

Microbial dispersal limitation to the McMurdo Dry Valleys of Antarctica

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Airborne microbial transport is assumed to occupy a central role in determining dispersal outcomes and extra-range dispersal has important implications for predicting ecosystem resilience and response to environmental change, particularly in Antarctica. Here we describe airborne and soil microbial diversity in the largest ice-free soil region, the McMurdo Dry Valleys, and identify that airborne bacteria and fungi form distinct assemblages from those in underlying soil. Extant soil communities could not be explained by recruitment from regular and persistent aerial inputs alone. Near-ground aerosols and those above the boundary layer for surface influence displayed only limited evidence of microbial exchange suggesting dispersal is largely a local process. Comparison with aerosols sourced from the nearest significant non-polar land mass at the limits of predicted microbial residence time during aerial transport to Antarctica suggested exogenous immigration of airborne microorganisms may be low. Comparison of our empirical data for airborne dispersal with predictions from current theoretical models suggests that biotic traits may exert deterministic influence on dispersal outcomes and this may need to be incorporated into future models. This study provides the first empirical support for dispersal limitation to the major ice-free soil region of Antarctica due to constraints on aerial transport, and yields new insight on potential microbial connectivity in the global system.

Photosynthetic pigment compositions of cyanobacteria in cryoconite in Greenland

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Cryoconite is a microbe-mineral aggregate found on glacier surfaces around the world. Cyanobacteria, photosynthetic prokaryotes, often dominate both the biomass and the carbon fixation via photosynthesis in cryoconites. Cyanobacteria contain pigmented compounds, mainly light absorbing pigments related photosynthesis (chlorophyll a and phycocyanin) and photoprotection (carotenoids and scytonemin). Therefore, composition and concentration of the intracellular pigment may directly affect the photosynthetic activity and the resistance to high-intensity solar radiation. In this study, we tried to reveal the relationship between species, pigment compositions and photosynthetic activity of cyanobacteria in cryoconite collected on Greenland glaciers. High-performance liquid chromatography identified chlorophyll a and carotenoids (zeaxanthin, echinenone, B-cryptoxanthin and B-carotene) as pigments of *Phormidesmis priestleyi* isolated from cryoconite on Qaanaaq Glacier of northwest Greenland. The dark-colored pigment, scytonemin, was identified in cryoconite collected from the Issunguata Sermia Glacier of southeastern Greenland, and its concentration spatially varied on the glacier. We measured the CO₂ concentrations in cryoconites by gas chromatography and mass spectroscopy. We discuss the light-adaptation strategies of cyanobacteria in cryoconite.

Comparative genomics of Psychrobacter reveal habitat-specific characteristics

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The diversity of habitats from which Psychrobacter have been isolated (e.g. cold marine environments, frozen soils, permafrost, and humans) provides a unique opportunity to examine habitat specific adaptations while reducing phylogenetic effects. Here, the genomes of 26 strains of Psychrobacter are compared to discern differences due to habitat. Phylogeny is established by comparing average nucleotide and amino acid identity. The pan genome of the genus is described and the gene content of strains and habitats examined. Amino acid characteristics that represent potential cold adaptation traits of genes are examined both genome-wide and within homolog groups. Psychrobacter strains associated with warm hosts have amino acid composition typical of mesophiles (e.g. higher proline and lysine content), distinct gene content (e.g. a collagenase-like protease), and less acidic proteomes than other Psychrobacter. Marine and terrestrial Psychrobacter share many genes not found in warm host Psychrobacter (e.g. FadB) and have many potentially cold-adapted core genes (e.g. ClpX, DsbC, GroEL/GroES and MutS2). Furthermore, terrestrial Psychrobacter were differentiated from marine Psychrobacter by the use of different cold adaptations and more hydrophobic and aliphatic proteins. These data suggest that terrestrial and marine Psychrobacter evolved from a mesophilic ancestor and are accumulating adaptations beneficial to low temperature growth as well as for their respective habitats.

Contaminant degradation in Arctic and sub-Arctic Alaska

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Effective remediation of military-relevant contaminants in Arctic and sub-Arctic regions is challenging due to extreme environmental conditions and remote site locations. Namely the cold, oligotrophic soils with permafrost beneath have contributed to the persistence of contaminants for decades. Microbial degradation shows promise of being a cost-effective, non-invasive method of clean-up. We conducted two sets of laboratory and field-scale studies to determine the efficacy of bioremediation of petroleum in Utqiagvik, Alaska and energetics at an Alaskan military range soil in Ft. Greely, Alaska. Both the contaminant concentrations and microbial attributes were measured under cold to freezing conditions. For petroleum hydrocarbons in the Arctic, the combination of fertilizer and plants resulted in the greatest decrease of aliphatic and aromatic fractions of hydrocarbons, the highest microbial activity, and the highest number of aliphatic degrading genes. For the energetics study, we tested the effects of constant versus fluctuating negative temperatures on the soil microbiome and its ability to degrade 2,4-dinitrotoluene. The microbial communities shifted as a result of fluctuating temperatures. Results from these studies inform the application of remediation technologies in cold, remote locations through the investigation of the environmental factors that promote degradation.

Caudovirales drive viral-host competition in Antarctic microbial communities

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Antarctica is seen as one of the most forbidding environments for life on Earth. Despite the extreme abiotic stressors experienced in this polar ecosystem, a higher than expected diversity of psychrotolerant and psychrophilic microorganisms can be found across Antarctic habitats. Recent studies have shown that virus-host interactions may also play a role in diversification through contributions to nutrient cycling. However, studies on viral-host interaction in psychrophilic communities remain scant and their role as community-determining factors for Antarctic communities is unclear.

In the present study we assessed the abundance and importance of virus-host interactions by determining the presence of anti-phage systems in Antarctic metagenomes. Our analyses revealed that microbiomes in Antarctic niches harbour widespread innate immunity systems, CRISPR-Cas adaptive immunity as well as newly characterized defense systems. The abundance of innate immunity systems was found to be linked to abundant taxa such as Proteobacteria. Caudovirales were also shown to be the most abundant phages in these communities corroborating the co-occurrence of immune systems which are specifically tailored against this order.

Taken together, our data provide crucial insights regarding viral-host interactions in cold environments. In these systems, such interactions may be substantially affected by global change, with severe impact to microbial community structure and biogeochemical cycles.

Ecological Controls on Bacterial Community Structure in Antarctic Dry Valley Soils

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The Dry Valleys of Antarctica possess a unique ecosystem where environmental influences on microbial communities are expected to be readily identified in the absence of complex trophic structures. As part of The New Zealand Terrestrial Antarctic Biocomplexity Survey (NZTABS), it was our goal to describe the composition of the microbial communities in the Dry Valleys and to elucidate the environmental factors and ecological drivers that influence their structure. Soil samples were collected at 480 sites from an area >250 square km encompassing the Miers, Marshall, Garwood, and Hidden Valleys, and high-throughput DNA sequencing was used to characterize the bacterial community structure across samples. Bacterial community composition was found to vary significantly with respect to many of the landscape and physicochemical variables measured. Additionally, results of null modeling suggest that homogenous selection and dispersal limitation represent important ecological drivers of bacterial distribution across the landscape. This work contributes to an improved understanding of the microbial ecology of the Dry Valleys, and results from this work are being used to develop predictive ecological models that can be applied to the management of Antarctica's ice-free areas.

