of the tree of life, and also including a rich virome. We will highlight some of the adaptive strategies that microorganisms developed to dwell within biofilms in a most extreme ecosystem. Among them, optimal resource exploitation, internal recycling of nutrients and metabolic interactions between photoautotrophs and heterotrophs enable the biofilm mode of life in glacier-fed streams. At the same time, we will also report on antimicrobial resistance in some of these biofilms, evidence that not all neighbours are friends. Finally, we present evidence on how glacier shrinkage may affect microbial energetics and related ecosystem processes. With these findings, we underline the necessity to shed light on an as yet unseen microbial life that is now vanishing as glaciers are melting before our eyes at an unprecedented pace.

Acidobacteriota diversity in arctic tundra soils

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Abstract

Climate change is affecting Arctic tundra ecosystems severely. Higher temperatures are driving increased microbial respiration of soil organic matter and the release of carbon dioxide and methane. To understand the mechanisms of microbial soil organic matter utilization, we examine the complex diversity of polar soil microbial communities with a focus on the ubiquitous but elusive members of the Acidobacteriota. Our aim is to uncover whether genetic and phylogenetic differences in Acidobacteriota species or strains are associated with differences in carbon and nitrogen utilization as well as predation of certain strains/species over others. We utilized the long-read capability of the Oxford Nanopore MinION to profile bacterial ribosomal operons of tundra soil Acidobacteriota communities and isolates. The inclusion of the hypervariable ITS region within the rRNA operon allows us conduct strain-level resolution of Acidobacteriota. These sequences along with metagenomic long-read sequences were then used to assemble complete Acidobacteriota genomes to annotate genes associated with organic matter utilization and pangenome markers to differentiate Acidobacteriota strains. Through this method we have been able to characterize multiple novel *Granulicella* strains in subdivision 1 of the Acidobacteriota and a cluster of phylogenetically distinct Acidobacteriota strains which include novel species. The complete genomes of these distinct strains will be analyzed further to identify functional and genetic differences that match up with differences in organic matter utilization. By understanding the complex diversity of Acidobacteriota, we can elucidate the mechanisms which shape microbial communities in polar soils.

Life beyond Earth: where and how should we look for it? - Permafrost as a key player to solve the task

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Abstract

The question "Are we alone?" is perhaps the most fundamental that affects mankind (after that of the origin of the Universe). How can we address the search for life in our Solar System? Mars, the icy ocean satellites of Saturn and Jupiter such as Enceladus and Europa are in the focus of the planetary research topic to search for life outside the terrestrial biosphere. These worlds are also called icy or permafrost worlds. While it is more likely to find remnants of life (fossils of extinct life) on Mars because of its past short time window of the surface habitability, it is probably more likely to find traces of extant life on the icy moons and ocean worlds of the gas giants Jupiter and Saturn. Nevertheless, even on Mars there could still be a chance to find extant life in niches near to the surface. Different approaches for the detection of traces of life in the form of biosignatures including pre-biotic molecules will be presented. The presentation will show in detail which infrastructure is needed for this enterprise from a scientific point of view and will give examples of future mission concepts to investigate the presence of life on other planets and moons. Finally, suggestions will be provided on methods, techniques, operations and strategies for preparation and realization of future life detection missions. It should be said, that the permafrost planetary analog field sites play a significant key role in all performed and even future space preparation investigations.

Active and dormant microorganisms on glacier surfaces

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Abstract

Glacier and ice sheet surfaces host diverse communities of microorganisms whose activity (or inactivity) influences biogeochemical cycles and ice melting. Supraglacial microbes endure various environmental extremes including resource scarcity, frequent temperature fluctuations above and below the freezing point of water, and high UV irradiance during summer followed by months of total darkness during winter. One strategy that enables microbial life to persist through environmental extremes is dormancy, which despite being prevalent among microbial communities in natural settings, has not been directly measured and quantified in glacier surface ecosystems. Here we use a combination of metabarcoding and metatranscriptomic analyses, as well as cell-specific activity (BONCAT) incubations to assess the diversity and activity of microbial communities from glacial surfaces in Iceland and Greenland. We also present a new ecological model for glacier microorganisms and simulate physiological state-changes in the glacial microbial community under idealized (i) freezing, (ii) thawing and (iii) freeze-thaw conditions. We show that a high proportion (>50%) of bacterial cells are translationally active on snow and ice, with Actinomycetota, Pseudomonadota, and Planctomycetota dominating the total and active community compositions, and that glacier microorganisms, even when frozen, could resume translational activity within 24 hours after thawing. Our data suggests that glacial microorganisms respond rapidly to dynamic and changing conditions typical of their natural environment. We deduce that the biology and biogeochemistry of glacier surfaces are shaped by processes occurring over short (i.e. daily) timescales, and thus are susceptible to change following the expected alterations to the melt-regime of glaciers driven by climate change. Better understanding the activity of microorganisms on glacier surfaces is critical in addressing the growing concern of climate change in Polar regions, as well as for their use as analogues to life in potentially habitable icy worlds.

Genome-assembled metagenomics to untangle bacterial diversity and functionality in Antarctic microbial endolithic communities

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Abstract

The capacity to dwell inside rocks enables microbes to push themselves at the edge of their biological potential and to spread and persist across the most inhospitable environments, including the ice-free areas of Antarctica. These regions include the McMurdo Dry Valleys, accounted as the closest terrestrial counterpart of the Martian environment and thought to be devoid of life until the discovery of these cryptic life-forms. Despite their interest as a model for early colonization of earth, little is known about the evolution, diversity, and genetic makeup of bacteria residing in these communities. To address this knowledge gap, we sequenced the metagenome of 108 endolithically colonized rocks collected over broad range of geo-environmental (e.g. altitudinal gradient, different rock typologies) and geography (i.e. Antarctic Peninsula, Northern Victoria Land, and McMurdo Dry Valleys). The derived catalogue includes 4,539 metagenome-assembled genomes representing 2,238 novel species, dominated by Actinobacteriota and Proteobacteria. Predicted genes were functionally annotated using the KEGG database. At least one gene encoding for anti-freezing proteins was present in each of the most abundant community members, across 15 phyla and 37 classes. Drought tolerance genes were less common. Moreover, 12 and 14 out of 15 phyla presented evidence for chemo-autotrophic carbon and nitrogen fixation, respectively. This first evidence suggested that cold tolerance is a key determinant for bacterial survival in such conditions whilst drought adaptation is less critical, or that other, not yet characterized mechanisms, have evolved in these organisms. Metabolisms for C fixation in addition to photosynthesis may be of importance in extremely dry environments, where water may be unavailable for photolysis. This is the largest attempt to define the amplitude of bacterial diversity and functionality of these extreme ecosystems supplying important insights on adaptability of life on our planet and how life may be able to persist on other planetary bodies.

Disentangling terrestrial microbial community composition in the Sør Rondane Mountains, East Antarctica

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Abstract

The sparse ice-free regions of Antarctica are the coldest deserts on Earth. Yet, ice-free soils harbor substantial microbial communities that can vary significantly in response to environmental and micro-climatic conditions. The factors responsible for driving the microbial diversity and community structure in inland nunataks of East Antarctica are still poorly understood. Within the MICROBIAN project, two sampling campaigns took place in the Sør Rondane Mountains during the austral summers of 2018 and 2019, resulting in more than 100 samples ranging from different types of barren bedrock to well-developed biological soil crusts. Bacterial and eukaryotic diversity was assessed by amplicon sequencing targeting the V1-V3 variable region of the 16S rRNA gene and the V4 region of the 18S rRNA gene with general bacterial and eukaryotic primers using the Illumina MiSeq v3 platform. To investigate the responses of these communities to soil driven geochemical variables (such as pH, TN, TOC, NH₄-N, etc.) across the sampled bedrock types (gneiss, granite, marble and moraine) we coupled a Spearman co-occurrence network of ASVs ($\rho > 0.7$ and p-value < 0.01) to random forest variable ranking and correlations with Spearman and Pearson statistics. A total of 13 clusters (modules) were observed, of which 8 gathered 82% of the ASVs and 97% of the reads in the network. Modules of ASVs that mostly occurred in granitic soils were dominated by filamentous Cyanobacteria and correlated well with increasing NH₄-N concentrations while unicellular Cyanobacteria dominated modules occurring in marble samples which correlated well with increasing pH values. One module occurring in gneiss soils was dominated by Proteobacteria and correlated with increasing TOC concentrations, whereas Actinobacteria dominated modules occurring in moraine samples which correlated with increasing TN concentrations. Chlorophyta was the most ubiquitous eukaryotic Phylum, and Metazoa were surprisingly found in the dry and oligotrophic moraine soils as well.

Influence of short term warming on microbial communities and functions in Arctic peat soil

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Abstract

Northern permafrost soils contain the largest terrestrial organic carbon pool. Microbes play an important role in converting soil carbon into greenhouse gases (GHG) so that their response to warming will feedback to the future climate. Temperature is an important factor governing microbe-mediated carbon turnover and therefore many studies investigated the impact of temperature on taxonomic and functional changes of microbial communities. However, the linkage of taxonomic and functional change in response to temperature change remains elusive due to the lack of studies combining both the taxonomic and metabolic response. Here, we studied the microbial composition and functional potential along a high-resolution temperature gradient ranging from 1 to 30 °C. The results show that microbial communities neither shift in continuous nor stochastic patterns under rising temperatures. The taxonomic response appears to partially reflect the differential temperature responses of individual taxa and the interspecies competition for resources. This taxonomic response was decoupled from the functional potential (metagenomics-based) across all temperatures and from the previously observed metabolic or metabolic shifts (metatranscriptomics) at key temperatures. With rising temperatures, a progressive decrease in species diversity (alpha diversity) was observed coinciding with an increased dispersion of GHG production rates. However, the reduction of alpha-diversity at higher temperatures might be a factor giving rise to the observed higher variability in GHG production rates at warmer temperatures.

High-resolution seasonal change of Chlorophyta ASVs in the snow in the Japanese beech forest

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Abstract

The colored snow, including green and red snow, caused by Chlorophyta was commonly found all over Japan, including Mt. Gassan, in the northern part of the main island (Honshu). Chlorophyta in the Japanese beech forest on the slope of Mt. Gassan has been well studied for a long time because the color of green snow is a noticeable addition to the accessibility. A recent study showed the seasonal variation of Chlorophyta (*Chloromonas* sp.) and micro-animals (tardigrades and rotifers). The abundance of micro-animals was significantly correlated with chlorophyll a concentration suggesting that those micro-animals prey on Chlorophyta. However, the type of Chlorophyta and predators were identified by their morphology (microscopic observation), and their changes in DNA sequence (Amplicon Sequence Variants: ASVs) level were not conducted yet. To understand the detail changes of Chlorophyta and their predators, 18S rRNA gene sequences were analyzed from the surface snow samples taken every 2-5 days from the end of April to the end of May, just before snow patches disappeared. The number of observed Chlorophyta ASVs decreased during a study period, and that was highest in the first period (24th Apr) and lowest in the last (20th May). The relative abundance of major Chlorophyta ASVs was seasonally variable. The most abundant ASV (ASV2: 99.3% identity to *Chloromonas alpina*) gradually increased from the middle of the season and reached 60% of total 18S rRNA gene sequences. On the other hand, other ASVs (ASV5: 100% identity to Uncultured algae from an Alaskan glacier, ASV8: 100% identity to *Chloromonas muramotoi*) decreased from the highest relative abundance in the early season. Therefore, this study shows the Chlorophyta genotype dynamically shifted during a month of snow melting, and may affect the ecological cycles in the snow.

Changes in microbial diversity and ecology in Arctic freshwater biofilms across a broad latitudinal gradient (56-83 °N)

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Abstract

Accelerated warming is altering the Arctic landscape in real time, with permafrost and sea ice melt accelerating habitat loss in the 21st century. This raises significant concerns over the future integrity of Arctic freshwater systems and, in turn, the diverse microbial ecosystems within. The latitudinal diversity gradient, the ecological theory of decreased diversity at higher latitudes, is evident in the reduction in fauna and flora across the Canadian Arctic, from the taiga treeline to the High Arctic. It is less clear, however, whether this gradient persists in the microbial diversity of these regions. Diverse freshwater ecosystems span the Arctic region. Benthic cyanobacteria-based microbial mats are almost ubiquitous in these ecosystems and containing diverse microbial communities. In this study, environmental DNA (eDNA) was collected from microbial mat samples collected from water bodies across a latitudinal gradient spanning the Canadian Arctic. Prokaryotic V4 16S and eukaryotic V9 18S rRNA gene DNA were sequenced from extracted eDNA samples by targeted amplicon sequencing to identify the prokaryote and microbial eukaryotic diversity within the mat samples, respectively. The latitudinal diversity gradient within the prokaryotic and microbial eukaryotic communities will then be assessed by three null hypotheses: (1) species richness, (2) functional diversity, (3) and the interactome having no correlation with latitude. Application of marker gene amplicon sequencing identified a significant inverse relationship between latitude and species richness in the prokaryote and eukaryote diversity of the microbial mat communities, associated with higher annual temperatures allowing the first null hypothesis to be rejected. Furthermore, taxonomic annotation of eukaryotic ASVs identified distinct functional compositions of the protist community between different Arctic ecozones. Future research aims to ascertain whether lower latitude ecosystems exhibit higher functional diversity and reduced interactions than the more vulnerable high latitude ecosystems.

