Funds were requested for participant support for the 5th International Conference on Polar and Alpine Microbiology which was held in Big Sky, Montana (USA) from 8-12 September 2013. This meeting was a continuation of the highly successful meetings previously held in Rovaniemi, Finland (2004), Innsbruck, Austria (2006), Banff, Canada (2008) and Ljubljana, Slovenia (2011), which brought together leading international researchers and students in this field. The overarching objective of the Big Sky meeting was be to bring together scientists, students and professionals to discuss all aspects of cold-adapted microorganisms and the roles they play in polar and alpine ecosystems. The sessions were arranged to (i) provide a forum for the discussion of the evolution of these organisms, (ii) their role in elemental biogeochemistry in a warming world, and (iii) to discuss metatranscriptomic, metaproteomic, and other genome-enabled approaches to understand how shifts in environmental variables impact microbially mediated elemental cycling in icy ecosystems. The conference provided a multi-disciplinary forum to explore emerging areas in the field and as always, will have a wealth of opportunities for the exchange of ideas and building of collaborations. The funds were used to defray registration and travel costs for 7 keynote speakers and 6 early career scientists.

SESSIONS (includes topics related to prokaryotes, eukaryotes, viruses, technological developments, and process related research)

- ***Sub-zero Microbiology: Links to Other Ecosystems***
- ***Microbial First Responders to a Changing World***
- ***Thresholds and Tipping Points in Polar and Alpine Environments***
- ***Subglacial Microbiology***
- ***Evolution of Psychrophilic Microorganisms***
- ***Biodiversity, Ecosystem Function, and Environmental Change: Past, Present and Future***
- ***Earth's Subzero Biosphere as a Model for Microbial Life on Other Icy Worlds***

Unlike past PAM Conferences, I chose to focus the Conference on “Discovery in a Changing World”, which has direct relevance to many of DOE’s missions. This theme allowed attendees to present and discuss new opportunities to bridge the knowledge gap between molecular and global-scale microbial phenomena, facilitating scaling of concepts and data across multiple levels of biological organization. This approach addressed directly the following DOE research areas:

- Characterize biological response to climate change with genomics and systems biology.
- Address multiple scales of time and space for processes underlying climate change.

- Understand the interactive genomic, environmental, and climatic influences on microbial elemental cycling.

Dr. Hugh Ducklow, an expert in the field of polar marine microbiology and climate change, provided the dinner lecture at the opening ceremony entitled “Changing Times in the Microbial Cryosphere”, which focused on microbial first responders to a changing Earth. The complete program is included on the meeting website:
http://polaralpinemicrobiology2013.montana.edu/

A thematic issue based on the proceedings of this meeting was published in FEMS Microbiology Ecology in 2014. The lead manuscript provided an overview of the conference (Priscu, J.C., J. Laybourn-Parry, M. Haggblom. 2014. Polar and alpine microbiology in a changing world FEMS Microbiology Ecology. 89:209-210).

2013 Polar & Alpine MICROBIOLOGY

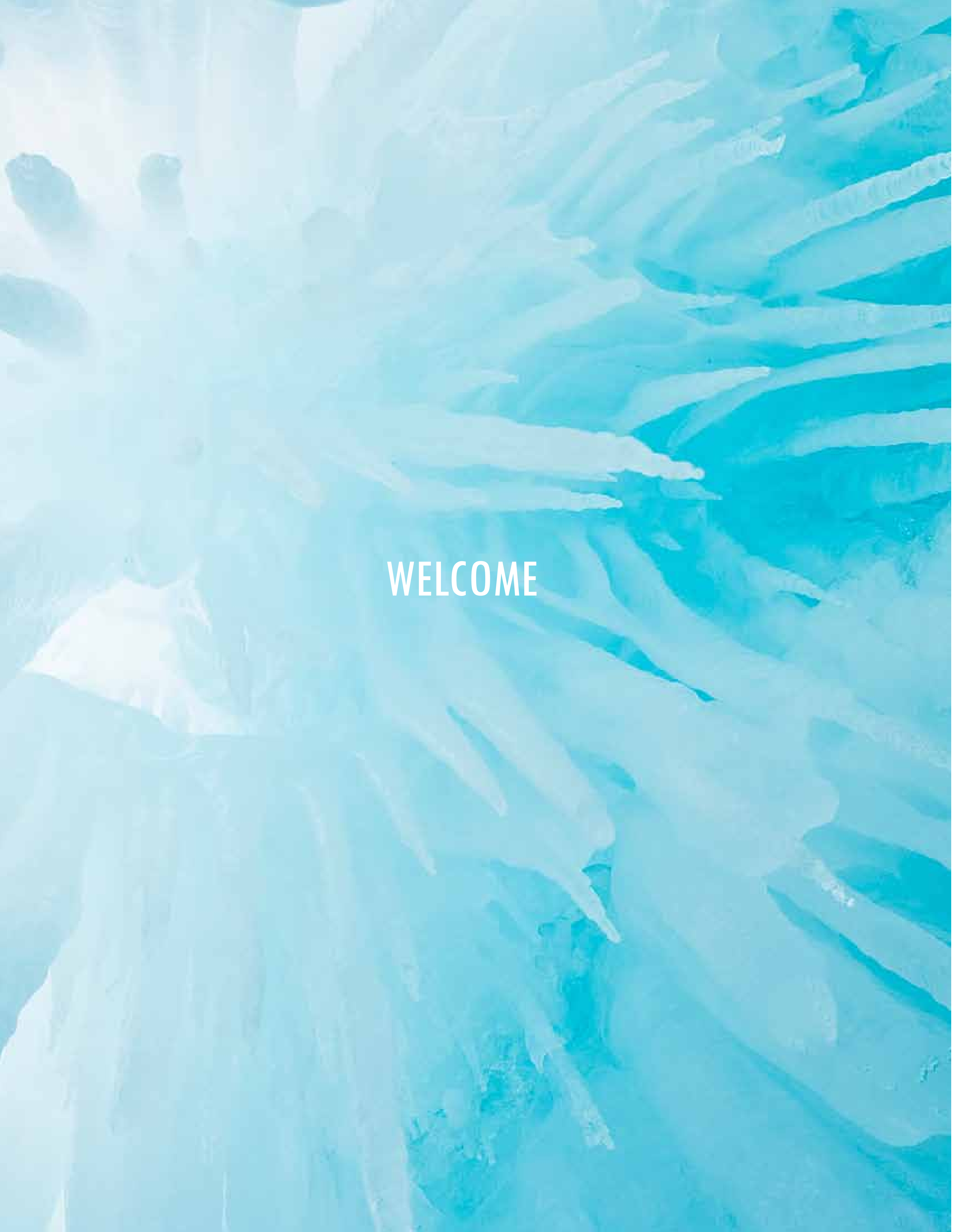
Discovery in a Changing World

PROGRAM & ABSTRACTS

The 5th INTERNATIONAL CONFERENCE on POLAR & ALPINE MICROBIOLOGY

SEPTEMBER 8-12, 2013 BIG SKY, MONTANA, USA

CONTENTS



WELCOME

INTRODUCTION

Dear Colleagues,

I am delighted to invite you to the Fifth International Conference on Polar and Alpine Microbiology (PAM5); this conference series will be entering its 10th year of gathering the scientific community for discourse and discussion on the latest in all the aspects of cold-living microorganisms. The conference will provide a multi-disciplinary forum to explore emerging areas in the field and as always, will have a wealth of opportunities for the exchange of ideas and building of collaborations. It is always a productive and energizing experience to be in the company of so many colleagues including rising stars and students. For those of you new to the conference, you will be challenged, stimulated and excited by the interest and findings featured.

This year's conference is held just 50 miles / 80 kilometers from Yellowstone National Park, an alpine environment that is home to over half of the world's thermal features in a stunning alpine environment. The unique beauty of our conference venue, the proximity to Yellowstone National Park and its natural wonders will surely inspire us all beyond our work.

We look forward to hosting you for another memorable and productive Polar and Alpine Microbiology conference.

Thank you,

John Priscu, Conference Chair

John C. Priscu

IT IS OUR PLEASURE TO WELCOME YOU TO PAM 2013

This is the 5th international meeting with the continuing goal to share and review discoveries and progress in polar and alpine microbiology research across disciplines.

PAM 2013 continues the tradition of the highly successful meetings previously held in:
Rovaniemi, Finland, 2004
Innsbruck, Austria, 2006
Banff, Canada, 2008
Ljubljana, Slovenia, 2011

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MO-BIO Laboratories

Montana State University

Thermal Biology Institute
at Montana State University

MEETING AT A GLANCE

TABLE

PROGRAM

SUNDAY 8 September 2013

1:00-5:00pm **REGISTRATION**

5:00pm Opening Western BBQ Dinner, Lone Peak Cafe

7:00-8:00 pm. OPENING LECTURE **Hugh Ducklow,** Madison Room
The Disappearing Cryosphere: Threat and Opportunity for Polar and Alpine Microbiology

8:00 Local mountain music and dancing, Huntley Dining Room

MONDAY 9 September 2013

SESSION 1 / SUB-ZERO MICROBIOLOGY: LINKS TO OTHER ECOSYSTEMS

Session Chair: **Jill Mikucki** *Session organizers:* **Dirk Wagner, Paula Matheus-Carnevali (early career scientist)**

8.30 - 9.00 KEYNOTE LECTURE **Kevin Arrigo**
Stanford University UNITED STATES
Climate Change Impacts in the Arctic Ocean

9.00 - 9.20 **Rachael Rhodes**
Oregon State University UNITED STATES
Excess methane spikes in Greenlandic glacial ice: in-situ production by psychrophiles?

9.20 - 9.40 **Janine Gorsch**
GFZ German Research Centre for Geosciences GERMANY
Deep biosphere of the El'gygytgyn Crater Lake/Far East Russian Arctic: How has the microbial community developed and changed since the impact 3.6 million years ago?