In situ hyperspectral imaging of the distribution and abundance sea-ice bottom algae

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Sea ice supports a unique assemblage of microorganisms that form the basic food supply for Antarctic coastal food-webs. Current core sampling techniques do not capture the natural variability in this assemblage, however, larger scale quantitative assessments of under-ice environments where these organisms are found are non-trivial. We tested a novel under-ice rig that remotely senses biophysical properties of 1m wide transects of fast sea-ice at millimetre-scale resolution. The payload consists of a hyperspectral imaging (HI) camera, a standard digital RGB camera, a spectroradiometer and an inertial measurement unit (IMU). The HI camera and the spectroradiometer estimated chlorophyll-a content at the sea water interface based on light transmitted through the ice column, the RGB camera provided under-ice structure through photogrammetric techniques and the IMU supported HI data composition. The payload slid underneath the ice at controlled speeds and the data was streamed to the surface in real-time. Three different transects 7 to 14 meters long were scanned with this method. This first deployment provided proof-of-concept of a novel underwater methodology capable of providing non-invasive and high resolution estimates of ice algal biomass, and some of its environmental drivers. Some preliminary results will be presented.

An Atlas of Arctic Marine Microbial Diversity Reveals the Uniquity of Sea Ice

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Microbial extinction is a controversial proposition due to the enormous population sizes of most microbes in the environment. Yet, ongoing melting of the million-year old Arctic sea ice cover may initiate such extinctions in microbes endemic to sea ice. While a number of meiofauna and algae have been identified as sea ice endemic by morphological analysis, little genetic evidence for endemism has been presented for sea ice microbes, including bacteria and archaea. In an effort to predict the potential for genomic extinction in sea ice as a result of ice loss, I will present biogeographical results from a set of 1500 samples analyzed using combined 16S rRNA, 18S rRNA, and ITS amplicon sequencing, along with phylogenomic analyses of metagenome-assembled genomes from 500 shotgun metagenomes of Arctic sea ice, seawater, sediment, and host-associated environments. These data reveal that many typical "sea ice bacteria" ESVs were found widely distributed throughout these habitats, particularly in particle-rich and host-associated environments like fecal pellets, suggesting that sea ice may be a secondary habitat for many of these copiotrophic bacteria. On the other hand, hundreds of ESVs were specifically associated with sea ice, particularly eukaryotic taxa including diatoms, dinoflagellates, ciliates, and others. Metagenome-assembled genomes recapitulated and extended previous findings of temperature-driven strain-level genomic variation in marine bacteria.

Uncovering microbial community diversity in Alaskan cryopeg brines

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Volumes of subzero liquid brine trapped in permafrost (cryopeg brines) are believed to have been isolated from the surface climate for many thousands, in some cases millions, of years. Inhabited by a surprising abundance of bacteria and viruses, cryopeg brines represent unique settings for asking questions about long-term adaptation to extreme conditions and the search for life in subsurface subzero brines of other planets or moons. We sampled cryopeg brines (-6°C , ~ 140 ppt salt) by drilling below a permafrost tunnel near Utqiagvik, AK, in multiple years to characterize the habitat and resident microbial communities. Most of the brines sampled contained remarkably high concentrations of bacteria ($\sim 10^8$ bacteria/mL) and millimolar amounts of nutrients and cryoprotectants. Amplicon sequencing of 16S rRNA genes revealed bacterial communities of low diversity (relative to subzero hypersaline sea-ice communities), sharing the dominant genera *Marinobacter*, *Gillisia*, and *Psychrobacter*. Temporal and spatial sampling patterns suggest an important role for physical stability (as well as substrate availability) in structuring these communities and enabling maximum carrying capacity under extreme conditions. Though sharing dominant genera, physically separated cryopeg brines varied in rare-member composition, suggesting the potential to develop differently in future, as environmental conditions change.

Excess carbon induces PHA production in Antarctic sea-ice bacteria

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Sea ice is a microbial habitat characterized by strong environmental gradients in time and space. In particular, low temperature and high salinity initially constrain microbial diversity in sea ice, but later algal-derived substrate supply is a key factor. Sea-ice bacteria possess different strategies to survive in the ice, however, these mechanisms are not thoroughly understood.

Polyhydroxyalkanoates (PHAs) are polyesters that serve e.g. as a pool for carbon storage, readily available for cellular processes. Commonly PHA is produced under excess carbon and low nutrient concentrations or during oxidative stress. PHA granules and *phaC* synthase genes have been detected from sea-ice bacteria, but the production mechanism and ecological significance is not known. We investigated if sea-ice bacteria are capable of PHA production and the genetic mechanism behind the production.

Batch experiments were conducted with two Antarctic sea-ice bacterial isolates. PHA-production was verified with transcriptomes, Nile-blue staining and GC-MS.

The results demonstrate that sea-ice bacteria are capable of producing PHAs. PHA production was induced in high and low nitrogen concentrations when excess carbon was available. We hypothesize, that PHA production in ice is related to the intermittent high availability of labile organic carbon (i.e. initial freezing and spring bloom). Thereafter there is carbon storage in PHA granules for enhanced survival in extreme environmental conditions.

Fungal community composition in permafrost and dynamics post-thaw

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Understanding the structure and function of the permafrost microbiome is critical to predict how permafrost ecosystems will respond to climate change. Despite the importance of fungi in soil carbon-cycling, the composition of fungal communities and their dynamics in thawing permafrost environments remain largely unexplored. We hypothesized that fungal community composition in permafrost would vary spatially across a landscape in response to soil physicochemistry, and that initial conditions would be important predictors of post thaw fungal community structure and function. To investigate this, we related fungal community structure to environmental composition in 59 permafrost samples collected across a landscape gradient in a boreal forest ecosystem near Fairbanks, Alaska and monitored community responses to thaw over 100 days of incubation at 4°C. Samples were dominated by Ascomycetes, with many of the most abundant OTUs grouping with fungi from other cold environments. Community composition varied spatially and a redundancy analysis model showed that 17% of the variation in community composition was explained by environmental variables, particularly nitrate and phosphorous concentrations, soil carbon composition, and soil texture. Initial community composition was a strong determinant of post thaw community composition, suggesting pre-thaw community characteristics may be important predictors of post thaw community structure and function.