Ecological networks of Antarctic cryptoendolithic communities

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Abstract

In the ice-free areas of the Antarctic deserts, the extremely low temperature, aridity, oligotrophy and UV irradiation are the main challenges for life; rock represents the main substratum for microbial colonization finding an ultimate refuge within rock airspaces. Therefore, endolithic life constitutes the predominant life-form in the ice-free areas of Antarctic deserts. Among endolithic communities, those dominated by lichens are the most complex and widespread. In the last decade, numerous studies started unravelling their diversity, composition and distribution along the Victoria Land of Antarctica. Inside the rocks, the spatial confinement forces each microbial component to a strict coexistence; however, the interactions established within these assemblages remain to date largely unexplored. This study provides a first co-occurrence network analysis, based on an extensive amplicon sequencing data of 72 rock samples, collected throughout Northern and Southern Victoria Land, in order to unravel the tight network of fungal functional guilds interactions and gain more insight into the ecological relationships driving the fungal component of antarctic cryptoendolithic communities. Results revealed a tangled network of correlations, mainly positive, gravitated around lichenized fungi (Lecanorales and Caliciales orders) and spread towards the saprotrophs and highly extreme-tolerant black fungi. Surprisingly, besides the large amount of negative interactions mainly reported among fungi with saprophytic ecology, lichens establish multiple competitive correlations with Chaetothyriales order, a component of fungal black screen, which protect the entire endolithic community from outer harsh condition.

Novel instrumentation for the in situ measurement of glacier algae physiology within ice

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Abstract

Microalgae on glacier surfaces are an important contributor to the biogeochemistry, albedo and net carbon production on the glaciers they inhabit. They may also hold the key to how early plants colonised land in the Ediacaran. In the aftermath of the Cryogenian Snowball Earth, cold-adapted Streptophyte algae may have given rise to the first land plants. By examining the photophysiology and adaptations of modern glacier Streptophyte algae, we can uncover key processes and strategies that have enabled these algae to survive in the present day and through their evolutionary history. However, these organisms are highly sensitive to their environment and do not survive well in culture so are relatively understudied. Here we present our first laboratory and field results from a new 'Photosynthetron' device developed through collaboration with Photon Systems Instruments (Czech Republic) as part of the iDAPT (ice Dependent Adaptations for Plant Terrestrialisation) Leverhulme Trust funded project. The aim of this novel instrumentation is to allow in situ quantification of algal physiology within surface ice on glaciers, allowing direct measurement of glacier algal responses to their environment. We will then be able to link the known physiological potential of algae collected from genomic and ex situ experimental data to the actual activity of these organisms in their native ecosystems, providing a new view of algal processes on ice today and a functional analogue to glacial algae of the past.

Cryogenian origins of multicellularity in algae

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Abstract

For much of Earth's history, cyanobacteria have been the dominant primary producers. However, during the Cryogenian (720-635 million years ago; mya), a period marked by two global glaciations, photosynthetic eukaryotes (Archaeplastida) became the major contributors to primary production, increasing levels of oxygen in the atmosphere. Clearly, the early radiation of algae transformed the biosphere, but establishing their relationships, the timescale and geological context of their evolution has been hindered by a lack of molecular and fossil data. Here we produce a time-calibrated phylogeny of early plant evolution, incorporating the latest molecular data with a reappraisal of the fossil record. By applying phylogenetic topology testing, we resolve many deep relationships within the Archaeplastida. Molecular clock analysis integrates this resolved phylogeny with 15 fossil calibrations to indicate an origin of Archaeplastida in the late Paleoproterozoic to early Mesoproterozoic (1712-1387 mya). Considering this time-calibrated tree, ancestral state reconstruction of cytomorphological traits reveals that many of the independent origins of multicellularity can be associated with the Cryogenian. Multicellular red algae emerge approximately 902-655 mya whilst the origin of Anhydrophyta (land plants and their close algal relatives) is dated at 796-671 mya. Recently, the Snowball Earth glaciations of the Cryogenian have been proposed as the driver for the evolution of all multicellular life. The analysis presented here provide credibility to this hypothesis. We consider mechanisms by which ancestral multicellular algae first established and then dominated on Snowball Earth. Further study of algae adapted to modern day cryospheric environments will inform us about ancient processes associated with the transition from unicellular to multicellular life.

Co-evolution of the Ess1-CTD axis in polar fungi suggests a role for phase separation in cold tolerance

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Abstract

Most of the world's biodiversity lives in cold (-2°C to 4°C) and hypersaline environments. To understand how cells adapt to such conditions, we isolated from fungal species that live in extreme polar environments two key components of the transcription machinery: the Ess1 prolyl isomerase and its target, the intrinsically disordered carboxy-terminal domain (CTD) of RNA polymerase II. Polar Ess1 enzymes are conserved and functional in the model yeast, *S. cerevisiae*. By contrast, polar CTDs diverge from the consensus repeat (YSPTSPS)₂₆ and are not fully functional in *S. cerevisiae*. These CTDs retain the critical Ess1 Ser-Pro target motifs, but importantly, substitutions at Y1, T4 and S7 profoundly affected their ability to undergo phase separation *in vitro* and to localize *in vivo*. We propose that environmentally-tuned phase separation by the CTD and other intrinsically disordered regions in proteins plays an adaptive role in cold tolerance by concentrating enzymes and substrates to overcome energetic barriers to metabolic activity.

Patchy and pink: Dynamics of a *Chlainomonas* sp. (Chlamydomonadales, Chlorophyta) algal bloom on Bagley Lake, North Cascades, WA

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Abstract

Snow algal blooms that darken snow surfaces and produce red or pink snow are produced by several species of related Chlorophyta, and are dynamic over space and time. *Chlainomonas* (Chlamydomonadales, Chlorophyta) is one of the three genera of true snow algae known to produce large pink or red blooms in alpine snow annually in alpine systems in the mountainous west of the US. The bloom dynamics of these taxa are likely dependent on environmental conditions; however, the system is still relatively uncharacterized. We have observed seasonal blooms of a *Chlainomonas* sp. from May through July from snow covering a lake in northwestern Washington State that is dominated by *Chlainomonas* sp. consistently over many years. In 2021 we characterized the bloom weekly to assess photophysiology, biodiversity, the life cycle of *Chlainomonas*, and the dynamics of pink color on snow surface over time. 2021 was a warm and dry spring and early summer, including a “heat dome” event where record high temperatures were observed in the region. Our data shows that the biodiversity (via ITS and 18S SSU rDNA) and lifecycle progression are dynamic over space and time through the bloom, but the photophysiology and pink color steadily decrease throughout the bloom and drop in relation to the high heat event.

Genomic and amino acid traits of cold adaptation in Antarctic cyanobacteria

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Abstract

Cyanobacteria are widely distributed in terrestrial shallow lakes in permafrost landscapes, ice shelf meltwater ponds and ice-covered lakes in Antarctica. They are important for primary production, food webs and biofilm formation. There is however relatively little data on the metabolic capacity and adaptation mechanisms to polar environmental conditions in particular low temperatures, freezing, variable light conditions and nutrient availability. Without such information, questions on the evolutionary persistence of cyanobacteria during both warming and glacial epochs, and impact of future climatic-driven environmental change cannot be addressed. We therefore performed comparative genomic analysis of dominant species in Antarctic terrestrial aquatic environments belonging to *Leptolyngbya*, *Phormidesmis*, *Pseudanabaena* and *Nostoc*. Clonal cultures of cyanobacterial strains were isolated from microbial mat samples of perennially ice-covered lakes in the McMurdo Dry Valleys and Dronning Maud Land, Antarctica, and high-quality draft genomes were assembled using a metagenomic approach. The cyanobacteria genomes contained pathways for nutrient uptake and processing including nitrogen assimilation, assimilatory sulfate reduction and/or nitrogen fixation. Genes associated with stress responses and a total of 81 putative biosynthetic gene cluster regions were identified across all genomes. Amino acid substitutions that could favor increased flexibility under low temperatures were identified including arginine/lysine ratio, proline usage and aromaticity in some of the genomes. Certain genes were consistently found to have a cold adapted copy including adaptive-response sensory-kinase *SasA*, sensor histidine kinase *RcsC*, vitamin B12 import ATP-binding protein *BtuD*, and chaperone protein *DnaK*. Several of the strains had multiple copy numbers of full-length Photosystem II D1 proteins associated with high and low light conditions and one strain contained a 'super rouge' D1 protein encoding chlorophyll f synthase that may allow far-red photosynthesis. Our results show that low-temperature cyanobacteria have genomic traits, amino acid modifications and photophysiology that support survival in the cold terrestrial biosphere.

Genomic characterization and identification of cold-adaptation signatures in metagenomic assembled genomes of Archaea from Arctic seawater

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Abstract:

Nitrification is a process that involves oxidizing ammonia to nitrite and nitrite to nitrate. Aerobic ammonia oxidation is the first rate-limiting step in nitrification catalyzed by ammonia-oxidizing Archaea and is responsible for providing primary producers with available forms of nitrogen in the surface layers of marine environments. Phytoplankton often outcompete nitrifiers for ammonia when waters are warmer and light penetration is higher. During the winter, competition is reduced as primary production is limited under ice coverage allowing nitrification rates to increase. As temperature, light penetration, and primary production increase in the Arctic, it is likely that ammonia competition will become greater. However, “true-psychrophiles” are less sensitive to substrate concentrations and have the potential to remain competitive for ammonia. Cold-adaptation can be measured by the following indices: arginine-lysine ratio, proline residue abundance, grand average of hydropathicity (GRAVY), aromaticity, aliphatic index, and acidic residue abundance. Each index is assigned a score where lower total scores are associated with a stronger cold-adaptation signature. If the nitrifiers are determined to be “true-psychrophiles”, they may maintain similar rates of nitrification, even when substrate concentrations are reduced. Metagenomic samples have been collected from seawater within the Western Arctic Ocean from the GEOTRACES 2015 cruise and sequenced using Illumina MiSeq (2x250bp). Salinity, temperature, particulate organic nitrogen (PON), nitrate (NO_3^-), nitrite (NO_2^-), and dissolved oxygen (DO) were measured. 128 co-assemblies were obtained resulting in 2735798 contigs. A total of 253 bins with an average size of 2 312 350 bp were recovered, twelve of which were of Archaeal origin. Cold adaptation indices will be calculated using Gentilhomme’s protocol ([https://github.com/agentilhomme/ Genomic-Signatures-of-OGT-2020-](https://github.com/agentilhomme/Genomic-Signatures-of-OGT-2020-)).

Intracellular metabolic signatures of pigmented algal blooms from the Greenland Ice Sheet

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Abstract

The Greenland Ice Sheet is inhabited by active microbial communities, including pigmented microalgae, which bloom on the melting ice surface. These algae darken the surface, significantly decreasing albedo and enhancing surface melt. There is increasing interest in the biology and ecology of ice microbial communities, yet we know very little about their metabolome and how it changes in response to environmental factors (e.g. light, temperature) that trigger blooms and pigment production. A challenge is the lack of adequate metabolomic workflows to acquire such data, from sample collection, filtration, preservation through to laboratory processing. It is important to ascertain if and how these steps introduce artefacts in the ice metabolome characteristics. Here we assessed the impact of algal cell density in surface ice samples and the effects of sample melt duration and melt temperature on analysed metabolomes. We collected high algal biomass ice that was melted under different conditions (5 to 20 °C, 15 min to 24 h) and increasingly dark coloured ice, from low to high biomass, that was melted at a set temperature of 10 °C. A biphasic solvent extraction allowed us to analyse the polar metabolome and lipidome using gas and liquid chromatography-based high-resolution mass spectrometry. We annotated 148 compounds from GC/MS analysis and 986 lipids based on reference retention times and mass spectra. In preliminary multivariate analysis we found that melt temperature and melt duration have no significant impact on the overall polar intracellular metabolome. This is an important finding which, if confirmed, reduces the complexity of on-ice sample handling. By contrast, the comparative multivariate analysis of high- and low-biomass ice revealed a clear separation in the polar metabolomes as a function of biomass content. Further analysis of possible changes in individual polar metabolites, the lipidome and cross correlation with cell counts are still ongoing.