9.40 - 10.00 **Jon Telling**
University of Bristol UNITED KINGDOM
Early melt ionic pulses within cryoconite holes of the McMurdo Dry Valleys, Antarctica: insight into microbial nutrient cycling and ecosystem function

COFFEE/TEA BREAK 10.00 - 10.40 (40 mins)

10.40 - 11.00 **Cristina Purcarea**
Institute of Biology Bucharest ROMANIA
Diversity of ice embedded microorganisms from Scarisoara Cave, Romania

11.00 - 11.20 **Jun Uetake**
National Institute of Polar Research JAPAN
Bacterial diversity of ice surface and moss gemmae aggregation on disappearing tropical glacier in Uganda

11.20 - 11.40 **Harry Langford**
University of Sheffield UNITED KINGDOM
Cell-mineral interaction and the bioaggregation of cyanobacteria with inorganic particulates upon glacier surfaces

11.40 - 12.00 **Sota Tanaka**
Chiba University JAPAN
Snow algal communities on mountain glaciers in the Suntar Khayata region, Eastern Siberia

LUNCH 12.00 - 1.20 (1 hour and 20 mins) Huntley Dining Room

SESSION 2 / MICROBIAL FIRST RESPONDERS TO A CHANGING WORLD

Session Chair: **Laurie Connell** *Session organizers:* **Ok-sun Kim, Nadia Mykytczuk (early career scientist)**

1.20 - 1.50 Keynote lecture **Josef Zeyer**
Federal Inst. of Technology Zurich (ETH) SWITZERLAND
Microbial structures and functions in glacier forefields: current scientific challenges

1.50 - 2.10 **Nadia Mykytczuk**
Laurentian University CANADA
Microbial carbon cycling in high Arctic permafrost polygons: responses to a warming climate

2.10 - 2.30 **Brian Lanoil**
University of Alberta CANADA
Few phylotypes consume added labile organic carbon in high arctic barrens soils

2.30 - 2.50 **Christopher Omelon**
The University of Texas at Austin UNITED STATES
Microbial respiration in cryptoendolithic habitats, Canadian Arctic

2.50 - 3.10 **Tina Santl Temkiv**
Aarhus University DENMARK
Sources and Types of Active Airborne Bacteria

COFFEE/TEA BREAK 3.10 - 3.50 (40 Mins)

SESSION 3 / THRESHOLDS AND TIPPING POINTS IN POLAR AND ALPINE ENVIRONMENTS

Session Chair: **Catherine Larose** *Session organizers:* **Yoo Kyung Lee, Laura Sanguino-Casado (early career scientist)**

3.50 - 4.20 Keynote lecture **Josh Schimel**
University of California Santa Barbara UNITED STATES
The interaction of physical and stoichiometric thresholds in regulating Arctic ecosystems.

4.20 - 4.40 **Nozomu Takeuchi**
Chiba University JAPAN
Geographical variations in cryoconite on glaciers in Asian high mountains.

4.40 - 5.00 **Laura Sanguino Casado**
Ecole Centrale de Lyon FRANCE
Viruses keep Arctic microbial adaptation from its breaking point

5.00 - 5.20 **Lee Taylor**
University of New Mexico UNITED STATES
Diversity of soil fungi does not decrease with latitude along the entire North American Arctic Transect but is structured by climate and vegetation

5.20 - 5.40 **David Van Horn**
University of New Mexico UNITED STATES
A Multi-Habitat Survey of Microbial Life in the McMurdo Dry Valleys, Antarctica

6.00 POSTERS (snacks and beverages provided)

8.00 Dinner on own

TUESDAY 10 September 2013

SESSION 4 / SUBGLACIAL MICROBIOLOGY

Session Chair: **David Pearce** *Session organizers:* **Irina Alekhina, Jon Telling (early career scientist)**

8.30 - 9.00 Keynote lecture **Brent Christner**
Louisiana State University UNITED STATES
Scientific Exploration of Subglacial Lake Whillans, West Antarctica

9.00 - 9.20 **Mark Skidmore**
Montana State University UNITED STATES
Geochemistry of subglacial Lake Whillans, West Antarctica: Implications for microbial activity.

9.20 - 9.40 **Trista Vick-Majors**
Montana State University UNITED STATES
Physiological Ecology of Bacteria in the water column of Subglacial Lake Whillans, Antarctica

9.40 - 10.00 **Amanda Achberger**
Louisiana State University UNITED STATES
Molecular Analysis of Microbial Communities inhabiting Subglacial Lake Whillans, Antarctica

10.00 - 10.20 **Alex Michaud**
Montana State University UNITED STATES
Microbial activity in the sediments of Subglacial Lake Whillans

COFFEE/TEA BREAK 10.20 - 11.00 (40 mins)

11.00 - 11.20 **Sergei Bulat**
PNPI, NRC Kurchatov institute RUSSIAN FEDERATION Elusive microbial life at the uppermost water layer in subglacial Lake Vostok, East Antarctica

11.20 - 11.40 **Terra Spotts**
Montana State University UNITED STATES Methane flux from subglacial sediments at Robertson Glacier, Canadian Rockies

11.40 - 12.00 **Trinity Hamilton**
Penn State University UNITED STATES Molecular evidence for an active endogenous microbiome beneath glacial ice

12.00 - 12.20 **Nina Gunde-Cimerman**
University of Ljubljana SLOVENIA
Differences between the Arctic black yeast Aureobasidium pullulans var. subglaciale and other three A. pullulans varieties uncovered by de novo genome sequencing

LUNCH 12.20 - 1.50 (1 hour and 30 mins) Huntley Dining Room

SESSION 5 / EVOLUTION OF PSYCHROPHILIC MICROORGANISMS

Session Chair: **Rachael Morgan-Kiss** *Session organizers:* **Eric Collins, Pierre Amato**

1.50 - 2.20 Keynote lecture **Daniel Shain**
Rutgers University UNITED STATES
Towards Understanding the Bioenergetics of Cold Adaptation

2.20 - 2.40 **Buford Price**
UC Berkeley UNITED STATES
Picocyanobacteria in ice: genomics, flow cytometry, live/dead tests

2.40 - 3.00 **Charles Lee**
University of Waikato NEW ZEALAND Distribution and Drivers of Archaeal and Fungal Communities in the Antarctic Dry Valleys

3.00 - 3.20 **Oddur Vilhelmsson**
University of Akureyri ICELAND
Endolichenic Proteobacteria and their roles in Arctic lichen symbiotic associations

3.20 - 3.40 **Rachael Morgan-Kiss**
Miami University UNITED STATES
The Antarctic Chlamydomonas raudensis: an emerging model for cold adaptation of photosynthesis

COFFEE/TEA BREAK 3.40 - 4.20 (40 mins)

4.20 - 4.40 **Stefanie Lutz**
University of Leeds UNITED KINGDOM Complexity of microbial ecology of a polythermal glacier surface and heterogeneity of cryophilic adaptive inventory

4.40 - 5.00 **Pierre Amato**
CNRS FRANCE
Survival of microorganisms to the main stress factors encountered in clouds

5.00 - 5.20 **Lucia Muggia**
University of Graz AUSTRIA
Alpine lichen communities as evolutionary hot beds of stress-tolerant fungi

5.20 - 5.40 **Anne Jungblut**
Natural History Museum UNITED KINGDOM
Using historical Antarctic collections and next generation sequencing to unlock the past: Has polar cyanobacterial diversity changed over the last 100-years?

5.40 - 6.00 **Max Haggblom**
Rutgers University UNITED STATES Acidobacteria Communities in Arctic Tundra Soils

6.00 Posters (snacks and beverages provided)

8.00 Dinner on own

WEDNESDAY 11 September 2013

ALL DAY OPTIONAL FIELD EXCURSION TO YELLOWSTONE NATIONAL PARK
PLEASE EXPLORE THE AREA ON YOUR OWN IF YOU HAVE OPTED NOT TO JOIN THE YELLOWSTONE EXCURSION, THERE IS MUCH TO SEE AND DO IN BIG SKY
Dinner on own

THURSDAY 12 September 2013

SESSION 6 / BIODIVERSITY, ECOSYSTEM FUNCTION, AND ENVIRONMENTAL CHANGE: PAST, PRESENT AND FUTURE

Session Chair: **Alexandre Anesio** *Session organizers:* **Hugh Ducklow, Jackie Goordial (early career scientist)**

8.30 - 9.00 Keynote lecture **Cristina Takacs-Vesbach**
University of New Mexico UNITED STATES
Microbial Responses to Increased Nutrients in a Changing Environment

9.00 - 9.20 **Jacqueline Goordial**
McGill University CANADA
Microbial life in permafrost and cryptoendolith environments in a hyper-arid Antarctic Dry Valley

9.20 - 9.40 **Thomas Rime**
Swiss Federal Research Institute WSL SWITZERLAND
Pyrosequencing-based assessment of the fungal communities in the cryosphere and soil depths of the Damma glacier, Switzerland

9.40 - 10.00 **Anna Lazzaro**
ETH Zurich SWITZERLAND
Microbial communities in the snowpack of alpine meadows and glacier forefields

COFFEE/TEA BREAK 10.00 - 10.40 (40 mins)

10.40 - 11.00 **Josef Elster**
University of South Bohemia CZECH REPUBLIC
Biogenic calcite structures in Green Lakes, James Ross Island, Antarctica

11.00 - 11.20 **Wim Vyverman**
UGENT BELGIUM
The imprint of glacial history on the biogeography of Antarctic lake-dwelling micro-organisms

11.20 - 11.40 **Catherine Larose**
University of Lyon FRANCE
The Dynamic Arctic Snowpack Microbial Habitat

11.40 - 12.00 **Rebecca Gast**
Woods Hole Oceanographic Institution UNITED STATES
Evaluation of Mixotroph Abundances in Polar Marine Environments by Quantitative PCR

12.00 - 12.20 **Dirk Wagner**
German Research Centre for Geosciences GERMANY
Extremophilic microorganisms in glacier forefields of the Larsemann Hills, East Antarctica