Hydrocarbon Biodegradation along Canada's Northwest Passage Shorelines

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The Arctic is at an increased risk of an oil spill as global warming drives the opening of Canada's Northwest Passage. Characterizing how native microorganisms respond to oil exposure and determining the extent to which oil is naturally degraded will inform relevant bioremediation approaches. This project will comparatively assess microbial community composition and functional community potential in a natural state and in an altered state—following a controlled small-scale oil spill experiment, through culturing techniques and molecular approaches including 16S rRNA and metagenome sequencing alongside appropriate statistical and bioinformatic analyses. Moreover, microcosm experiments will be utilized to understand hydrocarbon biodegradation under controlled conditions within a laboratory setting, thus, providing insight to contrast microbial shifts between simulated and in situ Arctic conditions. It is hypothesized that shifts in the Indigenous Arctic shoreline microbial communities will be observed following exposure to hydrocarbons reflecting increased community hydrocarbon metabolism.

Ice Nucleation Potential and Microbiology of Natural and Artificial Snow

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Proceeding climate change effects minimized snow cover in skiing resorts globally. Artificial snow production becomes increasingly important to secure revenues and operating times of skiing resorts. The efficiency of artificial snow production depends on the ice nucleation characteristics of the input substrate.

For artificial snow production, ice has to form in a relative short amount of time and travel distance before the water droplets reach the ground. Technological efforts went into modern snow production devices with this main challenge in mind. Ice formation is determined by physical factors (temperature, humidity, droplet size), thus most technological research is focused into this direction. However, microbial and chemical substrate composition are important for artificial snow production, when physical conditions are less optimal. Atmospheric ice nucleating particles (INPs) have a considerable impact on ice cloud formation. Those can be of inorganic, carbonaceous or biological origin. There is a large scientific interest to investigate their nature, origin, and abundance to gain a better insight on atmospheric processes especially in the light of climate research. The most active INPs can be found within the group of biological particles specifically microbes.

We compared natural snow, artificial snow, piste snow and water supplies with respect of their chemical, microbiological and INP characteristics, but also consider impacts to alpine ecosystems.

Population genomics of polyextremotolerant polar fungi

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Background. Many fungal species from polar environments can also be found in temperate, even tropical regions. The question is - can a single genomic configuration allow for the flexibility required to adapt to such diverse conditions? Or, alternatively, do these species harbour cryptic specialists, undetected by traditional phylogenetics? The few published non-medical fungal population genomic studies show that even in seemingly homogenous species cryptic diversification can often be detected.

Results. We sequenced whole genomes of fifty strains of the black yeast *Aureobasidium pullulans* and fifteen strains of its sister species *Aureobasidium subglaciale*. Although the species are closely related, the former is a ubiquitous generalist, while the latter is mostly confined to glacial habitats. Population genomic analyses revealed that *A. pullulans* is a true generalist: the strains belong to a homogenous and recombining population. *A. subglaciale* was similar in many aspects – but not all.

Conclusions. *A. pullulans* is a true generalist, with strains from a single recombining population – including the many glacial strains – inhabiting diverse habitats with no signs of specialisation for each of these habitats. *A. subglaciale*, despite being closely related and with similar population characteristics, has a fundamentally different ecology. Possible reasons for these different survival strategies and the implications of these results for other polar fungi, will be discussed.

Cold-adapted Enzymes: Analysis of Ess1, a key regulator of RNA polymerase II

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The folding and activity of cold-adapted enzymes is of great interest for understanding protein function and how organisms grow and divide in extreme environments. Peptidyl Prolyl Isomerases (PPIases) are enzymes that rotate peptide bonds within target proteins and to assist in the folding of newly-synthesized proteins, and regulate the activity of mature proteins by conformational isomerization. We study one such enzyme, called Ess1, that is conserved from yeast to humans (where it is called Pin1). In the budding yeast *S. cerevisiae*, Ess1 isomerizes the carboxy-terminal domain (CTD) of the large subunit of RNA polymerase II thereby regulating the binding of co-factor proteins to the CTD that are required for transcription and RNA processing (e.g. capping, elongation, termination). We have cloned Ess1 from three extremophile fungal species that thrive in arctic and/or high salt environments, *A. pullulans*, *H. werneckii*, and *W. ichthyophaga*. Sequencing and 3-D modeling suggest the enzymes are structurally conserved, but as is often the case for cold-adapted enzymes, the predicted surface charge densities are reduced relative to Ess1 enzymes from budding yeast and the human pathogen *C. albicans*. We are currently using genetic complementation tests in *S. cerevisiae* to determine functional conservation. The long-term goal is to understand the basis for Ess1-RNA pol II interaction and regulation of transcription under extreme conditions.

Hypogeous fungi (truffles) diversity and cultivation at the upper timber line

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Truffles cultivation is in need for new cultivation areas. Hypogeous fungi (truffles s. l.) are known to occur mainly in the Mediterranean climates but recent activities disclosed that hypogeous fungi are present in colder areas including a successful cultivation in boreal zones (Shamekh et al 2013).

The upper timber lane was never of interest of commercial truffle hunters thus it remained understudied until recently. The review study focused on high altitude areas around the globe where truffles (incl. genus *Tuber*) are expected to grow. We have sampled areas in the SE central Alps, Dinarides, western Himalayan (Pakistan) area and Inner Mongolia in China.

Among commercial truffes *Tuber aestivum* was collected in beech forest at high altitude (> 1500 m a.s.l.) (Grebenc et al., 2011) and *T. melanosporum*-related novel true truffle species *T. petrophylum* (Milenković et al., 2015). Novel ectomycorrhizae from the genus *Tuber* were retrieved also from Himalaya, Inner Mongolia and Alps (Ilyas 2013; Jabeen and Khalid, 2014) including a broadly distributed novel *Tuber* species limited to the upper timber line.

Results and preliminary economic calculations for cultivation suggest good chances for successful cultivation and potentially economically justified use of truffles either as a plantation culture or as a supplementary inoculation species for environmental restoration purposes, at high-altitude alpine conditions.

Fungi in Svalbard glaciers and Greenland Ice Sheet: Are they alike?

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In this study we investigated fungal communities from two different Arctic glacial locations, Svalbard and Greenland, by combining cultivation approaches and amplicon based next generation sequencing (NGS). In Svalbard we sampled different ice types and glacial meltwater in three polythermal glaciers (Midre-Lovenbreen, Pedersenbreen and Vestre-Broggerbreen), while on the Greenland Ice Sheet (GrIS) we investigated fungi in cryoconite holes, supraglacial water, and dark and clear surface ice, characterized by high and low loads of ice algae, respectively. Results from cultivation and ergosterol analyses in the GrIS samples revealed the highest fungal biomass in dark ice and cryoconite holes, while the most diverse fungal communities were detected in dark ice. In Svalbard, fungi prevailed in subglacial ice and glacial meltwater, with the most diverse communities found in the Vestre Broggerbreen glacier. Amplicon sequencing of samples from the GrIS habitats and Svalbard glaciers revealed the presence of 201 and 132 fungal taxa, respectively, and cultivation approaches identified 308 and 119 fungal isolates, respectively. Many fungal cultures were recognized as new.