Novel Antarctic yeast adapts to cold by switching energy metabolism and increasing small RNA synthesis

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Abstract

Numerous studies have investigated bacteria, archaea and algae from cryospheric environments, however, less work had been done on fungi inhabiting these environments. Fungi play key roles in the cryosphere as they are facilitators of primary biomass production through endophytic and lichenic relationships and are involved in the nutrients recycling, though their adaptation strategies to low temperatures are not well understood. In our study, we investigated the cold-adaptative strategies of the novel *Rhodotorula frigidialcoholis* yeast, isolated from ice-cemented permafrost in University Valley (Antarctic). Our finding suggests that under cold temperature, *R. frigidialcoholis* induces a metabolic switch from respiration to ethanol fermentation to overcome the Antarctic permafrost growth challenges. This was consistent with our observation of ethanol production at 0 °C, the coldest temperature reported for its natural production. In addition, *R. frigidialcoholis* showed an increase in sRNAs diversity and abundance when grown at 0 °C versus 23 °C. Our results imply that gene expression post-transcriptional regulation and mRNA silencing may be a novel evolutionary fungal adaptation in the cryosphere.

Profiling pigments in the psychrotrophic Antarctic bacteria by FT-Raman spectroscopy

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Abstract

Changes in the amount and type of produced pigments is a common defense mechanism for Antarctic bacteria. It is well known that pigments play a key role in adaptation to cold environments by modulating membrane fluidity and protecting bacterial cells from ultraviolet radiation. Thus, screening for pigments-producing Antarctic bacteria and understanding how pigments production is affected by different stress factors is crucial for microbial ecology and biotechnology. However, so far only limited knowledge was generated in the field of bacterial pigments due to time-consuming, expensive, and laborious analysis of bacterial pigments.

Raman spectroscopy is a non-destructive and rapid analytical technique with great potential for analysis of microbial pigments. For example, different carotenoid pigments have specific Raman spectra, and thus can be identified by Raman spectroscopy. In this study, a total of ten pigmented bacterial isolates from Antarctic green snow and meltwater ponds, grown under different temperature and light conditions, were studied by FT-Raman. HPLC-MS was used as a reference method for identification of pigments. FT-Raman analysis showed that all the studied bacteria produce different carotenoids, and that their profiles are different. Based on FT-Raman data, we could split all bacteria into four groups with distinct pigment profiles. Interestingly, effect of temperature and blue-light on pigment production and profile was strain-specific, and we did not observe a general pigment-affecting effect.

Microbial community selection and adaptation in snow

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Abstract

Arctic snowpack microbial communities are continually subject to dynamic chemical and microbial input from the atmosphere. As such, the factors that contribute to structuring their microbial communities are complex and have yet to be completely resolved. The driving forces that determine microbial community structure in the snow are likely the result of random stochastic processes and environmental conditions that vary both temporally and spatially. In addition, biological interactions in snowpacks alter community function and drive adaptation. Here, we present research on the role of microorganisms in the functioning of Arctic snow by highlighting the links between their biotic and abiotic components from field and laboratory studies. Our work focuses on biodiversity, microbial population dynamics and the influence of microorganisms on biogeochemical cycling, and their interactions with their physical and chemical environment. Results indicate that environmental selection plays a significant role in structuring snow microbial communities and that future studies should focus on activity and growth.

Illuminating microbial communities in the Finnish subarctic soils using omics approaches

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Abstract

Soil microbial communities have critical role in biogeochemical processes on Earth, but our understanding of their response to the ongoing climate change is poor. Arctic and subarctic soils harbor approximately 50 % of Earth's below ground carbon. Warmer climate leads to increased rate of soil organic matter decomposition in polar regions, but the overall impact to carbon and other biogeochemical cycles is difficult to predict without a deeper understanding of the soil microbial ecology. We analysed both metagenomic and metatranscriptomic data from soils in northern Finland covering a range of ecosystems from dry upland soils to water-logged fens, and obtained over 1000 manually binned and curated metagenome-assembled genomes (MAGs). We then searched for MAGs harbouring genes involved in methane cycling and driving methane effluxes as well as genes involved in denitrification, an important process driving N₂O emissions. Communities of potential denitrifiers were dominated by microorganisms with truncated denitrification pathways and differed across soil ecosystems. Upland soils showed a strong N₂O sink potential and were dominated by members of the Alphaproteobacteria. Fens, which had in general net-zero N₂O fluxes, had a high abundance of poorly characterized taxa affiliated with the Chloroflexota lineage Ellin6529 and the Acidobacteriota subdivision Gp23. Metatranscriptomics with double RNA approach was applied to elucidate the active functions and activity of microbial communities in these same soils. Our data shows differences in the composition and activity of the microbial communities along the climate gradient and these results give information on how environmental factors contribute to microbial activity and again its feedback effect to warming climate. By coupling an in-depth characterization of microbial communities with in situ measurements of GHG fluxes, our results suggest that the observed spatial patterns of GHG fluxes in the tundra and fen soils are related to differences in the composition of microbial communities.

Nutrient requirements of microalgae on the Greenland Ice sheet revealed by single-cell analyses

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Abstract

Microalgal blooms accelerate surface ice melt on glaciers and ice sheets by lowering ice albedo. Their growth requirements and direct role in biogeochemical cycling remain, however, elusive, due to the lack of species-specific elemental composition and nutrient uptake measurements. Here, we address this knowledge gap by studying glacier algal elemental composition and the dual assimilation of ¹³C-bicarbonate and ¹⁵N-ammonium or ¹⁵N-nitrate in a bulk supraglacial community and in single glacier algal cells, during in situ incubation experiments on the Greenland Ice Sheet. Our results reveal high phenotypic plasticity in glacier algal populations, indicated by the intercellular variability in ¹³C and ¹⁵N-assimilation and elemental composition. The uptake of ¹⁵N-ammonium or ¹⁵N-nitrate was insufficient to sustain the observed DI¹³C-based growth in glacier algae, pointing to the uptake of dissolved organic nitrogen as an additional nitrogen source. Furthermore, in our nutrient addition experiment, we observe a lack of microalgae productivity stimulation after ¹⁵N-ammonium, ¹⁵N-nitrate, and phosphate additions within the 30 hours incubation time. The overall potential lack of macronutrient limitation in glacier algal populations together with high cellular in situ C:N and C:P atomic ratios suggest a lifestyle highly adapted to the low inorganic nutrient environment they thrive in, likely enabling sustained growth throughout the summer season.

Do Arctic extreme winter warming events lead to microbial N immobilization and plant N limitation?

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Abstract

In Arctic soils, wintertime usually means subzero ground temperatures and only little unfrozen water available below a snow cover. While this period has less active nutrient cycling by microbes, some activity means that winter mineralization of e.g., nitrogen (N) can release a pulse of mineral N (ammonium, nitrate) into the soil solution, which can become biological available upon spring thaw. In springtime, plants may compete with microbes for the N pulse, but if thaw happens during winter, the N pulse could be immobilized by active microbes, which can decrease the size of the springtime N pulse, and therefore decrease the growing season N addition to the ecosystem. Many parts of the Arctic have with climate change seen an increase in the frequency of extreme winter warming events (WW events), which are periods of positive temperatures lasting 5-7 days and causing snow to melt and the upper soil layer to thaw. In a field scale experiment, we quantified the amount of mineral N released into solution upon soil thaw during a simulated WW event in Disko island, Western Greenland (69.28°N, 53.48°W) in late winter 2022. We used ¹⁵N tracing to determine which parts of the ecosystem that benefited from this N during the WW event. Our focus is on microbes in the rooting zone, and we use a combination of density gradient methods to separate bacteria from the soil and, using nanoSIMS, study which communities that took up WW event-released N. We further study how the WW event affected plant N availability in summer. Our research sheds light on the little studied impact of climate change-related WW events on the nutrient cycling of Arctic soils and the plant-root competition for N in the future, and we develop methods for studying this phenomenon in the broader Arctic.

Microbial carbon dynamics in cryogenic environments of the western Greenland ice sheet

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Abstract

Microbial activity on glacier and ice sheet surfaces is a major factor responsible for their darkening. Pigmented snow and glacial ice algal blooms magnify surface melt by enhancing light absorption, which in turn decreases the albedo. Additionally, the metabolic activity of cryogenic microbes both releases and consumes dissolved organic species. Understanding organic carbon dynamics is thus crucial to assess microbial community interactions. We assessed initial microbial community composition via 16S and 18S rRNA gene sequencing and followed the carbon dynamics linked to autotrophic and heterotrophic activity in incubation experiments over 24-day. Red snow algae and dark purple glacial ice algae-rich surface samples were exposed to light and dark conditions, and the dissolved organic matter (DOM) fraction was collected at specific time intervals for dissolved organic carbon (DOC) content and molecular composition analyses via Fourier transform ion cyclotron mass spectrometry. Our results reveal that DOC in all systems increased over time. An 8-fold increase in DOC was observed in the glacial ice algae experiments, under light conditions, and only a 5-fold increase under dark conditions. The same trend was observed in the red snow algae experiment, with higher DOC being produced under light conditions (4-fold increase) relative to dark (1.5-fold increase). Variations in DOC content and DOM molecular composition mirrored both the metabolic activity of the glacial algae, and the autotrophic/heterotrophic changes over time. Glacial ice algae DOM was molecularly less diverse than red snow algal DOM, but its complexity increased with time, especially under light conditions. Our study revealed first insights into the carbon dynamics of glacial ice- and snow algae dominated systems, and evaluated their role in the variability of organic species on the Greenland Ice Sheet surface.

Environmental conditions and biogeochemical cycling in supraglacial weathering crust habitats

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Abstract

Shortwave radiation that penetrates and is attenuated in glacial ice generates meltwater and porous matrices in the near-surface ice termed the weathering crust aquifer (WCA). There has been increased interest in this portion of the supraglacial system as an important driver in the turnover of carbon and nitrogen and their export to periglacial environments. In this study, we report on the optical properties of ice that comprises the WCA and its evolution from early in the melt season to the peak of summer. By monitoring photosynthetically active radiation (PAR) penetration through the ice using shallow boreholes, we observed similar light attenuation coefficients in ice from Isunguata Sermia (Western Greenland) and the Matanuska Glacier (Alaska). PAR at 1 m below the ice surface ranges from 6 to 11% of surface incidence and is sufficient to support photosynthetic growth. Additionally, the concentrations of cells and ATP biomass in samples from the WCA are higher than levels found in nearby supraglacial streams. Metagenomic analysis of WCA samples from the Matanuska Glacier reveals the complexity of its community and confirms that algae commonly reported on glacier and snow surfaces globally are highly abundant, as well as genes for photosynthesis, carbon fixation, and nitrogen assimilation. We discuss the significance of biogeochemical processing in the WCA and its implications for downstream systems as global temperature and melt season duration increase in the future.

Aerobic anoxygenic photosynthetic bacteria are common in endosphere and phyllosphere microbiomes of arctic and boreal plants

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Abstract

Green plants, algae and cyanobacteria convert energy from light into organic compounds using oxygenic photosynthesis. In addition to these organisms, photosynthetic systems are also widely present in evolutionary ancient anoxygenic photosynthetic bacteria, including aerobic anoxygenic photosynthetic bacteria (AAPB). AAPB are abundant in aquatic ecosystems in all climates, but they have been also detected in terrestrial ecosystems, including arctic and alpine glaciers, polar and desert soils and soil crusts, and, recently, in metagenomes of several plant phyllosphere microbial communities.

Here, we present results of systematic screening and characterization of AAPB in phyllospheres and leaf endospheres of 25 plant species by near infrared fluorescence imaging of culturable bacteria. In collaboration with seven high schools in Finland, we sampled in ten distinct locations across latitudinal gradient spanning from hemiboreal to oroarctic climate zones in Finland.

We show, that AAPB are consistently present in plant phyllosphere microbiomes in these climates, as they are detected in all sampled locations, and in virtually all plant species studied. Additionally, AAPB were also detected in the endosphere samples of several arctic and boreal plant species. Most of the characterized isolates represent alphaproteobacterial genera *Sphingomonas* and *Methylobacterium*, but AAPB representing putatively novel alphaproteobacterial lineages, as well as betaproteobacteria were also detected. Methylobacterial isolates were mostly present in the phyllosphere with weak host specificity, while *Sphingomonas* AAPB were also detected in endosphere of several plant species, with clear host specific lineages. All the observed AAPBs show typical LH1/RC fluorescence spectral properties with slight variation among each others. Intriguingly, the AAPB detected in this study represent bacterial taxa with plant growth promoting bacteria, prompting questions about putative role of AAP in plant-microbe interactions in these ecosystems characterized by strong annual fluctuations of light and temperature.