LUNCH 12.20 - 1.50 (1 hour and 30 mins) Huntley Dining Room

SESSION 7 / EARTH'S SUBZERO BIOSPHERE AS A MODEL FOR MICROBIAL LIFE ON OTHER ICY WORLDS

Session Chair: **Anna Lazzaro** *Session organizers:* **Beat Frey, Yongqin Liu, Nozomo Takeuchi, Jun Uetake (early career scientist)**

1.50 - 2.20 Keynote lecture **Kevin Hand**
Jet Propulsion Laboratory, CalTech UNITED STATES
Ocean Worlds of the Outer Solar System

2.20 - 2.40 **Paula Matheus Carnevali**
Desert Research Institute UNITED STATES
Microbial isolation from terrestrial ‘icy worlds’

2.40 - 3.00 **Jeffrey Kargel**
University of Arizona UNITED STATES
Cosmopolitan-to-Refugia Habitat Oscillations: Earth, Mars, Europa

3.00 - 3.20 **Emanuele Kuhn**
Desert Research Institute UNITED STATES
Microbial life in the 18 to 27 m ice core section recovered from Lake Vida, Antarctica

COFFEE/TEA BREAK 3.20 - 4.00 (40 mins)

4.00 - 4.20 **Shawn Doyle**
Louisiana State University UNITED STATES
Antarctic Basal Ice as an Analog for Icy Extraterrestrial Habitats

4.20 - 4.40 **Craig Herbold**
University of Waikato/Joint Genome Institute NEW ZEALAND/UNITED STATES
Global-scale microbial dispersal characterized through genetic analysis of the fumarolic soils of Tramway Ridge, Mt Erebus, Victoria Land

4.40 - 5.00 **Birgit Sattler**
University of Innsbruck AUSTRIA
L.I.F.E. Laser Induced Fluorescence Emission: Non-Invasive Tool to Detect Photosynthetic Pigments Applicable in Various Habitats of the Cryosphere

5.00 - 5.30 Closing Remarks **John Priscu**
Montana State University UNITED STATES

6.00 Dinner on own

LECTURE ABSTRACTS

7 SESSIONS

1 SEPT 9/8.30 - 9.00 KEYNOTE LECTURE

Climate Change Impacts in the Arctic Ocean

Kevin R. Arrigo
Department of Environmental Earth System Science,
Stanford University

The Arctic Ocean has undergone dramatic reductions in sea ice extent and sea ice thickness in recent years. As a result, satellite-based estimates of primary production in ice-free waters have increased dramatically over the last decade and a half. More surprisingly, massive phytoplankton blooms have been observed beneath fully consolidated pack ice in the Chukchi Sea far from the ice edge where sea ice cover has thinned and where melt ponds have proliferated in recent decades. The bloom extended for >100 km in from the ice edge and was characterized by extraordinarily high diatom biomass and rates of production. Biogeochemical evidence suggests that under-ice phytoplankton blooms are widespread on nutrient-rich Arctic continental shelves and that satellite-based estimates of annual primary production in these waters are an order of magnitude too low. These under-ice blooms represent a marked shift in our understanding of Arctic marine ecosystems and their early timing can potentially disrupt lifecycle strategies of both resident and migratory Arctic species.

1 SEPT 9/9.00 - 9.20

Excess methane spikes in Greenlandic glacial ice: in-situ production by psychrophiles?

Rachael H. Rhodes[1], X. Fain[2], C. Stowasser[3], T. Blunier[3], J. Chappellaz[2], J.R. McConnell[4], L.E. Mitchell[1] and E.J. Brook[1]
1) Oregon State University, USA; 2) Laboratoire de Glaciologie et Geophysique de l'Environnement, France; 3) Center for Ice and Climate, University of Copenhagen, Denmark; 4) Desert Research Institute, Reno, USA. Contact *rhodesra@geo.oregonstate.edu*

The cold, dry and severely oligotrophic ice of polar ice sheets is a different potential habitat to basal ice. Recent advances in trace gas measurement in ice cores have allowed sharp spikes of 35-80 ppb methane concentration to be revealed, superimposed on the known decadal-scale climate variability. These features are reproducible and too abrupt in nature to be preserved atmospheric signals. Excess methane in the NEEM-S1-2011 core from Greenland is found in thin (20-100 cm) and infrequent layers that are comparatively rich in carbon- and nitrogen-based impurities. This suggests that psychrophilic microorganisms are able to produce methane at temperatures < -20 ºC and dissolved organic carbon (DOC) levels < 120 ppbC. Possible metabolic pathways will be explored as the origin of the microorganisms deposited on the ice sheet surface is speculated upon. New results from a dry-drilled ice core from a low accumulation (10 $cm.yr^{-1}$) site in NE Greenland will provide opportunity for comparison and testing of hypotheses which link aerosol loading and in-situ trace gas production.

(NSF-OPP-0944552 and -0909541)

1 SEPT 9/9.20 - 9.40

Deep biosphere of the El'gygytgyn Crater Lake/ Far East Russian Arctic: How has the microbial community developed and changed since the impact 3.6 million years ago?

J. Görsch[1], J. Bischoff[1,2], M. Alawi[1], K. Mangelsdorf[1], Dirk Wagner[1],
[1]Helmholtz Centre Potsdam, German Research Centre for Geosciences;
[2]Helmholtz Centre for Polar and Marine Research, Alfred Wegener Institute, Potsdam, Brandenburg, Germany 14473

Despite apparent diverse and active microbial ecosystems in the deep subsurface, the research of the deep biosphere in Arctic environments is still limited. Molecular investigations of sediment material of the El'gygytgyn Crater Lake give us a unique view into the past of the last 3.6 million years of microbial life. Since its formation, the lake was unglaciated and thus led to a continuous accumulation of sediment deposits. These chronological layers contain information about the earlier climate history, and the evolution of life since the meteorite impact. To investigate this climate archive, the El'gygytgyn Crater Lake sediments were drilled in 2009 in the framework of the ICDP project Scientific Drilling in El'gygytgyn Crater Lake.

We started a molecular investigation of the upper 470 ka old sediments. Thereby, we revealed the existence of a diverse archaeal community. Additionally, we found a strong correlation between the biogenic silica and the diversity and abundance of Bacteria and Archaea. This indirect microbial response can be explained by the improved nutrient supply during an algal bloom within warmer periods. Moreover, we applied a multiproxy approach to differentiate between signals of live and dead microorganisms. With the aid of microbial biomarker analysis we detected increased amounts of bacterial and archaeal GDGTs during interglacial periods. These lipid compounds were measured as core lipids that remain stable outside intact cells over geological times and thus indicated a fossil microbial community. Living cells were confirmed by measurements of the potential methane production rate and thus by detection of metabolic active microorganisms in areas of higher archaeal diversity.

Secondly, we extracted DNA from sediments up to an age of 3.6 million years and ran qPCR for a quantitative characterization. To perform metagenomic analysis of recent community and ancient DNA, we separated extracellular and intracellular DNA and apply fingerprint techniques to find areas of high microbial activity. The insights of our study help to understand the development of the microbial community in the El'gygytgyn Crater Lake from the time of its creation.

Grants: Deutsche Forschungsgemeinschaft, DFG-WA-1554/14.

1 SEPT 9/9.40 - 10.00

Early melt ionic pulses within cryoconite holes of the McMurdo Dry Valleys, Antarctica: insight into microbial nutrient cycling and ecosystem function

Jon Telling[1], Alexandre M. Anesio[1], Martyn Tranter[1], Andrew Fountain[2], Thomas Nylen[2], Cristina Takacs-Vesbach[3], Terrill Yazzie[3], Jonathan Hawkings[1], Preeti Kaur[1], Michaela Musilova[1]

[1]School of Geographical Sciences, University of Bristol, Bristol, UK, [2]Portland State University, Dept. of Geology, Portland, US, [3]Dept. of Biology, University of New Mexico, Albuquerque, US

Ice-lidded cryoconite holes provide habitable oases for life on glaciers within the McMurdo Dry Valleys during the austral summer, yet many details of how these ecosystems function remain uncertain. In this study we followed changes in the biogeochemistry of cryoconite holes on Canada Glacier from the pre-melt season when they are still fully frozen, through the first melt pulse of ion enriched waters, to more fully developed cryoconite holes. We examine temporal changes in the geochemistry, microbial activity (photosynthesis, bacterial production, nitrogenase activity) and microbial diversity. We demonstrate how the first melt pulses are nutrient rich with different C:N:P ratios and stimulated rates of heterotrophic microbiological activity than both (melted) time zero frozen cryoconite holes and later season cryoconite holes. We suggest that these ionic pulse events can be viewed as natural nutrient amendment experiments giving new insight into limitations on growth and ecosystem function within these extreme habitats.

This research is supported by NSF grant ANT1115245 to AF/CT-V, and NERC grant NE/G00496X/1 to AMA.

1 SEPT 9/10.40 - 11.00

Diversity of ice embedded microorganisms from Scarisoara Cave, Romania

Itcus C[1], Hillebrand-Voiculescu AM[2], Pascu D[1], Rusu A[1], Ardelean I[1], Persoiu A[3], Brad T[4], Popa E[1], Onac BP[4,5], Purcarea C[1]

[1]Institute of Biology Bucharest, Bucharest, Romania
[2]Emil Racoviță Institute of Speleology, Bucharest, Romania
[3]Ştefan cel Mare University, Suceava, Romania
[4]Emil Racoviță Institute of Speleology, Cluj-Napoca, Romania
[5]Department of Geology, University of South Florida, USA

Scarisoara Ice Cave (Romania) hosts one of world's largest and oldest underground glacier. This study is the first characterization of prokaryotic and eukaryotic microorganisms from the subterranean ice block of this cave, thriving in both organic-rich- and clear ice, in relation with their chronological distribution and past climatic changes. Samples were collected from ice layers of different age, from present to ~900 cal. yrs. BP, and the diversity of microbial communities was assessed by classical cultivation and molecular techniques. Microorganisms from ice samples were cultivated at 4˚C and 15˚C in different media, in the presence and absence of light. Epifluorescence microscopy analysis indicates the presence of phototrophic prokaryotes and eukaryotes in sunlight-exposed ice. Total DNA was isolated from each ice sample and the bacterial and eukaryotic SSU-rRNA genes were amplified and analyzed by DGGE. The chemical composition of both deeply buried (>10 m inside the ice block) and surface ice layers were analyzed in relation to their age and organic content.