Microbial Bioactives and Their Role in Antarctica

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Dynamics of Subzero-Active Bacterial Communities in Arctic Tundra Soils

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Approximately one-third of the global soil carbon pool is sequestered in Arctic and boreal ecosystems and its decomposition is expected to be a significant contributor to atmospheric chemistry and climate. These soil ecosystems are permanently frozen or only thaw for a brief time in the summer and therefore degradation of soil organic material is slow and incomplete. Microbial life, however, continues into the subzero temperature range, and this activity contributes to carbon and nitrogen flux in these ecosystems, ultimately affecting global processes. We seek to delineate the subzero active microbial community in Arctic tundra soils and discern their roles in soil organic matter degradation and understand how different members of the microbiome modulate their responses to variations in temperatures and C/N pulses. The divergent life-styles of different microorganisms will be reflected in their ability to function in frozen soils and in their responses to environmental perturbations, leading to seasonal dynamics of activities. Microbial degradation of plant litter is substantial in frozen soils. From analysis of rRNA distinct members of the bacterial community were active in summer vs. winter season. Using a stable isotope probing (SIP) approach, we demonstrated bacterial genome replication at temperatures from 0 to -20 °C in seasonally frozen and permafrost soils. Our findings indicate that Arctic soils impact greenhouse gas production while frozen, as well as when thawed.

Effects of ocean acidification on Antarctic marine microbial communities

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Antarctic marine microbes are the drivers of productivity, elemental cycling and effect ocean biogeochemistry. Despite Antarctic waters being amongst the most vulnerable in the world to increased CO₂, little is known about their response to ocean acidification. A six-level dose-response experiment was conducted using 650 L incubation tanks (minicosms) adjusted to CO₂ levels (ranging 343-1641 μatm). Microscopy, flow cytometry and phylogenetic marker gene sequencing (16S and 18S rDNA) was used to investigate the effect of ocean acidification on the bacteria, archaea and eukaryotes community structure and interactions. These analyses showed that CO₂ significantly altered the composition of eukaryotic communities, with higher CO₂ levels favouring smaller taxa. No significant effect of CO₂ was seen on the bacterial community composition, but there was higher abundances in the higher CO₂ treatments. Network analyses indicated that this higher bacterial abundance was due to a reduction in grazing pressure by heterotrophic nanoflagellates, which were less abundant in higher CO₂ treatments. Our findings suggest that by 2100 under a “business as usual scenario”, ocean acidification could change the microbial community structure and interactions, thereby altering the ecosystem services these communities provide. The flow-on effects of such changes could have significant consequences for the Antarctic food web and elemental cycling if anthropogenic CO₂ release continues unabated.

Effect of ocean acidification on Antarctic marine microbes – a meta-analysis

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Southern Ocean waters are amongst the most vulnerable in the world to ocean acidification. Projected increases in CO₂ levels will cause changes in carbonate chemistry that are likely to be damaging organisms inhabiting these waters. A meta-analysis was performed to examine the effects of ocean acidification on Antarctic marine microbes occupying waters south of 60°S. Ocean acidification negatively impacted phytoplankton, with sensitivity differing between studies on single species in culture compared to natural mixed assemblages. Natural assemblages had a greater sensitivity than single species, with a decline in chlorophyll a concentration, productivity and photosynthetic health, as well as a shift in community composition, observed at CO₂ levels above 1000µatm for natural phytoplankton assemblages. In contrast, bacterial communities' abundance was positively impacted by acidification, with increases in abundance with increasing CO₂. Our analysis indicates that marine microbial communities in the Southern Ocean are likely to be susceptible to ocean acidification, altering the community composition of phytoplankton, reducing both the primary production and a shift in microbial community structure, thereby changing their contribution to critical ecosystem services. Poor spatial coverage and an understanding of the potential for microbes to acclimate and/or adapt to the changing conditions is largely unknown and requires further investigation.

Soil bacterial community assembly changes during primary succession

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Microbial community succession is the outcome of both deterministic and stochastic processes that vary through time and space. Based on previous works, we hypothesise that there is a transition from stochasticity to determinism during community succession after disturbance and community re-establishment. Here, we used a deglaciated-soil system to investigate the bacterial community assembly process along a 15-year chronosequence of deglaciation. We found that community assembly was stochastic in the first three years post-deglaciation, then transitioned to mixed influences from stochastic and deterministic processes (years 4-8), and was eventually governed predominately by deterministic processes after years 8. Furthermore, we found increased bacterial interactions along the deglaciation chronosequence, especially with increased negative correlations, thereby indicating increased determinism due to microbial interactions. Along the deglaciation chronosequence, bacterial community beta-diversity (both phylogenetic and compositional) rapidly increased and then decreased, indicating that bacterial communities diverged due to stochasticity and then converged as a result of deterministic effects. Our results filled the gap between the previously developed stochastic and deterministic dominated conceptual model. The observed patterns suggest that there are general rules governing the balance between stochastic and deterministic assembly processes during succession.

Ecophysiology of European cryotrophic Chlamydomonadales (Chlorophyta)

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Cryotrophic green algae from the order Chlamydomonadales (Chlorophyta) experience low temperature with episodic freeze-thaw cycles while irradiance fluctuates from sub- to superoptimal levels during all stages of their life cycle. The effective adaptation to these extreme conditions is manifested by their vigorous growth within the upper layers of the snow column documented from polar and alpine ecosystems worldwide. We study the ecophysiological diversity of snow algal communities in mountains in central Europe: Alps (Austria), Giant Mountains (Czech Republic) and High Tatra Mountains (Slovak Republic). Here, snow algae regularly populate two contrasting types of habitats. Cysts of *Scotiella cryophila* and *Chloromonas brevispina* were found to inhabit forested loci exhibiting medium to low light environment. Cysts and flagellates of *Chloromonas nivalis*-like species caused snow blooms at forested as well as at alpine sites. The alpine ecosystems above the timberline host flora specifically suited to the very high light intensities – e.g. *Chlamydomonas nivalis* and *Chlainomonas* sp. Our studies of the effect of temperature and light on photosynthesis in snow algal populations in situ and in the unialgal cultures at the laboratory conditions aim at characterisation of the protective processes that are indispensable for their survival. None of the studied samples however carries the hallmark of a true cryophile exhibiting photosynthetic optima above 10 °C.

High temporal resolution sampling of polar airborne microorganisms

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Evidence indicates that a plethora of viable microbial life is present in the atmosphere, that uses air as a long-distance transport vector. Antarctica is an excellent location to investigate long-range dispersal, due to its extreme isolation, simple ecosystems and vulnerability to the establishment of non-local taxa. Numerous studies have identified off-continent biological material throughout Antarctica. The generally accepted protocol for microbial air sampling is to pump air through a 0.2 μ m polycarbonate filter for long durations at low flow rates. However, as biomass in Antarctic air is very low, contamination is difficult to overcome and extremely long sample durations (up to two months) are necessary for meaningful samples. This limits insight into the Antarctic system and increases the chance of biased samples. We have developed robust protocols utilising liquid cyclone air samplers with high flow rates that drastically reducing sampling times to hours, contamination potential and sampling bias related to the desiccation of microorganisms. Customised modifications can prevent freezing of the collection liquid and have been successfully used to collect high temporal resolution air samples in the McMurdo Dry Valleys in January 2017 and 2018. These techniques provide us with a toolkit that will allow us to further understand a process suspected of underpinning microbial biogeography in Antarctica.