Temporal rhizobiome changes inferred from ancient DNA shotgun sequencing

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Abstract

The Arctic is known to warm much faster than the global average which leads to drastic ecosystem changes such as the migration of the tree line northwards, resulting in arctic greening. Alongside plant community changes, their associated soil and root microorganisms are expected to change subsequently. So far, rhizobiome analyses mainly focus on single plant species and their adaptation to experimental warming but knowledge about whole plant community changes and subsequently their associated microbes is scarce. Understanding past changes in the taxonomic composition and co-occurrences helps to infer biotic interactions and can be used to predict future ecosystem adaptation and turnover as a response to climate change. We investigated sedimentary ancient DNA (sedaDNA) from Lake Lama, Taymyr Peninsula (Arctic Siberia), covering the last about 23.000 years using shotgun metagenomics, enabling to decipher past community composition at ecosystem level. Preliminary evaluation of the sedaDNA data shows that mycorrhizal fungi experience a compositional shift with ongoing warming at the Pleistocene-Holocene transition from *Thelephoraceae* and *Tricholomataceae* dominated Pleistocene to Glomeraceae dominated Holocene. Alongside, we detected a decrease in lichen abundance. This coincides with the migration of woody taxa such as Pinaceae in the area. Further comparison to bacterial nutrient cyclers show shifts from C to N cyclers as well as an indication for podzolization with Fe increase. Additionally, XRF data will be used to understand variations in the arctic rhizobiome in correlation to soil development. The data show that shotgun metagenomics alongside XRF data is a valuable tool to reconstruct ecosystem turnover during soil development processes.

Exploring the functional potential of plant-associated microbiomes in alpine region to enhance cold stress tolerance in plants

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Abstract

Climate change-associated extreme weather events such as early spring frosts have increased in frequency and intensity over the past decades. Cold stress is one of the main limiting factors for fruit crop production worldwide. Plants and their associated microbial communities have developed complex adaptation strategies against cold stress. Plants growing in cold regions, such as alpine regions, are hypothesized to survive cold stress thanks to symbiosis with endophytic microorganisms. However, the structure and function of endophytic microbial communities associated with such plants are poorly understood. Our aim is to taxonomically and functionally characterize the endophytic bacterial communities associated with three wild cold-adapted Rosaceae plants (i.e. *Geum montanum*, *Alchemilla* sp., and *Dryas octopetala*) from alpine region. Plant samples were collected from seven different sites in Italy from two expositions (North and South). The bacterial community structure associated with the flowers, leaves, and roots were characterized using 16S rRNA gene (V5–V7 region) amplicon sequencing to identify potential candidate taxa for cold tolerance. In addition, targeted isolation methods were used to recover culturable psychrotolerant bacterial taxa through a combination of a low nutrient medium (Reasoner's 2A agar), long incubation time (up to 4 weeks) and low temperature (at 4 °C). Plant species, tissues, and sites were the main factors influencing bacterial richness, diversity, and community structure. Furthermore, we established a taxonomically diverse psychrotolerant bacterial culture collections (about 700 isolates belonging to 54 different genera) representing the majority of dominant genera detectable by culture-independent community profiling, including *Pseudomonas*, *Erwinia*, *Sphingomonas*, *Rhizobium*, *Massilia*, *Janthinobacterium*, *Duganella*, *Flavobacterium*, *Mucilaginibacter*, *Subtercola*, and *Galbitalea*. This study contributes to the understanding of plant-associated microbiomes in alpine regions, and highlight their potential as bacterial inoculants for the enhancement of cold stress tolerance in agronomically relevant fruit crops.

Simulated snow drives rhizosphere recruitment in subarctic soils

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Abstract

In the arctic and subarctic, climate change is resulting in reduced snowpack extent and earlier snowmelt. Altered snowpack conditions will likely have significant ecological consequences in subarctic regions. Changes in snowpack state will directly affect metabolisms and behaviors of individual organisms in both above- and below-ground (i.e., plants and soil microorganisms). These individual-based responses will have long-term consequences where plant and soil communities will eventually reassemble. The aim of this study was to determine the effect of snowpack condition on overall microbial community structure and rhizosphere recruitment across three subarctic plant functional groups. Soil microcosms were established using a tree, forb, grass, or no plant control and after about 150 days, senescence was induced. Half of the samples experienced freeze thaw conditions simulating the absence of snow, while the other half experienced a static sub-zero temperature to simulate the snowpack. After approximately 400 days of incubation, soil microcosms were destructively sampled for soil properties and microbial taxonomy. Microorganisms were differentially recruited on the plants based on the presence of snow. There was a strong relationship between simulated snowpack treatments and plant type in structuring prokaryotic rhizosphere communities. In contrast, fungal community structure was most strongly influenced by plant type, suggesting that fungi are less susceptible to freeze-thaw cycles compared to bacteria. These findings have important ecological implications for how rhizosphere microorganisms behave under changing snowpack conditions induced by climate change.

The dark side of the moon: the unique and disappearing taxonomic and functional diversity of a tropical African glacier-fed stream

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Abstract

The glaciers on Africa's 'Mountains of the Moon' will almost certainly disappear this century. Despite this, the glacier-fed stream (GFSs) microbiome remains unexplored, although potentially housing unique taxa and functional processes given their isolation in the tropics. Here, we investigated the taxonomic and functional diversity of microbial communities inhabiting a stream draining the Stanley Glacier, in Rwenzori National Park, Uganda. We found the stream to be chemically dilute in ions, enriched in nitrogen and dissolved organic matter, and elevated in photoautotrophic biomass and extracellular enzyme activity. Amplicon sequencing revealed that bacterial and eukaryote communities were dominated by cyanobacteria and diatoms, respectively. Among non-photosynthesizing bacteria, Gammaproteobacteria had the greatest relative abundances, followed by Alphaproteobacteria and Bacteroidia. Yet, unlike other GFSs, usually common Chrysophytes and *Polaromonas* spp. exhibited low relative abundances. Because of the high photoautotroph abundance, we investigated microbial metabolic potential utilizing metagenomics, specifically focusing on organic matter utilization. We found most microbes capable of organic carbon oxidation, with >80% of the community capable of fermentation and acetate oxidation. Furthermore, we found glycosyltransferase, sucrose synthase, and the glycoside hydrolase families to be the most abundant CAZymes families, and 58% of MAGs possessed cellulase genes, including 72% of the Bacteroidia and 91.5% of the Verrucomicrobiae. These two classes also contributed the most to xylanase (57.3% and 61.7% of MAGs, respectively), and are probably the main degraders of algal-derived polysaccharides in this system. Lastly, 122 MAGs (e.g. 31 Alphaproteobacteria and 37 Bacteroidia) possessed genes involved in galacturonic acid degradation, the main component of pectin (found in green algae).

Given the high abundance of photoautotrophs and elevated enzymatic activity, our results reveal that the unique microbial community of this GFS is well-adapted to the unique conditions and associated eukaryote community resulting from a tropical setting markedly different from other GFSs globally.

MicroModel: Microscale controls on greenhouse gas production

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Abstract

The relative roles of microbial community assembly versus soil organic matter quality in controlling the timing and magnitude of greenhouse gas emissions from thawing permafrost remain unknown. In this study, we use a combination of laboratory and modelling techniques to assess the magnitudes of these controls on aerobic carbon dioxide (CO₂) and anaerobic CO₂ and methane (CH₄) production. We incubated 16 soil samples from four cores, representing thermokarst lake and lagoon environments in Siberia at various stages of high-disturbance thaw. Cumulative CO₂ production ranged from 0.88-976 mg CO₂ per g soil and cumulative CH₄ production ranged from 0.01-124 mg CH₄ per g soil during the 430-day incubations at 4 °C and 16 °C. Ultra-high resolution soil organic matter characterization was measured on a subset of samples using Fourier-transform ion cyclotron resonance mass spectrometry (FT ICR-MS) at the start (t = 0 days) and the end (t = 430 days) of the incubation to determine which compounds were consumed and/or produced during the incubations. Microbial community composition was characterized using 16S rRNA gene sequencing at the start and end of the incubation to assess initial microbial assemblage and which species increased or decreased during the incubation. Relationships between CO₂ and CH₄ production, organic matter utilization, and microbial communities will be determined using statistical modelling. Preliminary results indicate the changes in microbial assemblage following permafrost thaw have the strongest influence on greenhouse gas production potentials, but organic matter quality influences the post-thaw microbial assemblage.

Culture collection from a glacier-fed alpine stream-a tool to study adaptations of biofilm bacteria to climate change

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Abstract

Biofilms conform the dominant microbial lifestyle in streams, yet relatively little is known about their ecology and roles in the biogeochemistry of alpine systems. A key step to addressing this knowledge gap is to obtain cultures of the different microbial components of alpine stream biofilms, and study the phenotypic and genotypic traits that allow them to survive and prosper in these ecosystems. We have thus far isolated over 400 bacteria from biofilms growing in experimental flumes fed by an alpine stream. The experimental setup mimicked predicted environmental conditions given several climate change scenarios that reflect higher stream water temperature and altered hydrological regimes (natural, constant, stochastic and intermittent). Isolates corresponding to relatively abundant genera in our communities include members of *Hymenobacter*, *Massilia*, *Rhodoferrax*, *Acinetobacter*, *Trichococcus* and *Flavobacterium*. Almost one fourth of the isolates recovered in the different media and growth temperatures exhibited structural coloration in the form of “rainbow diffuse” iridescence under natural light; a phenotype that has not yet been reported in bacteria from alpine or polar systems. Although the iridescent phenotype of bacteria has not been observed in nature, it has been speculated to have biological roles such as increased tolerance to desiccation, photoprotection, and thermoregulation in marine bacteria. These proposed traits could also be relevant for bacteria adapted to living in alpine streams specially given future climate change scenarios that predict increased drought periods and higher temperatures. Our isolate collection will allow us to further elucidate the role of various adaptive traits of biofilm bacteria to climate change, and it comprises a valuable resource for other future ecological and biotechnological research.

Detection of ice nucleating bacteria in low biomass polar air samples

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Abstract

It has been known for some time that bacteria have a role and can be active in the atmosphere directly through ice nucleation (IN) and its impact on cloud formation and albedo. This is particularly relevant in the Polar regions, where albedo has an important influence on global warming. However, until relatively recently, the study of microorganisms in the atmosphere had been limited by the technology available to study them at appropriate scale and resolution. In this study, we investigate the ease of detection of ice nucleating (IN) bacteria in the atmosphere and suggest methods for improved working with low biomass microbial biomarkers at or close to the limits of detection. Targeting bacterial ice nucleation genes and using primers as published in the literature, we work with low biomass Polar air samples and focus on those methodologies which generate a signal at or above the nominal limit of detection. In so doing we establish a functional methodology that can be applied to other low biomass atmospheric studies.

Cyanobacterial communities in Antarctic and sub-Antarctic lacustrine microbial mats

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Abstract

During the BelSPO funded CCAMBIO project, based on an extensive sampling of about 80 samples from 8 Antarctic Conservation Biological Regions (ACBRs) on the Antarctic continent and two sub-Antarctic islands, two goals were pursued. First, the diversity of cyanobacteria growing in the microbial mats of freshwater lakes was described, including a comparison of rare and abundant taxa and the determination of the proportion of endemic taxa. Second, the influence of geographic isolation and environmental parameters (pH and conductivity) were studied at three different spatial scales: circum-polar, continental, and bioregional. In total, 310 cyanobacterial OTUs were obtained and covered a large taxonomic diversity, with 6 orders containing 64 genera. The most frequent genera were *Leptolyngbya* (31.4 % of the OTU abundance), *Phormidesmis* (29.2 %), *Phormidium* (10.5 %), *Oscillatoria* (5.2 %), and *Cyanobium* (3 %). The cyanobacterial communities appeared dominated by filamentous cyanobacteria on the Antarctic continent, whereas the sub-Antarctic islands present a more balanced diversity, with a higher presence of unicellular morphotypes. A MetaMDS analysis on the Bray-Curtis dissimilarity matrix of OTU shows that the cyanobacterial community structures differ between Antarctica and the sub-Antarctic islands. Within Antarctica, the PERMANOVA analysis reveals that the differences in community structures between maritime and continental samples, even if significant, are smaller than with the sub-Antarctic islands. Based on our GenBank annotation, the geographic distribution of OTUs found in Antarctica and in the sub-Antarctic islands shows different patterns. Indeed, even if cosmopolitan taxa are important in both places, Antarctica shows a higher proportion of "cold" taxa (Alpine and Polar = 48.3 %), compared to the sub-Antarctic (Alpine and Polar = 15.2 %). The data suggests that the cyanobacterial communities are not structured according to the ACBRs. The factors explaining the cyanobacterial community differences appear to depend on the spatial scales we focus on.