The presence of bacteria and eukaryotes in all the analyzed samples was asserted by both culture dependent and independent methods. The composition of cold-adapted ice embedded microbiota varied with the age and organic content of their ice habitat. DGGE analysis and sequencing allowed bacterial identification in each ice sample up to 900 years BP. These findings can be further used to reconstruct changes in the microbial diversity over the past approximately 5000 years, in correlation with climatic and environmental changes recorded by this cave ice block.

AKNOWLEDGMENTS: This study was financially supported by ANCS-UEFISCDI Romania, grant PN-II-ID-PCE-2011-3-0742 (contract nr. 159/28.10.2011).

1 SEPT 9/11.00 - 11.20

Bacterial diversity of ice surface and moss gemmae aggregation on disappearing tropical glacier in Uganda

Jun Uetake[1], Sota Tanaka[2], Kosuke Hara[3], Yukiko Tanabe[4], Satoshi Imura[1], Hideaki Motoyama[1], Shiro Koshima[3]
1: National Institute of Polar Research, Tokyo, Japan 190-8518
2: Faculty of Science, Chiba Univ., Chiba, Japan, 283-8522
3: Wildlife Res. Center, Kyoto Univ., Kyoto, Japan, 606-8203
4: Waseda Inst. for Advanced study, Waseda Univ. Tokyo, Japan, 169-8050

Tropical region is still missing area of glacier biology, though most studies on glacier ever had been reported frequently from mid latitude to bipolar region.In tropical regions glacier retreat is more significant, especially glaciers in Mt. Ruwenzori where located between Uganda and Congo was expected to disappear within a decade.

Climate in Mt. Ruwenzori is very different from mid Latitude Mountains, most major difference are no seasonal cycle of air temperature and no long term frozen period. These features may support the presence of unique biological aggregation, which formed by gemmae of cosmoporitan moss (*Ceratodon purpureus*). Glacial moss gemmae aggregation (GMGA) is 18.7mm length, 12.7mm width and 8.36mm depth on average (n=96) and concentrated around glacier terminus and inside temperature of GMGA rose up around 10 degree despite located on the ice. On the bared bed rock which recently glacier ice was retreat, dried GMGA which fell from glacier were frequently observed and some of these become soil-like structure. However, no studies for microbiology of GMGA were conducted.

In order to investigate microbial community of GMGA and ecological relation ship between GMGA and glacier surface and soil on bared bedrock, we analyzed diversity and community strsucture of bacterial 16S rRNA. Cluster analysis of 81073 sequences belong to abundant OTU from 5 sites shows difference of bacterial community structure between GMGA and other glacier surface is similar and 62% of total 590 OTU from same glacier (3 sites) is mutual in all. Therefore, small environmental change such as invasion of mosses or mild temperature rise would not largely affect bacterial community. Otherwise, community structure of soil on bared bedrock is completely different from glacier samples including GMGA and species diversity is lower than glacier. This may indicate bacterial community of GMGA is unstable for large environmental change such as much temperature rise or dryness. These evidences imply that glacial ecosystem will disappear when glacier ice will completely melt.

1 SEPT 9/11.20 - 11.40

Cell-mineral interaction and the bioaggregation of cyanobacteria with inorganic particulates upon glacier surfaces

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Bioaggregates are key components of surface water and soil environments that form when cells adhere to each other and to organic and inorganic particles, aided by extracellular polymeric substances (EPS), creating mini ecosystems highly relevant for water quality and nutrient cycling. Cryoconite granules, photoautotrophic aggregates found upon glacier surfaces, can be considered exemplar bioaggregates. Their involvement in supraglacial nutrient cycling has been well documented, yet little is known about the cell-mineral interaction and aggregation mechanisms that cause these bioaggregates to develop. This study combines microscopy and spectroscopy to study these bioaggregates and the co-aggregation of cyanobacteria and mineral particles, finding that a variety of mineral powders readily co-aggregate with cyanobacteria. Various physicochemical conditions, including ionic strength, temperature and growth phase, were shown to affect both photoautotroph survival and attachment. Fourier transform infrared (FTIR) imaging suggested that EPS–mineral interactions dominated cell–mineral attachment. Elemental carbon showed greater evidence for hydrophobic and cationic protein interactions, whilst quartz showed greater evidence for polysaccharide and carboxyl group interactions, suggesting that an array of attachment mechanisms may exist. The above suggests that there is a strong biological control over the aggregation of aeolian particulate matter on glacier surfaces.

1 SEPT 9/11.40 - 12.00

Snow algal communities on mountain glaciers in the Suntar Khayata region, Eastern Siberia in Russia

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Snow algae are cold-tolerant algae growing on snow and ice and have been reported on glaciers in many regions of the world. Snow algae can reduce the surface albedo of snow and ice and significantly affect glacier melting. In addition, structures of snow algal communities vary from region to region so their effects on glacier melting may vary too. This is the first report on snow algal communities on glaciers in the Suntar Khayata mountains in eastern Siberia, Russia.

Two taxa of green algae and five taxa of cyanobacteria were observed on the surface of the glaciers. These taxa were Ancylonema nordenskioeldii, Chloromonas sp., Chroococcaceae cyanobacterium, Calothrix parientia and three taxa of Oscillatoriaceae cyanobacterium. The total cell volume biomass ranged from 29 to 3967 μL m-2, which is equivalent to that on Asian glaciers. The community structure showed that Ancylonema nordenskioeldii, which is common species on glaciers in Arctic region, was dominant in the ice areas, while Chloromonas sp. was dominant in the snow areas. The algal distribution is similar to other Arctic glaciers. The amount of cryoconite on the ice surfaces was 47 g m-2 which is similar to other Arctic glaciers, but much smaller compared with the glaciers in Asia. The small abundance of cryoconite may be due to lack of filamentous cyanobacteria, which play a role to form the cryoconite aggregate structure.

2 SEPT 9/1.20 - 1.50 KEYNOTE LECTURE

Microbial structures and functions in glacier forefields: current scientific challenges

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The genesis of soils in the forefield of receding glaciers involves a complex network of physical, chemical, and biological processes. Microorganisms are of particular interest since they act as pioneers and catalyze important biogeochemical processes in the early stages of ecosystem development. Numerous scientific projects have addressed the microbial structures and functions along the chronosequence. Many of these studies were confronted with similar scientific challenges. These include: (i) The huge heterogeneity in glacier forefields hampers the quantification of physical, chemical and biological parameters. A proper quantification should consider the dominant morphotypes (e.g. ice, moraines, sand hills, landslides, rivers, flood plains). (ii) Field projects have limited resources and therefore focus on specific point measurements along the chronosequence. Extrapolation of such point data to the catchment level requires geostatistical tools which consider the spatial and temporal variability. (iii) Glacier forefields are highly dynamic in time. Many parameters are subject to daily and seasonal cycles and to stress factors such as extreme meteorological events (e.g. floods, droughts). (iv) Some reports have a tendency to be descriptive and present correlations but not basic mechanisms. The development of models with predictive power requires field scale experiments to identify cause and effect relationships and their underlying key drivers.

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2 SEPT 9/2.10 - 2.30

FEW PHYLOTYPES CONSUME ADDED LABILE ORGANIC CARBON IN HIGH ARCTIC BARRENS SOILS

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Polar warming will lead to increased labile organic carbon in Arctic soils, both from the release of organic carbon stored in permafrost and increased plant production. We determined the activity and composition of the active heterotrophic bacteria in soil cores from the Canadian High Arctic by stable isotope probing (SIP) with a labile soil organic matter analogue, ^{13}C-labeled algal lysate. Respiration rates were significantly higher with substrate added compared to the controls. There was a significant decrease in diversity and a shift in community composition following addition of labile carbon. Members of the Actinobacteria, Proteobacteria, and Firmicutes were the primary consumers of the added carbon at all sites, with three sites dominated by Actinobacteria and the fourth dominated by Firmicutes. Multivariate and cluster analysis of samples from multiple sites showed a clear clustering of the labile carbon consuming communities, while there was less similarity between the unincubated soils from different sites. These results suggest the same few phylotypes are active and responsive to increased labile organic carbon across all sampling sites. These groups of bacteria should be the focus of future study, as they will be more likely to react to future climate change and play important roles in global warming feedbacks.