What shapes communities in snow?

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Bacteria are ubiquitous in snow and ice, with a high diversity of organisms organized in complex communities. The driving forces that determine microbial community structure in the snow are likely the result of random stochastic processes, but also environmental conditions that vary both temporally and spatially. We applied a neutral community model to determine the relative importance of stochastic (immigration, division and death) versus deterministic factors (competition, niche differentiation) in driving microbial community assembly within arctic snowpacks collected in Svalbard as part of the SnowNet initiative. In a 2016 campaign carried out in April during the maximum snow accumulation period, 90 snow samples were collected from 22 sites on 7 glaciers on Spitzbergen and Austfonna and analyzed in terms of their chemistry, physics and microbial taxonomy and abundance (16S rRNA gene sequencing, 16S qPCR). Based on our results, stochastic processes were shown to be more powerful in explaining community assembly than most spatial factors considered (geography and altitude). However, deterministic factors, such as chemistry, also played a role at local scales, especially for certain taxa. This study suggests that bacterial assembly in snowpacks is spatially structured through neutral processes, but that deterministic processes also have an effect.

Addressing contaminants in community analysis of the Antarctic aerosphere

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Microbial transport by air to and within Antarctica is believed to play a critical role in structuring the microbial-dominated Dry Valleys ecosystem. After overcoming the technical limitations of concentrating sufficient biomass for analysis, the problem of separating sample signal from background noise became the greatest challenge, as the highly sensitive collection process is likely to pick up any trace contaminating microbial signals. The importance of robust protocols from sample collection, to bioinformatic processing is therefore vital in detecting targeted biological signatures, which is particularly challenging as contaminating and targeted microbiomes often shared close resemblance. Here we present our methodology and preliminary results from airborne microbiological studies based our experience in the ultra-low biomass aerosol environment from Antarctic Dry Valleys and the Great Barrier Reef, including sampling design to detect different sources. Furthermore, we discuss moving beyond standard operating procedures with amplicon sequence variant calling and in silico decontamination which leverages frequency and prevalence information of multiple controls to identify and remove contaminating phylotypes. The outcome and of these studies may provide valuable lessons for fellow researchers working in low biomass environment where incidental contamination, which often resembles the subject matter, can be reduced but cannot be completely eliminated.

Biogeography of Arctic microbial nitrogen-cycling traits in the Svalbard shelf

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Global warming has been manifested in the decrease of Arctic sea ice extent and thickness. The thinner and younger sea-ice regime, that the Arctic has been facing, changed phytoplankton dynamics and Arctic's biogeochemistry. Understanding the sources of nitrogen that will feed this new sea-ice regime is necessary to forecast future marine ecosystem trends. In this study we present a comprehensive analysis of the biogeographic patterns of the microorganisms carrying out N-cycling processes combined with the distribution of N metabolic pathways along two oceanographic transects crossing fjord, shelf and oceanic domains along the western (Kongsfjorden) and northern (Rijpfjorden) coast of Svalbard. A total of 11 stations were sampled at three depths (surface, chlorophyll maximum and above the seafloor) and amplification of 16S rRNA gene and metagenomic analysis were performed using Illumina MiSeq. The prokaryotic data set comprises highly complex and diverse microbial structure, with a marked biogeographic pattern of the communities involved in N transformations. Strong links were identified between N-communities/N-pathways distribution and environmental gradients along the transects. Thaumarchaeota phylum was dominant at deeper stations and our results showed evidence of a close relationship between nitrite-oxidizing bacteria, such as those belonging to Nitrospinae, and ammonia-oxidizing microorganisms, like Thaumarchaeota suggesting a possible syntrophic relationship.

The diversity and biogeography of the Antarctic surface snow bacteriome

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90% of Antarctica is ice and snow-covered, and while environmental conditions are considered extreme by human standards, microorganisms thrive in these ecosystems. Yet, only few studies have investigated microbial diversity of Antarctic snow. The aims of this study were to identify the Antarctic snow surface bacteriome, to investigate cell activity and the presence of relic DNA, and to evaluate the impacts of human presence on microbial communities. By sampling a transect from Signy Island, Livingstone Island, down the Antarctic Peninsula to the Ellsworth Mountains, we identified the surface bacteriome of pristine Antarctic snow. We observed a latitudinal change in microbial communities, notably with a decrease in alpha diversity at southern latitudes. We identified indicator species within each location and interestingly, northern sites presented more endemic OTUs than southern samples, suggesting more variable and opportunistic communities in southern, more extreme systems. Then, we investigated the impact of human presence on the snow microbiome by sampling around the Lake Ellsworth drill site. Results suggest that while human presence had limited impacts on the snow bacteriome across Antarctica, intense human activities did impact with natural communities at specific locations.

Glacial influences on carbon mineralization pathways in Arctic fjord sediments

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Fjord sediments collect glacial runoff, including Fe minerals, and marine primary productivity. Microbial Fe reduction is dependent on the Fe(III) mineral form and influences the potential of Fe reducers to outcompete sulfate reducers for common organic carbon substrates. We hypothesize that glacial runoff supplies microbially-reactive Fe(III)-oxide minerals and allows Fe reducers to outcompete sulfate reducers. We measured the reactivity of Fe(III)-oxides from fjord transects and source sediment, then compared the balance between Fe and sulfate reduction at each station to the Fe(III)-oxide content and reactivity. We found that Fe(III)-oxide reactivity increased with distance from the head of the fjords and decreased with sediment depth. Fe(III)-oxides from glacial runoff sources were less reactive than sediments distal to the fjord head. The gradient of Fe(III)-oxide reactivity mirrored the change of microbial activity from sulfate reduction near the head of the fjord to Fe reduction at the mouth of the fjord. We conclude that glacial catchments supply large quantities of Fe minerals to fjord sediments, but benthic recycling of Fe by microorganisms appears to be required to transform the Fe(III)-oxides, such as hematite, to a reactive form so Fe reducers can compete with sulfate reducers for common organic carbon substrates. Recycling of reactive Fe(III)-oxides by Fe reducing microorganisms may play role in liberating Fe to the water column, mainly at the fjord mouth.

Effects of freeze-thaw and dry-wet events on microbial activity in soil

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Freeze-thaw and dry-wet events represent an important phenomenon in terms of soil hydrology and thermodynamics. The change in environmental conditions associated with these events may induce stress within the soil microbial community. Previous studies have frequently observed a pulse of CO₂ from topsoils after freeze-thaw and dry-wet events. The enhanced release of CO₂ to the atmosphere may have important implications for soil carbon storage and greenhouse gas emissions. However, the origin of this carbon and the mechanisms responsible for its release have not been well characterised. To better understand the short term response to these two stressors, we investigated the effect of freeze-thaw and dry-wet events on microbial activity in Antarctic soils using ¹⁴C isotopic tracking. Freeze-thaw and dry-wet events induced a strong physiological response in soil microbes. We observed a CO₂ pulse on rewetting and thawing from soil. Freeze-thaw and dry-wet events increased C supply to the microbial community and promoted internal C cycling. This increase in C supply may be due to the release of stress-induced osmolytes from the microbial community and their use after removal of the stress. Alternatively, it could be caused by cell death and lysis or by abiotic physical and chemical processes that release C into solution.