Human activity and its role on the presence of antibiotic resistance in snow, ice and meltwaters in the alpine space

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Abstract

Antibiotic (AB)-resistances are, according to the WHO, one of the biggest global challenges of the 21st century. However, research of antimicrobial resistance is still mainly focused on urbanized areas while only little is known about the presence of (multi-)resistant microorganisms in relatively remote regions. This work provides a detailed report about the current state of AB-resistance in cryospheric habitats in the Tyrolean alpine space and the impact of humans on this phenomenon.

Here we evaluated antibiotic susceptibility by growing bacteria isolated from three different glaciers and their melting waters and performing an optimized protocol of the agar-disk-diffusion to meet the needs of psychophilic and psychrotolerant microorganisms. With this approach, a total 72 % out of 266 bacterial isolates from snow, ice and freshwaters showed resistance to at least two of eight different antibiotics whereas the number of susceptible microbes was as low as 18 %. One of the main driving factors for the emergence of antibiotic resistance is the human use of antimicrobials. However, little do we understand yet how far these effects reach even remote regions. To evaluate the potential effect of anthropogenic influence on antibiotic resistance in cryospheric habitats, we combined the data from our antibiogram with data that indicate human presence (e.g. tracking data, level of urbanization, proximity to sewage treatment plants). This way we found a significant increase of AB-resistance in areas with direct human impact compared to seemingly less impacted areas. Nevertheless, resistant bacteria have been found in all sampling sites which highlights that further factors like intrinsic resistance mechanisms and global spreading mechanisms through different vectors have also to be considered when discussing antibiotic resistance in remote cryospheric habitats.

Longitudinal patterns of microbial assemblages suspended in glacier-fed streams

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Abstract

Glacier-fed streams are rapidly changing ecosystems dominated by microbial life. As glaciers melt, nutrients, organic matter, and microbial cells are exported into proglacial streams, all of which are likely influential to downstream ecosystems. Meanwhile, other sources of solutes, particulates, and cells within the hydrological catchment enter and gain influence downstream, and include habitats such as eroding stream banks, tributary streams, benthic stream biofilms from the mainstem, and permafrost thawing. Yet, the residence time and ultimate fate of microbial cells derived from the glacial environment itself is not known, even though they have the potential to colonize and reside in downstream sediments.

In this work we ask, how do suspended microbial assemblages change with increasing distance from source glaciers, and what kinds of environmental factors might correspond with changes in their downstream composition? To answer this, we sampled streamwater from longitudinal transects (from glacier to major outlets) of 5 streams, 1 in Greenland, 1 in Iceland, and 3 in the European Alps, to characterize patterns in suspended microbial communities with the distance from their source glacier. DNA was then extracted from streamwater samples, and the 16S rRNA gene sequenced to characterize bacterial assemblages.

Overall, we found that bacterial diversity increases with distance from the source glacier, and reflects changes taking place within the catchment. This was particularly true for the catchments in the Alps and Iceland, while patterns within the Greenland catchment were more ambiguous. In this ongoing work, we further hypothesize that 'cryosphere specific' ASVs will decrease with distance from the glacier, and more 'generalist' freshwater ASVs to increase with increasing distance due to elevated inputs from the adjacent terrestrial system.

This study will improve our knowledge of the fate of glacially-exported cells and help to predict potential changes to the genetic repertoire of downstream ecosystems with ongoing glacial shrinkage.

2000LAKES: alpine research and citizen science for the microbial conservation of high-mountain lakes

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Abstract

Alpine lakes (those located above the 2000 m tree line) are excellent sentinels of climate change as their chemistry and biology respond rapidly to environmental forcing. The Swiss alps are host to over 1500 alpine lakes, many of which have been newly mapped and thus never been studied. Microorganisms play major ecological roles in these ecosystems, including primary production, cycling of elements, and attenuation of contaminants, but it is uncertain how physical climatic changes may affect microbial communities and their activities in alpine lakes. 2000LAKES is a project joining citizen science and alpine research aiming to: (i) record and monitor the unexplored microbial diversity in Swiss alpine lakes, and (ii) engage citizens in science and spread awareness about environmental conservation through participation in our field campaigns. So far, we have sampled more than 40 lakes in the Alps and our 16S rRNA sequencing results confirm that alpine lakes are unique hotspots of microbial diversity. In addition, we have built "Microbialps", a collection of alpine bacteria isolates that will be made available for research, education and conservation purposes. We are currently working on developing a citizen science framework to engage local actors in our research and to explore the social dimensions of the importance of alpine lakes. In summary, 2000LAKES is an exciting collaborative project aiming to understand the ecological impacts of climate change in alpine lakes and to promote the microbial conservation of alpine microbial ecosystems joining forces between scientists and citizens.

Adaptive mechanisms of phytoplankton in a changing Arctic: Acclimation, microevolution and ecological shifts under heatwaves

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Abstract

Progressing climate change poses large challenges for the adaptation of Arctic organisms and ecosystems, including phytoplankton at the very base of the foodweb. Rapid adjustments to a changing and increasingly fluctuating Arctic environment can take place through physiological and evolutionary responses on several fundamental ecological levels: a single genotype, a population of the same species, and the entire multi-species community. Protist communities are often observed to be rather resilient to environmental change, but which of the mentioned levels drives the responses to rapid environmental change can have large ecological and biogeochemical implications. In dedicated experimental setups of different ecological complexity, we are investigating how phytoplankton responds and adjusts to heatwaves, and on which of the mentioned levels shifts can be observed. A special focus was set on intraspecific diversity and selection dynamics within species, the analysis of which still poses a large challenge, but can be an important mechanism of adjustment. Using a novel molecular approach to efficiently examine the composition of protist populations in diverse contexts, we investigated how phytoplankton communities respond to stable and fluctuating temperature scenarios, physiologically and ecologically. This will help us to better project ecosystem dynamics in a future Arctic.

Diazotrophs in the Arctic Ocean: Seasonal variation and glacial meltwater influence

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Abstract

Nitrogen fixation was up until recently not thought to occur in polar marine waters but has now been detected in several habitats of the Arctic Ocean. With ongoing rapid climate change in the Arctic, forcing the system into a new state with less sea ice, retreating glaciers and higher temperatures, it is critical to investigate how nutrient availability will be affected and in turn govern primary productivity. Knowledge about the microbes responsible for nitrogen fixation – diazotrophs - in this region is sparse. Here, we investigated diazotroph community composition at contrasting locations, seasons, and habitats by targeting the nitrogenase gene *nifH* through amplicon sequencing. The community connectivity and succession were explored over a glacier-to-ocean continuum during three months in a north-eastern Greenland fjord, as well as re-visited a second year with drastically different temperature and run-off conditions from the land-terminating glaciers. Further, a first full annual cycle describing diazotrophs in contrasting water masses around Svalbard, including the vastly overlooked polar night season, mesopelagic depths and sea ice covered waters is presented. Through this study, a broader understanding of the influence of season and connectivity to land and glaciers on diazotrophs is provided – a prerequisite for prediction of nitrogen fixation and nitrogen availability in the current and future Arctic Ocean.

Uncovering diversity and abundance of metal metabolism and resistance genes in Arctic and Antarctic regions with LCPDb-MET

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Abstract

Resistance to toxic metals, as well as their metabolism, is a topic of great importance for the fields of microbiology, ecology and overall environmental studies. This also applies to the field of polar microbiology, as Arctic and Antarctic regions are often characterized by high concentrations of metals, including toxic metals, which is a consequence of natural bioweathering of rocks. For many years now, the polymerase chain reaction (PCR) was the method of choice for the detection of bacterial genes involved in metal metabolism and resistance. The quality of such analyses is often heavily dependent on the choice of suitable primers. The use of incorrectly designed primers often leads to generation of biased, or even false, results. To overcome this problem, 291 published PCR primer pairs, designed to detect genes involved in metal metabolism and resistance were analyzed and benchmarked. The study showed that almost 95% of the analyzed primer pairs are not suitable for analysis of metagenomic samples. The primer pair's benchmark is available in the LCPDb-MET database. Created through a systematic literature review and multiple steps of manual curation and validation, the database is a high quality resource that can be used to greatly improve the quality of PCR results. This can be achieved by providing users with a ranked list of primers, allowing them to choose the best one for their application. Here we present the result of screening of over 150 metagenomes coming from Arctic and Antarctic regions using the LCPDb-MET database. The results provide a great insight into the diversity and abundance of metal metabolism and resistance genes in these regions, while simultaneously confirming the suitability of use of the LCPDb-MET database for screening of polar regions.

In-silico identification and characterization of *Psychrobacter* prophages

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Abstract

Psychrobacter spp. have been isolated from a variety of environments, mostly low-temperature geographical locations like Antarctica, Svalbard, and Alaska. These bacteria can grow in extremely low temperatures, therefore, they are considered psychrotolerants. They belong to the *Moraxellaceae* family which also accommodates two other genera: *Moraxella* and *Acinetobacter*, for which the majority of representatives were recognized pathogens. Various *Psychrobacter* species were also found in clinical samples and are considered to be opportunistic pathogens. This study focuses on newly in-silico identified prophages in *Psychrobacter* genomes. Until now, only one *Psychrobacter* phage has been described and similarity to *A. baumannii* prophage has been indicated. The *Psychrobacter* virome and potential involvement of prophages in their hosts' phenotype still remain unexplored.

In this study, we screened 266 available genomes of *Psychrobacter* spp. for the presence of prophages. Using PhiSpy algorithm and manual annotation, we identified 123 previously unindicated complete prophages within 84 *Psychrobacter* genomes. Among them 28 revealed to be polilysogens carrying up to four complete prophages, which, in total, also constituted more than half of all identified prophages. The novel prophages were subjected to insightful comparative genomics, including the investigation of their diversity within the *Psychrobacter* genus, which also revealed their modularity. Using protein-based similarity networking we explored the relationships with other (pro)phages infecting or carried by *Moraxellaceae* representatives and also other groups of bacteria. The majority of *Psychrobacter* prophages, which shared similar proteins with all known *M. catarrhalis* prophages and several *A. baumannii* viruses, were grouped together in one compact cluster. Moreover, the analyses showed that a range of *Psychrobacter* prophages are similar to viruses infecting other Gamma-, Alpha- and Betaproteobacteria which reveals their diversity. In this study, we explored the diversity of *Psychrobacter* prophages, revealed their potential impact on their hosts' phenotype, all in relation to the general biogeography of *Psychrobacter* spp.

Novel tools for identification of antibiotic resistance genes in polar regions

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Abstract

Antibiotics in the environment can create selection pressures that stimulate the growth of antibiotic resistant bacteria and additionally, they can promote horizontal gene transfer (HTG) of antibiotic resistance (AR) among microorganisms. Thus, the phenomenon of AR in environmental settings is considered as one of the biggest threats to public health. It has therefore become extremely important to monitor antibiotic resistance genes (ARGs) in various environments. Multiple studies show that bacteria present in polar regions may exhibit natural resistance to antibiotics and they carry various autochthonous ARGs. However, there are also reports revealing the occurrence of ARGs of clinical relevance (normally identified in pathogenic, hospital strains) in Arctic and Antarctic bacteria. This exemplifies the importance of development of reliable and sensitive tools for the detection of these genes. Such tools are Universal Primer Validator (UniPriVal) and the LCPDb-ARG database. The UniPriVal tool was created to allow in silico validation of PCR primers used to identify ARGs in various environments. Primers are ranked based on three parameters: specificity, efficacy, and taxonomic efficacy and placed in the LCPDb-ARG database. Both tools were used for in silico PCR based on Arctic and Antarctic metagenomic data available in public databases. Using the best ranked primers, 93 ARGs were detected in 18 metagenomic datasets. As a second part of the study, completely new primers were designed to identify *mcr1-mcr9* genes in various environments. The *mcr* genes confer resistance to colistin that is considered the drug of the last resort. Newly designed primers were validated using UniPriVal and specifically optimized. This resulted in the identification of *mcr-2* and *mcr-3* genes in samples from glacier moraine and feces of little auks from the Arctic. This finding was not possible using any other pair of primers described in the literature, which indicates the advantage of our primers.