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2 SEPT 9/1.50 - 2.10

Microbial carbon cycling in high Arctic permafrost polygons: responses to a warming climate

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The research is funded by U. S. Department of Energy Office of Science, Genomic Science Program (DE-SC0004902)

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The fate of permafrost soil organic carbon (SOC) under a warming climate and the consequences of microbial decomposition of SOC into CO_2 and CH_4 represent one of the most significant potential feedbacks from terrestrial ecosystems to the atmosphere. However, the magnitude and rate of microbial feedback is highly uncertain. This presentation will give an overview of research targeting ice wedge polygons on Axel Heiberg Island (AHI) in Nunavut, Canada, using combined -omic, geochemical, and isotopic approaches in field based gas flux measurements and long-term laboratory permafrost core thawing and microcosm experiments. With thawing, permafrost-affected peat deposits are currently described to be sources of CH_4 and sinks of CO_2, whereas our measurements of *in situ* flux measurements coupled with 18 month thawing experiments of intact mineral (~1% wt. SOC) soil cores from AHI ice wedge polygons indicates that they are consistent sources of CO_2 (20-60 mmol m^{-2} day^{-1}) and sinks for atmospheric CH_4 (-3 to -1 μmol m^{-2} day^{-1}). After 1.5 year of continuous thawing (4°C), intact cores exhibited steadily increasing CO_2 emissions for the first 1 year of thawing consistent with *in situ* CO_2 fluxes, but surprisingly atmospheric CH_4 uptake continued even for water-saturated cores, but at lower rates than seen *in situ* or under more aerated conditions. The $\delta^{13}C$ of released CO_2 both *in situ* and in thawed soils ranged from -14 to -32‰, indicating that heterotrophic respiration accounted for CO_2 flux from the soil. The microbial community in the native AHI soil/permafrost was dominated by Bacteria, with 1% of Archaea, and ~0.1% of Eukaryota. Bacteria were comprised largely of heterotrophs belonging to Actinobacteria, followed by α-Proteobacteria, including N_2 fixers (*Bradyrhizobium*, *Rhizobium*) and type II CH_4 oxidizers (*Methylocella Methylobacterium*). Metaproteomic analyses of native, thawed, and amended soil microcosms confirmed the activity of the above N_2 fixers and type II CH_4 oxidizers and indicated that the activity of microbial community increases with thaw and nutritional availability. The metaproteome data also suggested that the active microbial communities are limited by accessible labile, and perhaps young, organic carbon. The extractable component of the SOC pre and post thawing was predominantly comprised of lipids. The $\delta^{14}C$ of the PLFA revealed that even though the carbon from viable cells throughout the active layer is 5.5 kyr younger than that of the bulk SOC (6 kyr) at corresponding depth, the $\delta^{14}C$ of the PLFA is consistent with carbon originating from atmospheric CO_2, and actively incorporated through microbial activity during the past few hundred years. In both native and thawed state, it is the cold-adapted soil microbial community that is actively metabolizing SOC from deeper permafrost as well as exchanging CO_2 and CH_4 with the atmosphere. Matching the information provided by the meta-omic data with constraints from isotopic analyses of the membrane lipids, the SOC and C flux will make it possible to construct a metabolic network for the microbial degradation of permafrost SOC at AHI and, in doing so, take steps to improve current climate models.

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2 SEPT 9/2.30 - 2.50

Microbial respiration in high Arctic cryptoendolithic habitats

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Cryptoendolithic microbial communities are widespread in the Canadian Arctic, inhabiting rocks that provide space for growth, moisture retention, and protection from climatic extremes. Microbial activity occurs predominantly during summer months when air temperatures are above freezing, rainfall is frequent, and solar insolation is continuous. In order to characterize this microbial activity, we conducted field-based studies of carbon fluxes to measure [CO_2] and $\delta^{13}C$. Under dry, sunlit conditions, measurements of CO_2 or $\delta^{13}C$ showed no notable differences when compared to ambient air. Upon wetting, [CO_2] increased with a concomitant decrease in $\delta^{13}C$ values. Simulations of dark conditions resulted in further increased CO_2 flux from the rock, which subsequently decreased when exposed to sunlight. These findings suggest that microbial activity is activated by moisture, and that respiration rates outpace photosynthesis due to an unaccounted for source of carbon, causing a net flux from the cryptoendolithic environment to the atmosphere. The cryptoendolithic microbial community was subsequently characterized by 454 pyrosequencing, revealing that Cyanobacteria comprise up to 44% of the total population near the rock surface. In contrast, heterotrophic Actinobacteria and Alphaproteobacteria dominate at depth beneath the photic zone. Microscopic evaluation showed mineral surfaces deeper within the rock coated with both living microorganisms as well as organic matter morphologically similar to bacteria. The latter are believed to have been incorporated during sediment deposition, providing a rich energy source for modern heterotrophy that can explain the net release of CO_2. These organic coatings are absent in the top several millimeters of exposed rock faces, suggesting that they are fully oxidized to CO_2 as heterotrophic bacteria migrate deeper into the subsurface. If this organic matter is ancient and our observations of respiration outpacing photosynthesis are representative, then these cryptoendolithic environments are likely a long-term net source of carbon to the atmosphere, a rare phenomenon among ecosystems at the surface of the Earth. In light of widely accepted predictions of warmer and wetter summer periods, this pool of organic carbon may result in even greater CO_2 fluxes in future years as a result of expected higher levels of cryptoendolithic microbial activity. We thank NSF for support for this research under NSF-OPP-0909482.

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2 SEPT 9/2.50 - 3.10

Sources and Types of Active Airborne Bacteria

Tina Šantl-Temkiv[1], Mark Lever[2], Maher Sahyoun[3,4], Ulrich G Karlson[5], Niels W Nielsen[4], Jens H Sørensen[4], Ulrik S Korsholm[4], Kai Finster[1,3]
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Active airborne bacteria may shape atmospheric processes, e.g. the turnover of organic compounds, as well as patterns of bacterial biogeography. Little is known, however, what fraction of the ~4*10^{16} cells estimated to enter the atmosphere from terrestrial surfaces every second (Burrows et al. 2009) is active within the atmosphere. Viable airborne bacteria have the physiological potential to both withstand atmospheric stress and grow on organic compounds abundant in the atmosphere (Amato et al 2005, Šantl-Temkiv et al 2013). Nonetheless, bacterial activity within the atmosphere has yet to be confirmed. We present the methodology and preliminary results of a study that combines metagenomics and metatranciptomics of airborne bacterial communities with the analysis of aerosol origin. In addition, we outline an approach to investigate total and active bacterial communities in habitats that could serve as sources of airborne microbes. This approach will enable us to compare source bacterial communities to atmospheric communities, and determine whether bacteria from certain environments, e.g. growing as epiphytes on terrestrial plants, are pre-adapted to be active at atmospheric conditions.

References

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Acknowledgements

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3 SEPT 9/4.20 - 4.40

Geographical variations in cryoconite on glaciers in Asian high mountains.

Nozomu Takeuchi, Dept of Earth Sciences, Chiba University, Japan.

Cryoconite is microbial aggregate on glacial ice and can be found on glaciers worldwide. Cryoconite usually forms spherical granules by entanglement of filamentous cyanobacteria. However, their size, color, and inner structure vary among glaciers or regions, probably due to differences of microbial community or chemical and physical conditions on glaciers. Because of their effect on surface albedo and melting of glaciers, understanding such geographical variations and formation process of cryoconite is important. Cryoconite collected from various glaciers in Asian high mountains, including Himalayas, Tienshan, Qilian, Pamir, and Altai, were analyzed. The characteristics of cryoconite can be divided mainly into three groups, which were southern, middle, and northern types. The southern-type cryoconite was dark, contained relatively coarse minerals, and was found in Himalayan glaciers. The middle-type cryoconite was pale in color, higher content of organic matter, and more densely covered with cyanobacteria, and was found in Qilian, Tienshan mountains. The northern-type was dark, smaller in size, sparsely covered with cyanobacteria, and was found in Pamir and Altai mountains. The three geographical regions were corresponded to distinctive climate regimes: strong monsoon climate in south, dry and sunny climate in middle, and arctic cold climate in north, suggesting that the climate conditions is one of the factors to characterize the cryoconite.

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3 SEPT 9/3.50 - 4.20 KEYNOTE LECTURE

The interaction of physical and stoichiometric thresholds in regulating Arctic ecosystems.

Joshua Schimel, University of California Santa Barbara

Arctic ecosystems exist on the cusp of critical physical thresholds—the "zero-degree curtain" being the obvious one. Freezing dominates life for arctic microbes. However, the extreme environment indirectly drives microbial dynamics by inducing resource limitations that may have more immediately powerful effects on communities than the climate itself. In the low Arctic, where the climate is "balmy," vegetation is lush, fully covering the land. Yet, while plants grow with their leaves in the warm summertime air, microbes live in the insulated, cold soil. This limits decomposition and nutrient recycling, and produces a biotic system that is intensely nutrient limited, so much so that microbes don't have enough N to produce the extracellular enzymes necessary to break down plant detritus and keep nutrients cycling. As a result, the decomposition system lapses into N-induced constipation. However, when soils freeze, N is mineralized because different substrates become available. This shift is observable at all scales from soil nutrient pools down to cellular C-allocation patterns. Amino acids are used as N-sources during summer but as C-sources during the winter. In the high Arctic, on the other hand, water is limiting and soils dry enough that resource diffusion constrains microbial processes. Warming accelerates microbial activity, but it takes increased rainfall to connect microbes with their resources and so switch on processes such as nitrification. Understanding microbial life in arctic soils requires integrating the physical thresholds associated with freezing and drought with resource limitation and stoichiometric imbalances. Importantly, crossing physical thresholds can cause microbial systems to cross stoichiometric thresholds—together these transform microbial physiology and ecosystem function.

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3 SEPT 9/4.40 - 5.00

Viruses keep Arctic microbial adaptation from its breaking point

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Environmental Microbial Genomics, CNRS, Ecole Centrale de Lyon, Université de Lyon, Ecully, France.

Microbial adaptation to changes in the environment is the first step to evolution. The acquisition of genes and development of novel enzymes in response to environmental perturbations are critical to successful adaptation. But can microorganisms in extreme environments, such as the Arctic, adapt fast enough to respond to rapid anthropogenic changes? Pollutants are tilting biogeochemical cycles and climate change is causing glacial retreat and possibly introducing a flow of microorganism into new niches.

Rapid adaptation to environmental perturbations could be attained through transduction, virus mediated transfer of genetic material between bacteria. Viruses have been suggested to play a key role in polar environments, and the relatively high virus to bacteria ratio might provide the answer to how cold adapted communities are dealing with these changes. Moreover, the potential broad host ranges would make them effective vectors. As an example a strong signature of phages for Ralstonia, a known carrier of mercury resistance genes, was seen in the virome of an Arctic glacier relative to other environmental viromes.

Data on environmental viruses is scarce and tracking their interactions with bacteria has only been addressed through single strain based experiments. Nevertheless, CRISPRs (Clustered Interspaced Short Palindromic Repeats) provide a history of viral-host interactions and might document this crucial viral influence on Arctic microbial community adaptation. Thus comparative CRISPR metagenomics will be used to describe the possible interaction between viruses and microorganisms in different ecosystems.