Effect of environmental heat-shock stress on glacier microbiome

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Glacier ice covers a noteworthy area of the planet and is presently facing an accelerated melting rate, combined with a potential remodeling of the microbial composition as a result of exposure to a temperature variation when moving to a contiguous soil. We investigated the bacterial thermal response examining the changes in the gene expression pattern in the microbiome of a glacier ice core from Svalbard, and in the psychrophilic bacterial model *Glaciibacter superstes*, in order to determine the presence of an enzymatic biomarker. Thawed ice samples were submitted to a 7-day heat/freeze cycles experiment, followed by DNA/RNA extraction and investigation of the resilient microbial community and gene expression variations by Shotgun metagenomics and metatranscriptomics. Gene expression coding for aspartate transcarbamoylase (ATC), a key enzyme of pyrimidine nucleotides biosynthesis, was quantified by qPCR, showing changes in the microbial DNA synthesis. Cell viability was assessed after each step based on dead/live cell counting in order to correlate the specific increase in ATC expression with the cellular division. Corroboration of the ATCase gene expression pattern in both psychrophilic bacterium and ice microbiome is currently underway in order to propose an enzymatic biomarker for ice microbiome response to temperature variations when changing habitats due to glaciers' retreat.

Patterns in microbial diversity at, and between the polar oceans

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Biogeographic patterns between the polar oceans have been studied with increasing resolution in recent years given advances in molecular tools, common sampling practices and next generation sequencing. The results have shown that picoplankton assemblages in the polar oceans are more similar to each other than to oceanic systems between them – yet they are worlds apart. Regional oceanographic patterns of winter picoplankton have been examined in detail in the Antarctic Peninsula, which suggest widespread dominance of chemoautotrophic and mixotrophic microbial groups throughout the water column. Winter plankton studies in the Arctic are more limited, though also support this finding. This keynote will examine the relationship between microbial diversity, ecosystem function and shifts in physiochemical parameters and resources in these systems and identify the contrasts between them.

Microbial life in frozen soils – what can and what cannot?

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Microbial activity in frozen soils has recently gained increasing awareness and the fact that soil microorganisms can perform significant metabolic activity also under such conditions is apparent. This activity can affect e.g. soil carbon balances and element turnover in high latitude soils.

This presentation will synthesize investigations and method developments carried out by our group the last 10 years that have aimed at resolving how the properties of the soil matrix interact with fundamental metabolic drivers such temperature, liquid water availability and substrate availability. We explore how these properties and drivers combine to regulate rates of catabolic and anabolic microbial processes in frozen soils. The studies span from the fundamental soil physical properties that underpin microbial activity by regulating the presence and availability of water, over the partitioning of substrate utilization of both simple and polymeric compounds into catabolic and anabolic metabolism, to the adaptations to frozen conditions occurring at the cell level. Impacts on microbial population dynamics on the community level are also addressed.

The results are obtained from seasonally frozen soils from the major landscape elements of boreal and sub-arctic ecosystems at temperatures representing dominating winter time soil temperatures with snow cover of 30 cm or more. The fundamental aspects of soil freezing presented should also be relevant for other systems where freezing occurs.

Algal-fungal interactions on the Greenland Ice Sheet surface

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Darkening and the resulting acceleration in surface melt of the Greenland Ice Sheet (GrIS) is mainly driven by ice-algal blooms. To investigate the contribution of fungal communities to this microbially-driven albedo reduction, fungi were isolated from surface ice with high and low algal loads, supraglacial water, cryoconite holes and snow on the southwestern margin of GrIS. By combining cultivation and sequencing methods, the fungal diversity and abundance of the above-mentioned habitats were characterized. After a thriving population of fungi was found in key GrIS habitats, in-situ and ex-situ incubation experiments were performed to investigate the possible positive or negative impacts of fungi on ice algal survival and bloom development. Algae *Mesotaenium berggrenii* and *Ancylonema nordenskiöldii* were incubated with two species representing the GrIS fungi: 5% of *Penicillium* sp. spores and/ or *Articulospora* sp. mycelium at 4 °C under 14/10 h cycle of light-darkness ($181.45 \pm 24.5 \mu\text{mol m}^{-2} \text{s}^{-1}$ PAR) for 2 months. Samples for scanning electron microscopy, light microscopy, pulse amplitude-modulated (PAM) fluorometry, ergosterol quantification and secondary metabolites extraction were collected at five time points. PAM-fluorometry outcomes indicated that fungal-algal interactions were likely beneficial for ice algae. The data supporting a possible symbiotic relationship between the two fungal species tested and its implications will be discussed.

Meta-omics investigation of soil communities in the Finnish Arctic tundra

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Increased permafrost thawing due to pronounced warming in high latitudes might lead to a positive warming feedback loop, as previously frozen organic matter is metabolized by microorganisms releasing carbon dioxide and methane. Despite their importance, there is limited knowledge on the functional potential of microbial communities in polar soils, especially regarding their role in the degradation of organic matter and potential contribution to the greenhouse gas budget. We applied a genome-resolved metagenomic/metatranscriptomic approach to study microbial communities in 50 soil plots along a natural climate gradient in the Finnish Arctic. Communities were dominated by Proteo-, Actino- and Acidobacteria and active functional pathways were mostly those involved in the breakdown of amino acids, carbohydrates and lipids. Recovered genomes were related to common soil taxa such as the nitrogen-fixing *Bradyrhizobium* (Alphaproteobacteria) and *Granulicella* (Acidobacteria), while others appear to represent distinct lineages distantly related to *Candidatus Koribacter* and *Candidatus Solibacter* (Acidobacteria). Further phylogenomic and functional analyses are being currently carried out. These will allow us to investigate the metabolic potential of the soil communities in more detail, for example, regarding the importance of carbon, nitrogen and sulphur cycles in the tundra ecosystem along fine-scale climatic variation.

Total and active microbiome from perennial cave ice

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Ice caves are one of the scarcely investigated cold habitats. Our survey of the temporal microbial distribution in the 13,000-years old ice core of Scarisoara cave (Romania) unraveled structural and functional microbiome patterns in relation to depositional and post-depositional processes and climate variation. The Prokaryotic and fungal communities' structure across the cave ice block was determined by 16S rRNA gene and ITS2 Illumina sequencing. Microbial abundance and diversity of total and active bacterial communities showed large variations across the ice core in relation with substrate geochemistry. The cave microbiome was dominated by Actinobacteria and Proteobacteria, with a high representation of species commonly found in cold environments, while the active bacterial community was shared between Proteobacteria and Firmicutes, with taxa variations based on ice age and TOC content. Euryarchaeota and Crenarchaeota archaeal taxa alternated in ice strata in relation with deposition climate pattern and ice geochemistry. Fungal community from 2,000 years old ice strata was majorly represented by Ascomycota and Basidiomycota, with a climatic-driven taxa distribution. This first investigation of cave microbiome entrenched in perennial ice strata since Late Glacial could help understanding the global microbial response to post glacial warming.