New classes of PHA synthases within polar region bacteria

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Abstract

Polyhydroxyacids (PHAs) are intracellular bacterial storage materials. Their main function is to store carbon as an energy source to be used in starvation periods. They are composed of polyesters of hydroxyalkanoic acids with chains of various lengths. Enzymes responsible for the polymerization process are the PHA synthases encoded by the *phaC* gene. Currently, four classes of this enzyme were discovered and described. PHA synthases of classes I, III and IV are involved in production of short chain hydroxyalkanoates (scl-PHA) and PHA synthase of class II are synthesized medium side chain PHAs (mcl-PHA). In 2020 synthase a class V polyhydroxyalkanoic acid synthase was proposed based on the amino acid sequence of a *phaC* gene from an Antarctic bacterium. Here we investigated *phaC* amino acid sequences from 20 genomes of Arctic and Antarctic bacteria. In genomes of eight strains more than one PHA-synthase class was identified, with up to four *phaC* genes in an Arctic *Janthinobacterium* sp. 1167. Some of the AA sequences clustered with known PHA synthase classes, some with the proposed class V. A few sequences showed no similarity to any known synthase class. Preliminary research suggests these additional synthases could be responsible for amending the basic PHB polymer in units of various lengths, thus making an unusual PHA, which properties may prove useful in many industrial applications.

Fast and persistent responses of alpine permafrost microbiomes to in-situ warming

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Abstract

We quantified the in situ responses of the alpine permafrost microbiome and virome to warming, using a soil transplantation experiment on the long-term permafrost monitoring summit in the Alps as a model ecosystem over three years. Field-simulated warming led to augmented microbial biomass in the permafrost, mainly owing to the abundance increase in copiotrophic prokaryotic taxa (e.g. *Noviherbaspirillum*) over metabolically restricted bacteria (i.e. *Patescibacteria*). Mostly ascomycetous sapro-pathotrophic fungi profited from warming, superseding basidiomycetous yeasts. Less than 1% of all metagenome reads were found to be viral sequences. The most abundant virus was Kloseneuvirus which strongly decreased with transplantation. Further, the classes Caudoviricetes and Megaviricetes strongly decreased with warming-induced transplantation. Our findings provided first insights on the structural acclimations of the alpine permafrost microbiomes and viromes to simulated warming which may improve the prediction of the future changes that mountain soil ecosystems will undergo due to climate change.

The *Comamonadaceae* family in the cryosphere

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Abstract

Bacterial taxa of the *Comamonadaceae* family (Betaproteobacteria) are widespread in the cryosphere and frequently represent the dominant species in samples of snow, glacial ice, meltwaters and recently-deglaciated sediments. It has been suggested that their physiological abilities may be advantageous for adaptation to cold environment providing them with selective benefits over other microorganisms. However, members of this family are closely related at the 16S rRNA gene sequence level, which complicates searching of patterns in their habitat preferences. In order to gain finer resolution of the distribution of *Comamonadaceae* taxa within the cryosphere and adjacent polar habitats, we extracted the 16S rRNA gene sequences of *Comamonadaceae* from almost 400 metagenomic samples collected from various sources (i.e. cryoconite holes, subglacial sediments, proglacial soils, and glacier rivers). We determined amplicon sequence variants (ASVs) providing us with a more precise resolution of genetically distinct lineages; ASVs were taxonomically determined by mapping on a phylogenetic tree constructed from nearly full-length sequences of *Comamonadaceae* and other Burkholderiales representatives. We found the majority (85 %) of ASVs affiliated to *Rhodoferrax*, *Polaromonas*, and *Delftia*, genera which we found to be ubiquitous among samples of various sources, but their proportional abundances differed suggesting potential environmental selection. Within these genera, various genotypes showed different distribution among samples, suggesting environmental overdispersion of closely related species. The fate and microdiversity of *Comamonadaceae* recovered from the cryosphere will also be discussed.

Microbial ecology of co-inhabiting prokaryotes in snow and ice biomes on the GrIS

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Abstract

Microbial communities blooming in the summer melt season on snow and ice surfaces are dominated by eukaryotic green algae (Chlorophytes and Streptophytes, respectively) and their diversity is usually extremely low. We know from amplicon-based studies that the phylogenetic diversity of co-inhabiting prokaryotes is far greater. This suggests that prokaryotic genomes account for a major part of the functional variety in these snow and ice biomes. We hypothesize that the functional potential of the prokaryotic community is linked to their eukaryotic partners and thus differs between surface snow and ice biomes. We analyzed metagenomes sequenced from glacial snow and ice-algae-rich samples from the Greenland Ice Sheet (GrIS), both at a genome resolved (MAGs) and contiguous-sequence based level. Our results show the existence of a prokaryotic core community found to be present in both biomes. However, 10% of MAGs and 20% of total functions were linked to either snow or ice biomes. Functions involved in nitrogen and sulfur assimilation were enriched in the ice habitats. Additionally, as exopolysaccharides (EPS) are thought to play key roles in community dynamics in these extreme environments, we investigated EPS production and degradation potential using the carbohydrate active enzyme database (CAZy). We combine these data with paired metatranscriptomic data to provide a more in-depth understanding of the prokaryotic co-community on snow and ice surfaces during summer melt at the GrIS. The resulting dataset will serve as a backbone in future studies investigating relationships between prokaryotes and cold-adapted glacier ice and snow algae.

Screening for bacteria with antiviral activity in Swiss alpine lakes

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Abstract

Viruses are one of the main mortality causes among human populations worldwide and yet, the range of antivirals nowadays available is alarmingly limited. It is therefore urgent to discover new antiviral compounds to fight against viral pathogens. In alpine lakes, extreme environmental conditions and low nutrient concentrations may limit the abundance of bacteria grazers. Consequently, bacteriophages can exert an important evolutionary pressure on bacteria inhabiting alpine lakes. Our hypothesis is that these lakes may be excellent environments for the discovery of novel antivirals of bacteria origin. To test this hypothesis, we conducted a field campaign in 24 alpine lakes in Switzerland and obtained a culture collection of 223 isolates of bacteria. All isolates were infected with a cocktail of environmental phages and the resultant phage yield was determined. Potential resistance to bacteriophage infections was detected in 75 out of 223 bacteria cultures isolated from the studied lakes. In addition, we conducted virus inactivation experiments spiking Influenza virus and human echovirus in water from each lake to determine if the bacteria communities in the lake water produce extracellular enzymes capable of inactivating human pathogens. Our results showed that the bacteria communities in two of the lakes could inactivate human Influenza virus and echovirus. In summary, we have successfully identified antiviral activity among bacteria communities of Swiss alpine lakes. This work may hopefully lead to the discovery of new antiviral compounds. Furthermore, our findings emphasize the importance of the conservation of alpine lakes as hotspots of microbial diversity and unknown metabolic richness.

Giant virus presence on Greenland Ice Sheet environments through metagenomes

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Abstract

Giant viruses are ubiquitous in marine locations and are known to infect algae. These giant viruses exert a pressure on the algal population and are responsible for cycling biomass within the marine environments. Algae are also known to be present on the surface of glaciers and ice sheets, but viral control on algal blooms is unknown within this cryogenic environment. Metagenomic libraries from red snow, dark ice and slush samples show Giant Viral marker genes. The red snow algae samples yield a potential Mimiviridae Giant Virus Metagenome Assembled Genome. Transcripts from the same sample supply evidence that this potential Mimiviridae VMAG could be active in this environment. These preliminary results demonstrate that Giant Viruses are present on the Greenland Ice Sheet in environments and could act as potential control of snow algal blooms.

Isolation of viruses infecting Acidobacteria from Arctic tundra soil

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Abstract

Acidobacteria are phylogenetically and physiologically diverse soil bacteria and play important roles in key ecological processes, such as biogeochemical cycles. Little is known about virus-host interactions in tundra soils, where Acidobacteria are abundant. Here, we report the isolation of the first known virus isolates infecting Acidobacteria from Kilpisjärvi tundra soils, Lapland, Finland (69° N). The five isolated viruses have double-stranded DNA genomes of 63–309 kbp in length and 51–58% GC content. Over a half of predicted open reading frames (ORFs) in each virus had no homologs in public databases. From the five isolates, two were closely related, having around 88% overall nucleotide identity, while the others were not similar one to another. Among the annotated ORFs, the predicted functions included DNA replication and modification, RNA processing, transcription and translation regulation, virion structural components, and cell lysis. Putative auxiliary metabolic genes involved in carbon and phosphate metabolism were also predicted. The presence of ORFs putatively encoding tail structural proteins suggested that the isolated viruses display tailed particles and belong to the order Caudovirales.

Culturing of the glacier ice algae *Ancylonema Nordenskiöldii*

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Abstract

Dark pigmented microalgae, glacier ice algae, inhibit the ice surface of the Greenland Ice Sheet. They contribute to the darkening of the ice surface, resulting in an increase of ice melt. No cultures of the glacier ice algae *Ancylonema alaskana* or *Ancylonema nordenskiöldii* have been established to date. Since no stable laboratory cultures are available, basic knowledge of growth rates and growth requirements are not known. By performing screenings of different media at different concentrations, pH, light intensities and temperature conditions, and solid vs liquid media, cultures of *A. nordenskiöldii* have been established for the first time, kept alive, and growing for nearly 2 years. To confirm the identity of the cultures, sanger sequencing was carried out using a region of the ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (*rbcL*) gene. With these cultures, growth curves have been recorded and an estimated doubling time calculated. These can later be used in biogeochemical models to estimate glacier ice algae growth and their further spread on the Greenland Ice Sheet.

Building bridges between researchers and local Greenlandic communities

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Abstract

Greenland is central for understanding the Arctic and the effects of climate change, resulting in high international interest and numerous researchers coming to Greenland for sampling. Despite research in the Arctic being valuable for society locally and globally, knowledge is generally not shared with local Greenlandic communities, and local knowledge is often not included and perceived as a valuable contribution to natural science studies. It is a problem that there is an imbalance in local communities not having access to the research conducted in Greenland. Our study will investigate how Dialogue Based Communication can lead to more collaborative and equitable exchange of knowledge between international researchers and local Greenlandic communities with both parties benefitting. This study will contribute to the EU ERC-Synergy research project, Deep Purple, which investigates the physical and microbial processes that darken the Greenland Ice Sheet and accelerate sea level rise. By mapping out the perceptions between researchers and locals and learning from previous experiences and cases of science communication, we will identify possible barriers and challenges preventing equitable exchange of knowledge. These results will be used to develop a communication product which will facilitate an inclusive Dialogue Based Communication product which has the intent to facilitate exchange of knowledge between the researchers of Deep Purple and local Greenlandic communities. The communication product will be developed using a new approach to scientific communication including aesthetics and interactive formats with the intent to explore new ways in which natural science can be shared.

Microbial diversity in ice samples collected in the vicinity of Concordia Base, Antarctica

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Abstract

Despite the surfaces of icy moons may be so diverse that no one location on Earth can perfectly reproduce those conditions, planetary scientists and astrobiologists agree that Antarctic polar plateau may represent a good analogue. There, specific conditions mimicking processes found on icy worlds may lay the foundation for ways in which their exploration fits into the overall strategy of Space Agencies Programs. Antarctic ice sheet, may also serve as excellent proving grounds for microbial adaptation, given that resident microorganisms may have acquired the ability to resist sub-zero temperatures, wide temperature fluctuations, high doses of solar UV radiation, osmotic pressures, and very low nutrient availability. This study is a part of the BacFinder project and aims to investigate the microbial diversity in snow/ice surface of the Polar Plateau in the vicinity of the Concordia Antarctic Research Station, the most confined and extreme environment on Earth. Yet, human fluxes can alter the eventual resident microbial composition in this pristine environment. We here investigated, for the first time, microbial diversity on polar plateau surface and the amplitude of human impact in its composition around Concordia Station. To accomplish this goal, we sampled ice/snow surface in monthly intervals (to highlight possible effect of seasonality) over one year and at distances of 0m, 500m, and 1000m. Using high throughput amplicon sequence approach, we found that Fungi were mainly represented by Basidiomycota (49%) and Ascomycota (42%), whilst Bacteria mainly by the phyla Bacteroidetes (68%) and Proteobacteria (26%). Despite Ascomycota is the largest phylum of the fungal kingdom, a greater predominance of Basidiomycota was here found; yet a conspicuous presence of basidiomycetous yeasts is reported in cold environments. We found that bacterial core was more similar in term of biodiversity within the samples in the winter season, probably due the harsh and stable winter condition.