3 SEPT 9/5.00 - 5.20

Diversity of soil fungi does not decrease with latitude along the entire North American Arctic Transect but is structured by climate and vegetation

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Fungi are ubiquitous in Arctic soils, where they function as symbionts and decomposers and may affect the carbon balance of terrestrial ecosystems subjected to climate change. Yet little is known about the composition of fungal communities in soil at high. Key questions include how fungal species and communities are distributed with respect to latitude and what environmental factors drive their distributions. We sampled soils from six locations along a transect representing all five bioclimatic subzones of the Arctic and sequenced large clone libraries of fungal ITS amplicons. We recorded 1267 Operational Taxonomic Units (OTUs), which spanned eight phyla, 22 classes, 70 orders, 108 families, and 177 genera falling into all major functional groups. Ascomycota (844 OTUs) and Basidiomycota (344 OTUs) dominated the fungal communities. While the most abundant OTUs were distributed across multiple continents, fungal communities showed niche preferences with regard to regional climate, local soil factors and plant communities, as well as frost-driven patterned-ground features. As a result, fungal community composition changed progressively from one subzone to the next. Unexpectedly, fungal species richness at the plot scale did not decline with latitude. This result was due to a decrease in richness of ectomycorrhizal species balanced by an increase in lichen species with increasing latitude. Our results show that dominant fungal species are capable of rapid, wide dispersal, and may be impervious to climate change. However, overall fungal community composition is tightly correlated with climate and other environmental factors, and thus will be likely be affected by ongoing warming.

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3 SEPT 9/5.00 - 5.20

A Multi-Habitat Survey of Microbial Life in the McMurdo Dry Valleys, Antarctica

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The McMurdo Dry Valleys, Antarctica, are a microbially dominated ecosystem with an absence of vascular plants and limited invertebrate diversity. An analysis of bacterial 16S rRNA gene sequence data was performed using ~450 samples collected for a variety of studies from four distinct habitats: soils, streams, lakes, and cryoconites. Approximately 2.1 million high quality sequence reads were generated representing ~39,000 operational taxonomic units (OTUs, 97% identity). On average soils were the least diverse habitat while samples from streams (sediments and microbial mats) were the most diverse with ~200 and 500 OTUs per 1000 sequences, respectively. The phyla level taxonomy varied greatly among habitat types: the most abundant phyla were Cyanobacteria in streams and cryoconites, Proteobacteria in lakes, and Acidobacteria in soils. Principal coordinate analyses of all samples using a phylogenetically informed distance matrix (UniFrac) demonstrated discreet clustering by habit type with overlap found only between the cryoconite and stream samples. Among habitats there was no evidence of clustering by geographic location. Further clustering was observed within habitats according to mat type (orange, black, etc.) in streams, habitat severity (salinity, elevation, etc.) in soils, and sampling location in lakes. Results from this survey suggest the Dry Valleys contain diverse microbial communities with environmental filtering determining the composition among and within habitat types.

This research is supported by NSF grant 1142102 to CDTV and DJVH, and 0838879 to CDTV, JEB and MNG.

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4 SEPT 10/8.30 - 9.00 KEYNOTE LECTURE

Scientific Exploration of Subglacial Lake Whillans, West Antarctica

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Subglacial Lake Whillans (SLW) is one of numerous lakes that comprise an extensive drainage basin beneath the lower portion of the Whillans Ice Stream on the Siple Coast of West Antarctica. The surface area of SLW is 59 km^2 ± 12 km^2 and radar observations suggested the lake was ~800 mbs with a maximum water column thickness of 5-6 m. Water enters the lake from the upstream direction and drains downstream at rates of ~10 m^3 s^{-1}. Based on morphometry and fill-drain cycles, SLW has a volume of <0.5 km^3 and the residence time of the lake is estimated to be < 10 y. During January 2013, a hot water drilling system was used to create an access borehole for direct sampling and to conduct measurements for constraining the physical, chemical, and biological characteristics of SLW. A microbiologically clean access strategy was achieved through the use four complementary technologies [(*i*) filtration, (*ii*) ultraviolet (UV) irradiation, (*iii*) pasteurization, and (*iv*) chemical disinfection] that reduced microbial contamination and viability in the drilling fluid and on equipment deployed in the borehole. At 0802 on 27 January, the drill was at 801 mbs and there were indications of unloading on the load cell. Two minutes later, the head above the downhole pump (stationed at ~110m depth) rapidly rose and remained at 80 mbs, indicating hydrostatic equilibration between the borehole and lake water. The water recovered from Niskin casts in the lake contained microbial cell concentrations of 0.9-1 x 10^5 cells mL^{-1}, which were appreciably higher than values observed in water from the drilling system and borehole (2-7 x 10^2 cells mL^{-1}). Significant rates of macromolecular synthesis, respiration, and CO_2 fixation were measured in samples obtained from the water column and sediments, indicating the presence of viable microorganisms and providing evidence for a microbial food web in SLW. Molecular diversity analysis of the water and sediments has provided key data to assess the composition and physiological potential of microorganisms inhabiting the SLW ecosystem.
The WISSARD project is supported by the National Science Foundation's Division of Polar Programs through grants 0838933, 0838896, 0838941, 0839142, 0839059, 0838885, 0838855, 0838763, 0839107, 0838947, 0838854, 0838764 and 1142123.

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4 SEPT 10/9:00 - 9.20

Geochemistry of subglacial Lake Whillans, West Antarctica: Implications for microbial activity.

Mark Skidmore[1], Andrew Mitchell[2], Carlo Barbante[3], Alex Michaud[4], Trista Vick-Majors[4], John Priscu[4]
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Subglacial Lake Whillans is located beneath the Whillans Ice Stream in West Antarctica. The lake is situated beneath 800 m of ice and ~ 70 km upstream of the grounding line where Whillans Ice Stream terminates into the Ross Sea. Water and sediment samples were recovered from the lake, using clean access drilling technologies, in January, 2013.

Isotopic analysis of the lake waters indicates basal meltwater from the ice sheet as the dominant water source. Geochemical analysis of the lake waters reveal it is freshwater with total dissolved solids concentrations about 1/70th that of sea water. However, mineral weathering is a significant source of solute to the lake water with a contribution also from sea water. Nutrients N and P are present at micromolar concentrations.

The sediment porewaters from shallow cores (~ 40 cm depth) of the subglacial lake sediments indicate increasing solute concentration with depth, with up to ~ five times greater solute concentrations than in the lake waters.

Collectively the aqueous geochemistry indicates an environment favorable for microbial activity. Thus, microbially-driven mineral weathering appears likely beneath the Whillans Ice Stream, as has been demonstrated in other subglacial systems, including in subglacial sediments of the neighboring Kamb Ice Stream.

Funding: NSF-OPP 0838933 and Italian National Program for Antarctic Research

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4 SEPT 10/9:20 - 9.40

Physiological Ecology of Bacteria in the water column of Subglacial Lake Whillans, Antarctica

Trista Vick-Majors, Alex Michaud, and John Priscu, Department of Land Resources and Environmental Sciences, Montana State University, Bozeman, MT, USA, 59717.

Recent recognition of the widespread nature of liquid water beneath the Antarctic ice sheet has generated new interest in subglacial aquatic environments as microbial habitats. These environments have been hypothesized to contain active ecosystems and encompass stores of organic matter and nutrients of unquantified significance to Earth's biogeochemical cycles. We report here on the collection of the first intact water samples from Subglacial Lake Whillans (SLW), and provide the first direct evidence for active microbial life in a subglacial water column.

SLW lies 800 m beneath the ice surface of Whillans Ice Stream, West Antarctica. Remote sensing data indicate that the lake lies near the end of a hydrological flow-path and periodically flushes into the sea under the Ross Ice Shelf. Epifluorescent microscopy showed that water collected from SLW in clean Niskin bottles contained ~10^5 cells mL^{-1}. Metabolic activity was measured both directly and indirectly by measuring (i) cellular ATP concentration, (ii) respiratory electron transport activity, and (iii) cellular incorporation of ^{14}C-acetate, ^{14}C-bicarbonate, ^{14}C-leucine, ^{3}H-thymidine, and ^{3}H-leucine.

ATP levels (avg +/- SD = 3.7 +/- 0.4 pmol L^{-1}) in the lake samples were significantly ($p<0.05$) greater than levels in drill borehole water and blanks indicating active biosynthesis of this critical metabolic compound. Time series measurements of electron transport system activity and radiolabelled substrate incorporation (except for acetate) were also significantly ($p<0.05$) greater than killed samples. Bacterial growth efficiency (BGE = BP/(BP+BR)) based on ^{14}C-labelled leucine incubations was 0.12, which is relatively low compared to other Antarctic lakes. ^{3}H-leucine incubations amended with combinations of C, N, and P revealed phosphorus limitation of heterotrophic activity in SLW. Taken together, these results show that SLW contains active microbial consortia and have implications for nutrient cycling under Antarctic ice.

Funding provided by NSF-OPP grant 0838933.

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4 SEPT 10/9:40 - 10.00

Molecular Analysis of Microbial Communities inhabiting Subglacial Lake Whillans, Antarctica

Amanda Achberger[1], Carlo Barbante[2], Andrew Mitchell[3], Alexander Michaud[4], Jill Mikucki[5], John Priscu[4], Mark Skidmore[6], Tristy Vick-Majors[4], and Brent Christner[1]
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A complex hydrologic system consisting of lakes, streams, and water saturated sediments exists beneath the Antarctic Ice Sheet. Although subglacial aquatic environments are hypothesized to harbor active microbial communities, direct sampling of these potential ecosystems has been lacking. During January 2013, the Whillans Ice Stream Subglacial Access Research Drilling (WISSARD) Project created a ~800 m borehole to access Subglacial Lake Whillans (SLW) and collected water and sediment samples. The biotic and abiotic particulates larger than 10, 3, and 0.2 μm were fractionated and concentrated *in situ* on 142 mm filters using a custom filtration device that was lowered into the lake. In addition, the upper 40 cm of lake sediments were retrieved and sampled at 2 cm intervals. Nucleic acids were extracted from the samples and phylogenetic analysis based on the V4 region of the 16S rRNA gene was used to characterize the prokaryotic microbial community structure in SLW. The significance of the molecular data for deciphering ecosystem processes in SLW are discussed. This research was supported by the National Science Foundation through grant ANT 0838941 and a Graduate Research Fellowship award to A.A.