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Diversity of DNA and RNA viruses in polar regions

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RNA viruses may be as abundant as DNA viruses but studies on RNA viruses are scarce. Metagenomic studies of RNA viruses in freshwater lakes in the Arctic (Svalbard) have shown that, as we described for Antarctic RNA viruses, most of them belong to the order Picornavirales. We have characterized their genetic variability (quasispecies), which may represent a mechanism of adaptation.

Polar regions harbour a great diversity of DNA viruses. We have carried out extensive bioinformatic analysis and assembled >9.000 new circular ssDNA viral genomes from polar regions that group in >100 clusters, largely increasing the existing database (~1.300 circular ssDNA viruses, <10 families). Additional analysis including ~32.000 circular ssDNA viral genomes, assembled from published viral metagenomic studies, group them within the >100 clusters we described. Interestingly, many clusters are composed exclusively of polar viruses, suggesting new viral families adapted to polar environments. Sequence variability, similar to RNA viral quasispecies, has been suggested in circular ssDNA viral genomes but this has not been explored. We have identified complex quasispecies (high sequence variability) in several polar circular ssDNA viruses.

These studies illustrate the power of our metagenomic approach to identify new viruses from polar regions. High genetic variability may represent a mechanism of rapid virus adaptation to changing conditions in natural ecosystems and facilitate virus colonization.

Bacteria living on air: trace gas chemoautotrophy is abundant in Antarctic soils

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Antarctic soils, despite exposure to extreme environmental conditions, support high microbial diversity. Often in these environments, photosynthetic bacteria are the dominant primary producers. However, in two East Antarctic sites, Robinson Ridge and Adams Flat, bacteria capable of a novel chemotrophy were recently discovered. There, the oxidation of atmospheric hydrogen and carbon monoxide supported primary production of the microbially-dominated, phototroph-lacking surface soils. The ability to literally 'live on air' was attributed to two genes, the relatively unknown RuBisCO type IE (*rbcL1E*) and the high-affinity 1h/5-[NiFe]-hydrogenase large subunit (*hhyL*) gene. We used QPCR to detect the abundances of these genes, relative to 16S rDNA, throughout ten new sites spanning two major regions in eastern Antarctica; the Windmill Islands and Vestfold Hills. Soil physiochemical and OTU abundance data showed that low moisture, carbon and phosphorus content of the soils, and larger particle sizes, were major abiotic drivers for trace gas fixation. Higher abundances of Actinobacteria, Candidatus Eremiobacteraeota and Dormibacteraeota, and other novel phyla were positively correlated to the genetic determinants of trace gas chemoautotrophy. While further research is required to quantify the expression and activity of trace gas chemoautotrophy in these ecosystems, this work highlights the widespread potential for Antarctic soils to be undertaking this trace gas chemosynthesis.

Diversity of bacterial biosynthetic genes across Fildes Bay, King George Island

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Polyketides (PKSs) and Non-ribosomal peptides (NRPSs) are mega enzymes responsible for the biosynthesis of a large fraction of important natural products. Molecular markers targeting biosynthetic genes, such as Ketosynthase (KS) of PKSs, as well as Adenylation (AD) domains of NRPSs have been used to assess the diversity and distribution of biosynthetic genes of bacterial isolates and complex microbial communities. In this study, the distribution of PKS and NRPS genes of the Fildes Bay at Fildes Peninsula, one of the largest ice-free and biodiversity rich areas in Antarctica, was assessed by using PCR-based strategies couple with high-throughput sequencing. To assess the distribution of biosynthetically rich bacteria, such as Actinobacteria, Cyanobacteria and Proteobacteria, 16S rRNA gene amplicon sequencing is included. Taxonomical relative abundance distribution revealed Acidobacteria, Bacteroidetes and Proteobacteria as the most abundant phyla. Comparing with other ecosystems, such as temperate and tropical soils, the number of OTUs obtained for PKS and NRPS genes is lower. A phylogenetic placement analysis will allow us to determine to which class the biosynthetic domains are associated to, including potential novel chemical diversity and biotechnological applications. This study will allow us to reveal the biosynthetic capacity of Fildes Bay soils, not yet assessed, and help identifying prolific starting points for future novel bioactive molecules discovery efforts.

Metagenome assembled genomes (MAGs) from freshwater Siberian permafrost

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The oldest undisturbed permafrost of the Northern Hemisphere is in the Kolyma-Indigirka Lowland region of Siberia. The deepest layers are aged up to 2 Ma years old. Borehole samples were aseptically retrieved in 2015 from permafrost bordering the Alazeya River. 30 MAGs were created from depths of 3.5, 7.2, 14.1 and 14.8 m. These depths were chosen due to the variable geology. The syncryogenic permafrost of the Yedoma suite has never thawed since deposition 26-60 K years ago for samples 3.5 and 7.2 m. Our deepest epigenetic permafrost is from the Olyor suite, 14.1 and 14.8 m, and is 0.8-1 Ma old. All these samples are of freshwater origin with total anions <3.1 and cations <1.9 mmol/100 g soil. The Alazeya River site has no record of being marine influenced. However the assembled genomes are phylogenetically related to microbes commonly found in deep subsurface marine environments, such as Atribacteria and archaeal Marine Benthic Group D, whose assembled genomes have been found in marine environments. These MAGs contained genes that would allow these organisms to exist in thin films of unfrozen brine within the permafrost. The phylogenetically identified MAGs display a microbial presence similar to that found in other low energy and deep subsurface environments, such as the deep subsurface and the sea floor. Supported by NSF DEB 1442262 & NSF IIA 1358155 & RGA#AAAA-A18-118013190181-6.

Cyanobacteria from polar regions, a field identification guide

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Cyanobacteria play pivotal role among the primary producers in Arctic and AntArctic ecosystems. They are capable of surviving extended periods of freezing and desiccation yet re-establish their metabolic activity quickly after rehydration. Such properties allow them to dominate both aquatic and disturbed terrestrial environments.

Recent studies on composition of cyanobacterial assemblages have utilized next generation sequencing techniques (NGS) despite some disadvantages. For example, presence of extensive sheaths hampers DNA isolation resulting in some species left undetected. Optical microscopy though remains an indispensable method in determination of cyanobacteria in the field. Association of long 16S rRNA gene sequences with cyanobacterial morphotypes are also necessary for reliable identification of environmental sequences obtained by NGS.