Comparison of extraction methods for recovery of nucleic acids from subglacial sediments

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Abstract

Obtaining high-quality nucleic acids from extreme environments is challenging, especially when microbial biomass is low. To address this issue, we designed a methodological study aiming to compare established extraction protocols in terms of DNA and/or RNA yields and characterization of bacterial and archaeal diversity. In the proposed study we will use a subglacial sediment sample collected from the Issunguata Sermia glacier terminus (West Greenland), which will be sterilized (γ -irradiation) and spiked with a self-designed mock community containing strains typical of the subglacial microbiome (i.e. combination of bacterial taxa *Polaromonas glacialis* DSM 24062, *Methylophilus sp.* DSM 102653, *Thiobacillus sp.* DSM 612, *Desulfosporosinus meridiei* DSM 13257, and an archaeon *Methanococoides burtonii* DSM 6242). A blank sample and a non-sterilized true sample will be extracted alongside using similar extraction protocols. The following extraction kits and methods (9 in total) will be used and compared: DNeasy PowerSoil[®] Pro kit, DNeasy PowerMax[®] Soil kit, RNeasy PowerSoil[®] Total RNA Kit complemented with DNA Elution Kit, E.Z.N.A.[®] Soil DNA Kit, FastDNATM Spin kit, NucleoBond RNA Soil and DNA Set for NucleoBond RNA Soil, successive extractions using the FastDNATM Spin kit, successive extractions using the DNeasy PowerSoil[®] Pro kit, and the Griffith's protocol (CTAB - phenol-chloroform-isoamyl-alcohol protocol). Following the extractions, we will quantify nucleic acid yields using a Qubit fluorometer, and a real-time PCR assay will be used to evaluate the success of different extraction protocols in the recovery of the mock community's DNA. Additionally, we will perform PCR amplification of the 16S rRNA gene followed by next-generation sequencing. Finally, we will assess the quality of the sequence reads and characterize the microbial community composition recovered using downstream analyses.

Impact of a temporary lagoon in the high-altitude microbial communities in the Barrancas Blancas area (Chile)

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Abstract

The high mountain deserts represent examples of harsh environments characterized by extreme aridity, intense solar UV radiation and extreme shifts in daily temperature. The Barrancas Blancas area in the high Atacama Andes of Chile (~5000 m a.s.l, 68°39' W, 27°02' S) is a unique spot for the study of extremophilic microorganisms due to the harsh surroundings. In this area the water is scarce, and it is the main limitation for life and activity. The water could be present in glaciers, snowfields and ice-rich permafrost. Melting and thawing processes originate seasonal lakes and lagoons which can impact the activity of microbial life. Specifically, in Barrancas Blancas, there is a small temporal lagoon with a range size of 1.5 to 3.0 km². We propose that this temporary lagoon is a hotspot for life and therefore we designed a DNA/RNA-based study along a moisture transect through the lagoon to evaluate the effect on shaping the microbial communities and processes. Water and soil samples of different depths along the transect were taken in spring 2022. For the molecular analysis, we used a novel protocol to separate the intracellular DNA (iDNA) which represents the living community (active or dormant) from the extracellular DNA (eDNA) which might represent dead communities. Preliminary data shows recoverable DNA and the 16S amplicon sequencing data shows highly specialized microbial communities with respect to the moisture gradient and the permafrost dynamics

BCCM/ULC: a public culture collection to conserve ex situ the polar cyanobacterial diversity and taxonomic reference strains

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Abstract

The BCCM/ULC public collection (<https://bccm.belspo.be/about-us/bccm-ulc>) aims to gather a representative portion of terrestrial, freshwater and marine cyanobacterial strains from different ecosystems with a focus on the polar diversity (140/272 strains). Amongst the 243 strains, for which the 16S rRNA gene sequence was determined, 93 OTU's (99% 16S rRNA similarity) were recognized. It includes the taxonomic references (or 'type') for two taxa collected in Antarctica, *Plectolyngbya hodgsonii* and *Shackletoniella antarctica*. The collection's goal is to preserve the deposited biological material, to valorize it by performing research on it, to provide it to interested parties for fundamental and applied research, and to provide services linked to the identification of the Cyanobacteria for the scientific community. An ISO 9001 certificate was obtained for the public deposition and distribution of strains, as part of the multi-site certification for the BCCM consortium. A dozen genomes are presently being sequenced. For example, for the FRIA project BI-HABITAT, four genomes were sequenced and assembled: *Nostoc spp.* ULC180 (coverage: 94.11 %, assembly: ~6.3 Mb), ULC008 (coverage: 98.11 %, assembly: ~6.1 Mb), and ULC046 (coverage: 85.5 %, assembly: 6.2 Mb), as well as *Phormidium autumnale (Microcoleus favosus)* ULC128 (coverage: 99.71 %, assembly: ~7.1 Mb). Given their origin from the harsh environments of polar biotopes, the discovery of genes related to particular adaptations as well as novel molecules may be expected. Accordingly, methanolic extracts obtained from *Phormidesmis priestleyi* ULC0026 (sister to ULC007 for which the genome was already published) and from *Plectolyngbya hodgsonii* ULC009 showed, respectively, bioactivity against the fungus *Cercospora sp.*, an important causal agent of plant diseases, and against *Candida sp.*, that can cause human infections (candidiasis).

Antarctic ascidian-associated bacterial culture collection reveals genomes rich in biosynthetic gene clusters and genomes harboring signatures of cold adaptation

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Abstract

Natural products synthesized by host-associated microbes from polar regions pose tremendous potential for addressing human health challenges. One prominent example is the newly recognized verrucomicrobium, *Candidatus Synoicohabitans palmerolidicus* associated with the Antarctic ascidian *Synoicum adareanum*. This bacterium is of interest in part due to its genome-encoded biosynthetic capacity to produce palmerolide A, a macrolide with antimelanoma specific activity. Here we tested the hypotheses that the *S. adareanum* microbiome may harbor a wealth of biosynthetic novelty, and that the host-associated bacteria contain genomic signatures unique to evolutionary selection pressures experienced in polar ocean systems. A large cultivation effort was launched targeting psychrophilic bacteria, and although palmerolide A-targeted PCR screens thus far have been negative, at least 30 unique bacterial cultures were identified through 16S rRNA gene sequencing. Our cultivation strategy utilized single carbon sources, increasing the phylogenetic breadth of cultured, slow-growing bacteria from this ascidian host to include 4 additional classes and three phyla. Through mining 22 whole genomes, we identified 135 candidate biosynthetic gene clusters dominated by ribosomally-synthesized and post-translationally modified peptides, amino acid metabolism, nonribosomal peptide and polyketide synthases. To evaluate traits of cold adaptation, publicly available genome sequences were compiled from organisms belonging to the same genus as the Antarctic isolates but from low/mid-latitude marine environments (+/- 45 degrees latitude). Comparisons of pairs of predicted orthologs from both the Antarctic and low/mid-latitude genomes revealed that proteins of Antarctic organisms often exhibit specific biases in their amino acid composition typically found in cold adapted proteins. Protein intrinsic disorder analyses indicated that proteomes of Antarctic isolates were often less disordered than their lower latitude counterparts. The results from this secondary metabolite and cold-evolution study open the doors to the secondary metabolic repertoire of the ascidian microbiome and may guide future engineering of cold-adapted microbes for efficient production of natural products.

Biodiversity and biochemistry of ice-based bacterial communities in East-Antarctica

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Abstract

Active microbial consortia are present in the oligotrophic and perennially ice-covered Lake Untersee within the Wohlthat Mountains, East Antarctica. The lake is dammed by the adjacent Anuchin Glacier with a 0.68 km² large ice wall and has been subject of numerous hydrological and biological studies. The glacier itself consists of two ice lobes and a dark-colored medial moraine that is fed by a nearby Nunatak. Based on shallow surface ice cores, we hypothesized that different origins of these ice lobes and the medial moraine are reflected in the stable water isotope ratios, ice chemistry, and microbial community composition. The stable water isotope ratios with respect to the Vienna Standard Mean Ocean Water (VSMOW) indicated that the isotopic enrichment differed according to their respective ice sources. Further, the ice along the medial moraine was most likely of deep Pleistocene origin. The ice lobes also differed in their chemistry, such as nitrate, sulfate, ammonium, magnesium, and total phosphorus contents. Based on 16S rRNA NGS amplicon sequencing, the most abundant ribosomal sequence variants (RSVs) belonged to the phyla Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes, and Cyanobacteria. A network analysis revealed that 48% of all RSVs were unique and most of them were present along the medial moraine. Alpha diversity indices differed significantly – but not across all sites. Further, a constrained analysis of principal coordinates indicated that microbial communities of one ice lobe and the medial moraine clustered together while samples from the second ice lobe did not show a clear pattern. Overall, differences in biological, isotopic and chemical signatures across the Anuchin Glacier support our initial hypothesis. To answer if these differences are more pronounced at a larger geographical scale requires sampling with higher spatial resolution.

Greenland ice sheet as a model for microbial macroecology

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Abstract

Ecological processes at large scales are studied in complex ecosystems that are shaped by multiple factors at various scales. Moreover, many fundamental (macro)ecological questions become difficult when applied to microorganisms, due to the complexity and dynamics of their communities. As a result, microbial macroecology is still in its infancy. Here we present research that overcomes these problems by using a simple model ecosystem – the surface of the Greenland Ice Sheet (GrIS). The principal aims of the project are to gather a unique microbial community data set from the surface of the GrIS and to use this data set to test key macroecological hypotheses concerning assembly rules of microbial communities and spatial patterns in the distribution and diversity of phylogenetic vs. functional groups of microorganisms at different taxonomic levels. We expect this research will bring novel insights into two fields of ecology – macroecology and microbial ecology – by combining the expertise and methodologies of both disciplines. Here we present the progress of the project entering its analytical phase with the first sequencing result from the final sample set from the Greenland ice sheet surface.

Vertical and spatial distribution of microbial populations in Svalbard soil

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Abstract

The effects of climate change on Arctic soils and its inhabitants have not yet been well understood, therefore spatial biodiversity and microbial biogeography in polar habitats represent growing interests. A total of 56 soil samples were obtained in April 2018 and August 2019 from active layer cores collected in Svalbard, Norway (79°N) in close proximity to the Bayelva long-term climate monitoring station. The samples were from different soil layers up to 0.6 m depth and the distance between collection sites varied from 30 m to 375 m. The total community genomic DNA was extracted from 1 g of soil using a QIAGEN PowerSoil DNA Kit. Metagenome libraries were prepared using the SMARTer ThruPlex DNA-seq with 350 bp average fragment size and sequenced on Illumina NovaSeq. The metagenome sequencing reads were assembled into 169 genomes with $\geq 50\%$ completeness and $< 10\%$ contamination and taxonomically identified with GTDB-Tk. The abundance and distribution of metagenome assembled genomes (MAGs) across all samples was studied. Among the MAGs, 1 archaeal and 11 bacterial phyla were identified. The most dominant phylum with 60 MAGs was Acidobacteriota, followed by Actinobacteriota (n=52), Chloroflexota (n=24), Proteobacteria (n=16), Planctomycetota (n=5), Gemmatimonadota (n=3), Verrucomicrobiota (n=3), Thermoproteota (n=2), and 4 singleton MAGs from the phyla Bacteroidota, Cyanobacteria, Eisenbacteria, and Methlomirabilota. MAGs distribution computed with metaWRAP's showed that MAGs correlated to other MAGs from the same location or depth but not from different sites or the same phylum. The current study showed that microbial populations in the Svalbard active layer are season, site and niche specific. More metagenome monitoring studies from the same location are needed to determine factors responsible for distribution of microbial populations.

Steps towards the analysis of Greenland Ice Sheet metaproteomes

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Abstract

Microbial communities dominated by eukaryotic algae thrive during summer melt on the Greenland Ice Sheet and on other supraglacial environments globally. Chlorophyte and cryptophyte algae grow on snow, while the dominant algal species on bare ice are streptophytes (*Zygnematophyceae*). The environmental conditions in which algal blooms develop include low temperature, high light, and low nutrients. These eukaryotes have specialised cellular mechanisms allowing them to survive, grow, and divide in these extreme conditions. However, despite our knowledge of species distribution and associated abiotic conditions, little empirical data currently exists that specifically examines these cellular adaptations. We aim to address this knowledge gap by identifying protein groups essential for the maintenance of cellular homeostasis under relevant environmental conditions. This includes the development of a novel workflow to analyse metaproteomes from snow and ice samples from the Greenland Ice Sheet. With this workflow, we quantify the abundance of algal protein under field conditions, as well as proteins from bacteria and fungi. Following a validated protein extraction protocol prior to LC-MS/MS analysis, we identified proteins using a predicted protein database built from metagenomic data representative of a Greenland Ice Sheet community similar to the analysed protein sample. We identified 11% of the recorded MS2 spectra that were assigned to bacterial, fungal, and algal proteins. Before applying this workflow to targeted environmental samples, further work will be undertaken to improve both the protein extraction efficiency and the MS data analysis in order to enhance the number of identified algal proteins.