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4 SEPT 10/10.00 - 10.20

Microbial activity in the sediments of Subglacial Lake Whillans

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Subglacial Lake Whillans is situated 800m below the surface of the Whillans Ice Stream (WIS), in a region of the continent that drains much of the water from below the West Antarctic Ice Sheet. Water draining below the WIS creates a system of drainage channels, lakes, and saturated sediment. The saturated sediment near the upper reaches of the WIS has been estimated to be up to a kilometer thick. These saturated sediments have been thought to contain a large reservoir of organic carbon and support viable microorganisms. We collected ~ 40 cm sediment cores during January 2013 to determine the geomicrobiological characteristics of the surface sediments. Biological incorporation of ^{14}C-acetate, ^{3}H-leucine and ^{3}H-thymidine in 4^{o}C, dark incubations was significant in the upper 2 cm of the sediment column. Rates of ^{3}H-leucine and thymidine incorporation were similar to ^{3}H-leucine rates measured in the perennially ice-covered lakes in the Taylor Valley, Antarctica. Fixation of ^{14}C-bicarbonate only occurred 38-40cm below the surface of the cores. Our results reveal the presence of an active microbial assemblage in the sediments beneath Lake Whillans consisting of heterotrophic and chemoautotrophic organisms.

Funding: NSF-OPP 0838933

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4 SEPT 10/11.00 - 11.20

Elusive microbial life at the uppermost water layer in subglacial Lake Vostok, East Antarctica

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The objective was to estimate microbial content of accretion ice originating from frozen water of the subglacial Lake Vostok buried beneath 4-km thick East Antarctic ice sheet as well as first samples of the lake water (RAE57-58) with the ultimate goal to discover the life in this extreme icy environment.

As a result, the DNA study constrained by Ancient DNA research criteria along with cell enumeration by flow cytometry has pointed out that the deepest closest to the ice-water boundary accretion ice (3764m) contains the very low microbial biomass generating no reliable DNA signals in PCR and is comparable with background contamination level (a few cells per ml).

The comprehensive analyses of the first lake water (mixed with a drill fluid at ratio 1:1) sample froze on a drill bit at 3769.3m depth upon the subglacial Lake Vostok entry (February 5, 2012) are finally got finished. The cell concentrations in the sample showed 167 cells per ml (counted by flow cytofluorometry) coming up with several bacterial phylotypes identified by sequencing of several regions of the 16S rRNA genes. Amongst them all but one were considered to be contaminants (in our contaminant library, including drill fluid findings). The remaining phylotype successfully passing all contamination criteria is proved hitherto-unknown type of bacterium (group of clones, 3 allelic variants) showing less than 86% similarity with known taxa. Its phylogenetic assignment to bacterial divisions or lineages was also unsuccessful despite of the RDP has classified it belonging to OD1 uncultured Candidate Division. Archaea were not detected nor in deepest accretion nor in the lake water sample.

Thus, the unidentified and unclassified bacterial phylotype for the first time discovered in the uppermost water layer in subglacial Lake Vostok might represent ingenious cell populations in the lake. The proof will (and further discoveries may) come with analyses of several new bigger and cleaner lake water (frozen-in-borehole – from full cylinder until moon-shaped ice) samples which are under study now.

4 SEPT 10/11.20 - 11.40

Methane flux from subglacial sediments at Robertson Glacier, Canadian Rockies

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Methane is over 20 times more effective than CO_2 as a greenhouse gas. Thus, its atmospheric concentration and the processes controlling it are an important component of the global climate system. Recent research has shown methanogenesis in subglacial sediments, and it has been proposed that there is the potential for large methane reservoirs beneath the Antarctic Ice Sheet. However, the net contribution from subglacial systems to the global methane budget is poorly understood due to a dearth of empirical data.

Here we demonstrate, using measurements via the static chamber method, the flux of methane from recently exposed sediments at Robertson Glacier, Canadian Rockies. Methane concentrations were measured from samples collected from gas flux chambers, placed on the sediment surface, in transects both parallel to and perpendicular to the glacier terminus. Measurements were made over a melt season, July to September, and used to determine both spatial and temporal variability in the methane flux at this retreating, temperate glacier. The chamber farthest from the glacier terminus, approximately 50 m down valley, had an average flux close to zero whereas the chambers nearest the terminus had the highest average fluxes. Smaller volume gas flux chambers were also employed to measure fluxes at 5, 10 and 15 cm depths. The highest methane efflux was measured at a depth of 15 cm in sediments exposed by ice front retreat only days prior to measurement.

Shallow sediment cores were also collected adjacent to the static chambers and frozen immediately. Methane was measured from the thawed core samples to create a vertical concentration profile for the sediment cores. Methane concentrations are higher than atmospheric in all cases. Linkages between core profile methane concentrations and net methane fluxes are discussed based on diffusion and other processes in the sediments.

Funding: NASA Exobiology Grant NNX10AT31G and GSA Research Grant

4 SEPT 10/11.40 - 12.00

Molecular evidence for an active endogenous microbiome beneath glacial ice

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Geologic, chemical and isotopic evidence indicate that Earth has experienced numerous intervals of widespread glaciation throughout its history, with roughly 11% of present day Earth's land surface covered in ice. Despite the pervasive nature of glacial ice both today and in Earth's past and the potential contribution of these systems to global biogeochemical cycles, the composition and phylogenetic structure of an active microbial community in subglacial systems has yet to be described. Here, using RNA-based approaches, we demonstrate the presence of active and endogenous archaeal, bacterial and eukaryal assemblages in cold (0–1□°C) subglacial sediments sampled from Robertson Glacier, Alberta, Canada. Patterns in the phylogenetic structure and composition of subglacial sediment small subunit (SSU) ribosomal RNA (rRNA) assemblages indicate greater diversity and evenness than in glacial surface environments, possibly due to facilitative or competitive interactions among populations in the subglacial environment. The combination of phylogenetically more even and more diverse assemblages in the subglacial environment suggests minimal niche overlap and optimization to capture a wider spectrum of the limited nutrients and chemical energy made available from weathering of bedrock minerals. The prevalence of SSU rRNA affiliated with lithoautotrophic bacteria, autotrophic methane producing archaea and heterotrophic eukarya in the subglacial environment is consistent with this hypothesis and suggests an active contribution to the global carbon cycle. Collectively, our findings demonstrate that subglacial environments harbor endogenous active ecosystems that have the potential to impact global biogeochemical cycles over extended periods of time.

Funding: NASA Exobiology Grant NNX10AT31G

4 SEPT 10/12.00 - 12.20

Differences between the Arctic black yeast *Aureobasidium pullulans var. subglaciale* and other three *A. pullulans* varieties uncovered by *de novo* genome sequencing

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Aureobasidium pullulans is a polyextremotolerant black yeast-like fungus from the order Dothideales. The species is of interest because of its many biotechnological applications such as production of pullulan (polysaccharide polymer), aureobasidin A (antimycotic) and various extracellular enzymes. It is used as a biocontrol agent in agriculture and is also considered by some authors to be an emerging opportunistic human pathogen.

In Zalar et al. (2008) we described its four varieties: *A. pullulans* var. *pullulans*, *A. pullulans* var. *melanogenum*, *A. pullulans* var. *namibiae* and *A. pullulans* var. *subglaciale*, which occupy different ecological niches. *A. pullulans* var. *subglaciale*, was so far isolated only from Arctic glaciers, while the other three varieties can be found in numerous habitats, from plant surfaces and household dust to coastal ponds of hypersaline water. Recently we performed *de novo* genome sequencing and analysis of four varieties of the species. Annotation of the genes was performed with the help of transcriptome sequencing. The differences between varieties and with other phylogenetically related fungi were analysed on the genomic and (predicted) proteomic levels and will be discussed in light of the exquisite stress tolerance of the species, of its preferences for different habitats and conditions that were observed for individual varieties, particularly the cold adapted Arctic var. *subglaciale*. The question whether substantial differences between the genomes justify the elevation of *A. pullulans* varieties to a higher taxonomic level will also be addressed.

The availability of the genomic sequence of *A. pullulans* var. *subglaciale* is expected to facilitate research into this species, and this should improve our understanding of its lifestyle considerably different from the other three ubiquitous species.

Reference:

Zalar P, Gostinčar C, de Hoog GS, Uršič V, Sudhadham M, et al. (2008) Redefinition of Aureobasidium pullulans and its varieties. Stud Mycol 61: 21–38.

5 SEPT 10/1.50 - 2.20 KEYNOTE LECTURE

Towards Understanding the Bioenergetics of Cold Adaptation

Daniel H. Shain Rutgers University

Adaptation to survive at low physiological temperatures is likely a multi-step process involving many components of the cell (e.g., membranes, enzymes). Our data suggest that a critical requirement of cold adaptation is the ability to maintain relatively high intracellular ATP (5'-adenonsine triphosphate) levels. In fact, all psychrophiles that we've examined to date paradoxically increase ATP levels as temperatures decline within their viable temperature range. We interpret this as a compensatory mechanism to off-set the inherent reduction in molecular motion associated with cold temperature. The biochemistry underlying this metabolic response may be partially explained by the silencing of regulatory enzymes (e.g., 5'-nucleotidase, AMP deaminase) that typically stabilize ATP levels by removing AMP from the adenylate pool. Other changes seem necessary, however, and may include the convergent evolution of ATP synthetic machinery in both the cytosol and mitochondrion.