We had studied cyanobacterial populations by isolation of more than 150 strains of cyanobacteria from Alaska and Svalbard in Arctic and compared them with more than 100 cyanobacterial strains from various sites in the AntArctic. We compared 16S rRNA gene phylogeny of studied strains with sequences and respective strains from other areas.

Here we present morphology from 16 genera showing distinct diacritical features of thin filamentous, coccal and heterocystous polar cyanobacteria of genera *Geminocystis*, *Geitlerinema*, *Gloeothece*, *Leptolyngbya sensu lato*, *Microcoleus*, *Nodosilinea*, *Nostoc*, *Phormidesmis*, and *Pseudophormidium*, etc.

Drivers and scales of plant-fungal communities in patterned-ground ecosystems

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The composition and growth rates of plant communities are strongly affected by their interactions with Fungi and Bacteria. How plant communities will respond to a warming Arctic might depend largely on their co-assembly with microbes. However, the rules that govern the co-assembly of these three kingdoms, Plants, Fungi and Bacteria, remain elusive.

We tested the drivers and scale-dependency of plant-fungal-bacterial community co-assembly across the Arctic, by sampling 3580 soil cores, plant communities, and environmental data from a sub-meter to a continental scale along the North American and Eurasian Arctic transect, which span all five bioclimatic subzones of the Arctic. We contrasted communities of bare, cryoturbated patterned-ground and adjacent vegetated features. DNA was extracted from soils and bacteria and fungi were sequenced. Initial analyses show that plant and fungal communities are highly correlated along and across the two transects. At a cross-continental scale, they are significantly structured by transects, which correlates with distinctly different climates, geologies and pH. Along each transect plants and fungi are structured by bioclimatic subzones, and at local scale by patterned ground features. We conclude that pan-arctic plant and fungal communities are foremost positively correlated with each other and both are affected by a complex of abiotic filters with climate representing the strongest filter, followed by soil pH, soil disturbance, and texture.

First Gaze at Microbial Community of the Marine Permafrost Through Metagenomics

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Permanently frozen marine sediments found along the East Siberian Sea coast were formed 100-120 K years ago. In August 2017, permafrost cores from a remote site on the Chukochy Cape were collected using a slow rotary drill. Total carbon ranged from 1.7 to 2.2%. Methane was detected at 5.4 m and 15 m. Concentrations of Cl⁻, SO₄²⁻, Na⁺ and Mg²⁺ increased with depth. The genomic DNA from 7 permafrost samples was used to obtain metagenome sequences. Microbial communities dominated by Bacteria (78-98%) and Archaea (1-21%), while Eukaryota were a minor component (1-3%). The highest abundance of methanogenic Methanosarcinales (11%), Methanomicrobiales (6%), and methylotrophic Thermoplasmata (1%) was detected in samples with methane. Other sequences were from halophilic, sulfate or sulfur reducing Archaea. Bacterial community at 1.75 m comprised of 31% Actinobacteria that decreased to 15% at 18.8 m. On the contrary abundance of the anaerobic, spore-forming, sulfate, sulfite, and metal-reducing Firmicutes increased with depth from 7 to 36%. Abundance of sulfate and sulfite reducing Deltaproteobacteria were 4-11%, other Deltaproteobacteria were related to halophilic and marine myxobacteria. Metagenome analyses from the marine permafrost showed presence of sulfate-, sulfite-, and metal-reducing bacteria and Archaea previously isolated only from thermophilic environments.

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Determining possible origin, structure and function of microbial communities

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Sea ice and its snow cover are critical for global processes including climate regulation and biogeochemical cycles. Despite an increase in studies focused on snow microorganisms, the ecological role of snow inhabitants remains unclear, and thus, is excluded from predictive models of sea ice retreat related to climate change. In this study, we applied high throughput 16S rRNA gene and metagenomic sequencing to samples collected from a vertical profile through the snow overlying sea ice in a Greenlandic fjord to investigate sources and selection of the microbial communities in the atmosphere, four layers of snow, sea ice brine and seawater. Microbial communities from all snow layers were dominated by Alteromonadales, Rhizobiales, Saccharomyceta and Actinomycetales and were superficially more similar to atmospheric communities than to sea ice or seawater communities. The surface snow community functional profile was characterized by resistance to photochemical stress, potential for primary production, and high versatility in the utilization of carbon from various sources. The larger microbial community in the basal snow layer may have been fed by relatively nutrient-rich sea ice brine resulting in potential growth of copiotrophic psychro- and halotolerant members. The origin of those snow-associated members (especially when similar ones exist both in sea water and the atmosphere) was evaluated by sequence level similarities with taxonomic and functional units.

Microbial Communities along Consecutively Connected Habitats in East-Antarctica

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The ultraoligotrophic Lake Untersee is the largest and deepest surface lake of Central Queen Maud Land in East Antarctica. It is located in a cirque-like valley which is dammed by the Anuchin glacier at its northern tip which provides the only known water source for the lake. Water-loss only occurs through ablation and sublimation of the perennially lake ice cover. Lake Untersee pelagic and benthic microbial communities are relatively well studied. However, the Anuchin glacier is still unexplored even though its potential role as major contributor of nutrients and biota to the lake ecosystem.

Based on 16s rRNA gene targeted PCR and subsequent Illumina tagged sequencing, we show that aerial deposition of biota on the glacier leads to distinct microbial communities in glacier ice and cryoconite holes. These communities ultimately become part of the Lake Untersee ecosystem. Significant differences in microbial diversity were also recorded between supraglacial habitats and the lake ice cover, suggesting a shift in glacier microbial communities once they melt into the lake. The highest relative abundant phyla in lake, glacier and aerosol samples belong to Actinobacteria, Cyanobacteria, Bacteroidetes, Firmicutes, and Proteobacteria.

The glacier can be considered as a vector for the colonization of Lake Untersee and hence shapes the Lake Untersee ecosystem. The microbial input from englacial and subglacial zones to the lake are unknown and require further investigation.

Characterising the response of mycorrhizal networks to agents of global change

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New Zealand's alpine regions face acute pressures from the combined effects of species invasions and relatively high rates of climate change, yet the response of endemic plant communities to these pressures remains poorly understood. Mycorrhizas are ubiquitous and critical trophic associations between plant roots and soil fungi in alpine zones. The mutualism is diffuse, so that single fungi may be associated with multiple plants and vice versa. The complex mycorrhizal networks that emerge can have profound effects on plant community dynamics and ecosystem function, and may be sensitive to agents of global change, but very few empirical studies have examined these effects. We applied a factorial combination of warming by Open-Top Chamber and invasive *Calluna vulgaris* removals in a field experiment in Tongariro National Park, New Zealand. In the third year of treatment, soil cores were collected at 5 random locations in plots. DNA was extracted from 6-8 individual root fragments per core. Plant species were identified through a RLFP-based fingerprinting method, while fungi were identified through sequencing of the internal transcribed spacer of the fungal rRNA operon, on the Illumina Hi-Seq platform. Interaction networks will be assembled on a per plot basis to assess how plant-fungal networks differ under treatments. Here, I will focus on the molecular techniques I used to identify the plant species.