A novel psychrophilic model organism: de novo snow alga genome

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Abstract

Green algae thrive in diverse environments, including high elevation alpine and glacier regions worldwide where they are exposed to high light levels, intense UV radiation, cold temperatures, and low nutrient availability. Despite these challenges, they are primary producers that support a rich community in the snow microbiome. Globally, blood-red snow algal blooms contribute to accelerating snow melt via the reduction of snow surface albedo. We have grown the first successful culture of snow alga that genetically matches with a red-pigmented species. Under lower light and warmer laboratory conditions, cells proliferated as green biciliates but were conspecific with the immotile orange species *Sanguina aurantia* seen in the field. We proposed this as a potential mechanism for how snow alga colonize the snow surface each summer, green motile cells swim up after overwintering where they then shed their cilia and accumulate astaxanthin as a hypothesized adaptation to intense UV exposure. The availability of culture provides an invaluable opportunity to sequence and assemble a reference snow alga genome. Using a hybrid approach, we incorporated Oxford Nanopore long-reads, Illumina short-reads and high-throughput chromatin conformation capture mapping (Hi-C analysis) to generate a de novo draft genome of *S. aurantia*. Our current assembly metrics indicate a complex genome with a size of 180 Mbp, 55% GC content, N50 of 4 Mbp, and is made up of 107 contigs. By comparison to other algal species, both temperate and cold-adapted, we hope to identify shared and unique gene families related to the abiotic stressors of life on snow. As a new potential model organism to study psychrophilic adaptations, this work will set the foundation for future algal evolutionary research as well as fill gaps in our current knowledge of how snow algae contribute to the decline of snowfields worldwide in an ever-warming climate.

Different resistance mechanisms to desiccation of a pair of *Nostoc* sp. strains from aquatic and terrestrial habitats of Antarctica

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Abstract

Cyanobacteria are photosynthetic autotrophic microorganisms that can survive in a variety of extreme environments around the world, such as polar regions. They usually live in association with other organisms and form biological soil crusts in terrestrial environments or thick benthic mats in aquatic environments, where they can develop particular structures such as benthic pinnacle mats. Cyanobacteria have developed different resistance traits to cope with extreme and contrasted environments, such as the production of pigments to absorb UV radiation, or a polysaccharidic matrix to withstand desiccation. However, a better understanding of their ecophysiological mechanisms is necessary to clarify how these processes work. In the present study, the ecophysiological performance of two *Nostoc* sp. strains was investigated under dehydration and subsequent re-hydration stress. The chosen pair of strains shares 100 % of 16S rRNA gene similarity but have different ecologies. Strain ULC180 and ULC008 from the BCCM culture collection were isolated from a granitic outcrop in the Sør Rondane Mountains (East Antarctica) and from an Antarctic lake (Larsemann Hills, East Antarctica), respectively. To determine their capacity to withstand desiccation, both strains were cultured in BG110 medium, then left dehydrating onto filters placed into a desiccation chamber until complete desiccation (Fv/Fm around 0) and re-hydrated for up to 72 h. Samples for pigments, exopolysaccharide (EPS) and RNA extractions were taken when the desiccation was complete and after 10 min, 2 h, 24 h and 72 h of rewetting whilst Fv/Fm was measured before sampling. Our preliminary EPS and pigments results suggest a higher resistance of the terrestrial strain to desiccation. However further analyses of the gene expression by RNA-seq are in progress for a better understanding of the different mechanisms developed by these two strains.

High concentrations of volatile fatty acids and methane production upon thaw of yedoma permafrost

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Abstract

Northern permafrost ecosystems store about 50% of the global below-ground organic carbon pool, and due to the present and projected climate warming, permafrost soils are subject to widespread thaw, resulting in microbial decomposition of previously frozen organic carbon and the release of greenhouse gases (GHGs). This might be one of the most important climate-carbon feedbacks from terrestrial ecosystems to the atmosphere. Yedoma permafrost are particularly organic- and ice-rich and are thus extremely vulnerable to global warming. This study investigated a vertical section (90 cm - 250 cm depth) of Yedoma permafrost from a thermokarst area in Fairbanks, Alaska. Concentrations and dynamics of volatile fatty acids (VFAs) and overall anaerobic microbial activity, including acetoclastic methanogenesis, were determined shortly upon thawing of the permafrost. The results showed high concentrations of VFAs, especially acetate, immediately or shortly upon thawing, thus indicating an accumulation of fermentation and acetogenesis end products before permafrost thaw. Further, anaerobic respiratory processes were observed to be subject to a lag-phase before establishment of sustainable populations were achieved, and a decoupling of acetate producing processes and acetate consuming processes was thus observed. The presence of alternative terminal electron acceptors, such as nitrate and sulfate, was relatively low and a significant production of methane was observed just 40 days upon thawing, indicating that methanogenesis could be the predominant process in the investigated permafrost soil in a near future.

Characterization of particulate organic matter in algae-dominated glacier ice environments

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Abstract

The terrestrial cryosphere is considered a unique biome and is home to diverse microbial communities, including microalgae. These microalgae produce 'sticky' extracellular polymeric substances that bind cellular materials and mineral dust into mineral-organic aggregates. In turn, these aggregated particulates darken the snow and ice surfaces and increase melting by lowering their albedo. Information on the chemical nature and reactivity of such particulate organic matter is critical to understanding its potential to fuel snow and ice microbial communities and assess the dynamics of carbon on glaciers and ice sheets globally. In this study, we evaluated various chemicals (ranging from polar to non-polar solvents and from acidic to alkaline solutions), extraction conditions (temperature, time), and sample preparation methods (sonication, freeze shock), to obtain the most efficient method for the extraction of organic matter (OM) from algae-dominated, but carbon poor (< 1 wt %), particulate-rich ice samples from Iceland and Southeast Greenland. To validate our extraction protocols, we complemented these natural samples with a synthetic reference mineral-organic mixture. We estimated the extraction yield by total organic carbon analysis and measured the composition of extracted OM using high-resolution mass spectrometry. We achieved recoveries between 12 and 87% of the total organic carbon, depending on the extraction method. This is up to 6-times higher than previously reported (1-15%) for low carbon sediments. These results allowed us to gain insights into the source and nature of particulate OM of algae-dominated ice surfaces and improve our understanding of this understudied component of the glacier carbon pool.

Soil N, P and K mineralization and CO₂, CH₄ and N₂O production from Kurungnakh Island, Lena River Delta, Siberia, at different incubation temperatures

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Abstract

Global warming causes permafrost thawing, exposing additional organic matter for decomposition. Yet, additional warming and increase of CO₂ concentration in the atmosphere enhance net primary productivity (NPP) of arctic vegetation. Some authors argue that such higher NPP would be constrained by nitrogen (N) and phosphorus (P) availability in future, and indeed such constraints were identified experimentally. Thus, arctic terrestrial ecosystems would be most likely a source than a sink of carbon in future. However, nutrient mineralization is also a temperature sensitive process, due to the effect of temperature on the activity of the enzymes responsible for extraction of these nutrients from the organic matter. Thus, the response of nutrient availability to warming remains a source of uncertainty on future climate-carbon feedbacks. Additionally, increased temperature affects the production of different greenhouse gases differently, converting the ecosystem in either a source or sink of CO₂, methane (CH₄) and nitrous oxide (N₂O). To address these questions, we incubated active layer samples from organic and mineral horizons from three sites in Kurungnakh Island, Lena River Delta, Siberia, keeping the original moisture conditions in the field, under 4°C and 15°C, to assess the effect of the additional warming in the N, P and K mineralization and availabilities, and in the production of CO₂, CH₄ and N₂O.

Biodiversity of Antarctic lichen bacterial communities (a comparison of cDNA and gDNA 16S rRNA gene amplicon sequencing)

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Abstract

Lichens have achieved an astounding ecological success, evidenced by their ability to colonize barren territories across nearly every latitude, from the Arctic to Antarctica. This success is mainly due to the components that make up a lichen and their activity: the heterotrophic fungus, the photoautotrophic partner, as well as the microbiome inhabiting the lichen. While the former two components have been studied thoroughly, the microbiome (which is predominantly bacterial) and its relationship with the remaining components has not yet been fully understood, especially in the context of its contribution to the survival in unfavourable conditions, such as those in polar environments, where the abundance of nutrients may vary extremely. Thus, the aim of this study was to investigate the bacterial composition and determine the active bacterial fraction of six Antarctic lichens from two sites on King George Island, Maritime Antarctica: a nitrogen-rich site in the vicinity of a penguin rookery, and a nitrogen-depleted area surrounding Jardine Peak. This was achieved with the use of 16S rRNA gene amplicon sequencing of genomic, as well as complementary DNA. Preliminary results show a discrepancy between the bacterial composition of the total vs. active lichen bacteriome in the varying nutrient habitats, with Acidobacteria defining the nutrient-depleted area and Bacteroidetes the nutrient-rich site.

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The impacts of browning on the structure and function of sub-Arctic alpine dry heath communities

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Abstract

High latitude ecosystems are experiencing vegetation changes in response to long-term warming. The trend is often in the direction of increased productivity and vegetation cover ('Arctic greening'); however, we also observe declines in vegetation productivity and cover due to additional stress and damage associated with abiotic and biotic extreme events ('Arctic browning'). There are many potential drivers for Arctic browning events, all of which can have detrimental consequences to vegetation with cascading effects for other organisms and ecosystem processes, most notably for carbon exchange. Microorganisms are abundant in these ecosystems, significantly contributing to the carbon cycle. Plants have been the primary focus of browning studies, while very little is known about plant-soil interactions under such conditions. We conducted vegetation surveys, gas flux measurements (CO₂ and CH₄), and analyzed the structure and function of the soil microbial community in a naturally occurring browning site near the Latnjajaure Field Station, northern Sweden. There were two dominant plant species, *Empetrum nigrum* (E) and *Cassiope tetragona* (C), experiencing browning, so we demarcated healthy (H) vs browning (B) plots for each species. Plant species diversity between the plot types was distinct, with browning plots supporting more diversity than healthy plots. Browning plots for both species became a net source of CO₂, and the BC plots were the greatest net sink for CH₄. Bacterial alpha and beta community diversity differed between the vegetation types, while the beta diversity also differed between BE and HE plots. HC plots had the highest 16S gene copy abundance, while BE plots had the highest 18S gene copy abundance. This study demonstrates that Arctic browning influences plant-soil interactions resulting in shifts in the structure and function above and belowground with consequences for net carbon exchange.

Seed microbial diversity and composition of *Silene acaulis* across a European latitudinal gradient

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Abstract

Seed is an essential stage in the life cycle of a plant. Increasing evidence shows the vital role of seeds in transmitting a core microbiome from one generation to the next; an initial inoculum of beneficial microbes will help the plant's health and fitness. This study explores the unknown seeds bacterial endophytes community in the foundational Alpine-Arctic plant *Silene acaulis* and how the microbial communities vary spatially and temporally. To reach this scope, capsules containing seeds have been collected since 2018 from five regions: High Arctic, Subarctic, Central Alpine, and Southern Alpine. The DNA extracted from the surface-sterilized seeds was processed by Illumina sequencing. The results explore the seeds' bacterial communities at a resolution from Phylum to Species-level. The dominant bacteria and shared core microbiome are detected across regions, individuals and time. The unique bacteria Phyla-Species present across regions and years are detected with a particular focus on critical ecological bacteria. In addition, we are trying to understand how much the plant growth region explains microbial community composition.

List of participants – PAM2022

Institutions and abbreviations

AWI = Alfred-Wegener-Institut für Polar- und Meeresforschung (Alfred-Wegener-Institute for Polar and Marine Research)

CUNI = Charles University in Prague

CRREL = US Army Cold Regions Research and Engineering Laboratory

DLR = German Aerospace Center

EPFL = École polytechnique fédérale de Lausanne (Swiss Federal Institute of Technology in Lausanne)

GFZ = GFZ German Research Centre for Geosciences

IBB-PAS = Institute of Biochemistry and Biophysics Polish Academy of Sciences

MPIMM = Max Planck Institute for Marine Microbiology

NCPOR = National Centre for Polar and Ocean Research, Ministry of Earth Sciences, India

NHM = The Natural History Museum London

NMBU = Norwegian University of Life Science

LUKE = Natural Resources Institute Finland

QMUL = Queen Mary University of London

SUNY Upstate = State University of New York Upstate Medical University

UiT = The Arctic University of Norway

ULiège = University of Liège

UNIS = University Centre of Svalbard

UNITUS = Università degli Studi della Tuscia (Tuscia University)

UNN = Northumbria University Newcastle

WSL = Swiss Federal Institute for Forest, Snow and Landscape Research

WWU = Western Washington University

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