5 SEPT 10/2:20 - 2.40

Picocyanobacteria in ice: genomics, flow cytometry, live/dead tests

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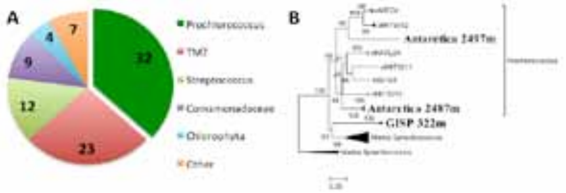
Using scanning laser fluorescence spectroscopy, we measured *in-situ* profiles of Chl in GISP2 and WDC (W. Ant.) ice cores at 1 mm intervals over ~3 km depth. Using flow cytometry to map Chl and phycoerythrin autofluorescence, and size (via scatter relative to beads) in unstained cells of size <1 μm in melted ice, we discovered cells at every depth that matched cultures of *Prochlorococcus* and *Synechococcus.* In ice that we provided, our collaborators K. Vergin and S. Giovannoni (OSU) obtained 454-generated 16S sequences from GISP2 at 322m and from WDC at 2487m and 2497m. The figure shows (A) major taxa including *Pro*-like sequences and (B) a clone library prepared using highly specific primers targeting the 16S-23S ITS region of *Pro* and *Syn* at 3 depths. In some cases these sequences were strikingly divergent from known modern strains. From live/dead tests of stained cells run through a 1 μm prefilter onto a 0.1μm membrane filter, our students James Bui and Ajeeth Adhikari found that at all depths more than half of all submicron-size cells in ice melts were alive. ~3% of cells from GISP2 and ~1% of cells from WDC were *Pro* or *Syn.* With J. Morris (MSU), R. Lenski (MSU) and R. Kodner (WWU), we propose to study evolutionary changes in *Pro* and *Syn* genomes with time (depth) in ice. We hope to determine what *Pro* and *Syn* genes have changed the most, how the community has changed, whether the established ecotypes of modern *Pro* and *Syn* were as dominant in the ancient ocean as in the modern, and whether the carbon fixation pathways of *Pro* and *Syn* have adapted to changing atmospheric CO_2 concentrations over the times encompassed by our samples.



5 SEPT 10/2.40 - 3.00

Distribution and Drivers of Archaeal and Fungal Communities in the Antarctic Dry Valleys

Charles K. Lee, Ingrid Richter, Lisa Dreesens, Eric M. Bottos, Craig W. Herbold, S. Craig Cary

International Centre for Terrestrial Antarctic Research, University of Waikato, New Zealand

Recent molecular evidence has shed new lights on the microbial ecology of Dry Valley soils, demonstrating distinct biogeographical trends and environmental drivers for bacterial and cyanobacterial communities. Our understanding of archaea and fungi in the Dry Valleys, however, remains comparatively limited, and the ecology of these taxa in the Dry Valleys are largely unresolved due to the lack of systematic surveys across environmental gradients.

Here we present findings from recent studies that examined Dry Valley archaeal and fungal communities. Contrary to earlier findings, we were able to detect widespread presence of archaeal communities in inland areas, but the observed diversity was low and dominated by *Thaumarchaeota* Marine Group 1.1b. There appears to be significant interactions between environmental heterogeneities and archaeal distribution, and phylogenetic analysis of Dry Valley archaeal lineages provided hints at their functional roles.

Meanwhile, a regional scale survey of fungal communities revealed significant biogeography for fungi that is highly heterogeneous and localized and thus parallels biogeographical patterns reported for bacteria in the Dry Valleys. This is in stark contrast to the common belief that fungal signals detected in the Dry Valleys were primarily contributed by dormant spores and detached from local environmental drivers. These findings perfectly augment the results from our landscape-scale survey of the Dry Valley, and collectively they provide a holistic view of fungal ecology in the Dry Valleys.

This research was supported by the New Zealand Marsden Fund (UOW0802 & UOW1003) and Antarctica New Zealand (K020).

5 SEPT 10/3.00 - 3.20

Endolichenic Proteobacteria and their roles in Arctic lichen symbiotic associations

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Lichens form a conspicuous and important part of Arctic and sub-Arctic vegetation, often occurring as the only visible vegetation in cold, arid areas such as glacial morains and nunataks. While generally described as bipartite mutualistic associations between fungi and algae or cyanobacteria, lichens are also hosts to lichen species-specific communities of other endolichenic bacteria, typically dominated by *Alpha*- and *Betaproteobacteria*. In the present study, we attempt to elucidate the functional roles and colonization mechanisms of endolichenic *Proteobacteria* by a multi-pronged approach including both genomic and metagenomic analysis, as well as biochemical and physiological analysis of cultured strains.

Analysis of 28,000 contigs from the bacterial component of the *Peltigera membranacea* metagenome yielded mutiple hits on several proteobacterial genes potentially involved in lichen secondary metabolite resistance, inorganic phosphate mobilization, biopolymer degradation and several other potentially important functions in thallus colonization and symbiosis. Phenotypic analysis of 50 endolichenic proteobacterial isolates from crustose, fruticose and foliose lichens indicated that hydrolytic activity is common among these bacteria, as is inorganic phosphate mobilization, whereas little evidence was found of some other proposed functions such as antimicrobial action or biofilm formation. Ongoing genome sequencing of several of these strains is expected to yield further insights.

The work presented was supported by the Icelandic Research Fund (IRF grant 120220021), the University of Akureyri Research Fund, and the KEA University Fund.

5 SEPT 10/3.20 - 3.40

The Antarctic *Chlamydomonas raudensis*: an emerging model for cold adaptation of photosynthesis

Rachael M. Morgan-Kiss[1], Jenna M. Dolhi[1], Sarah Stahl[1], James A. Raymond[2], Andor J. Kiss[1,3]
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Permanently low temperature habitats dominate our planet and psychrophilic microorganisms thrive in cold environments. Environmental adaptations unique to psychrophilic microorganisms have been thoroughly described; however, the vast majority of studies to date have focused on cold-adapted bacteria. The combination of low temperatures in the presence of light is one of the most damaging environmental stresses for a photosynthetic organism: in order to survive, photopsychrophiles (i.e. photosynthetic organisms adapted to low temperatures) balance temperature-independent reactions of light energy capture/transduction with downstream temperature-dependent metabolic processes such as carbon fixation. *Chlamydomonas raudensis* UWO241 (UWO241) is a psychrophilic green algal species and is a member of the photosynthetic microbial eukaryote community that provides the majority of fixed carbon for ice-covered lake ecosystems located in the McMurdo Dry Valleys, Antarctica. The water column exerts a range of environmental stressors on the phytoplankton community that inhabit this aquatic ecosystem including: low temperatures, extreme shade of an unusual spectral range (blue-green), high salinity, nutrient deprivation and extremes in seasonal photoperiod. More than two decades of work on UWO241 has produced one of our most comprehensive views of environmental adaptation in a cold-adapted, photosynthetic microbial eukaryote. Here we will review past research focused on UWO241 physiology and environmental adaptation in the context of the first transcriptome of this enigmatic extremophile. This work was supported by NSF Office of Polar Programs (0631659 and 1056396).

5 SEPT 10/4.20 - 4.40

Complexity of microbial ecology of a polythermal glacier surface and heterogeneity of cryophilic adaptive inventory

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Mittivakkat glacier in SE-Greenland is a polythermal glacier with low average temperatures allowing long snow and ice persistence and its remoteness warrants low levels of contamination from anthropogenic inputs.

By using a multi-disciplinary approach we have assessed the microbial ecology of a whole glacier over an area of 1 km^2 and during the high melting season in July 2012 when the so far most extreme melting rate for the Greenland ice sheet has been recorded. On Mittivakkat, the fast melting was accompanied by dramatic changes in microbial surface habitats and dominant microbial communities. We investigated the carbon and nutrient fluxes from snow to ice, to cryoconites and to glacial forefronts and the effect of cell retention at the glacial surface on albedo which appears to have a strong bio-component and was massively decreased (down to 20%) by algal pigmentation and hence colouring of the snow and ice. The low nutrient (< 1 ppm) and trace metal (< 100 ppb) contents combined with slow weathering of nutrient-scarce minerals and the high irradiation levels provide an extreme setting for algal growth. Nevertheless, snow and ice algae showed high metabolic activity and they were by far the dominant species at the glacial ecosystem scale. Although cryoconites can be self-sustaining and are usually regarded as hot spots for nutrient cycling, cell counts suggest that snow and ice algal communities support them. Snow and ice algal pigment, lipid and functional group distributions and compositions revealed a broad and rapidly changing cryo-organic adaptation inventory. The spatial and temporal heterogeneity in pigment and lipid composition and abundance between samples correlated well with the functional group distributions showing a clear trend among microbial communities and adaptation strategies. Microbiological, biochemical and geochemical analyses are complemented by shotgun metagenomic Illumina sequencing data revealing the microbial diversity (16S and 18S rRNA) and prokaryotic and eukaryotic functional gene inventory of three glacial surface habitats (green snow, red snow, biofilm; 25 Gb of data and ~ 90 million reads each). To our knowledge this is the first multi-tiered evaluation of the microbial ecology of an entire glacial surface ecosystem, the temporal and spatial changes in algal communities and adaptation inventory and resulting effects on the physical glacial properties.

Grant acknowledgements: European Union Seventh Framework Programme FP7/2007-2013/ n° 262693 [INTERACT] and University of Leeds.

4 SEPT 10/4.40 - 5.00

Survival of microorganisms to the main stress factors encountered in clouds

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Microorganisms are present in low altitude clouds at concentrations of $\sim10^4$ bacteria mL^{-1} and $\sim10^3$ fungi mL^{-1}. The monitoring of clouds since 2003 at the puy de Dôme station (1465 m a.s.l., France) revealed the presence of recurrent microorganisms among the cultivable bacterial community: *Pseudomonas* spp. and *Sphingomonas* spp. notably were present in 55% and 45% of the samples collected, respectively, and they represented ~30% of the total heterotrophic bacteria cultivable on R2A at 17°C.

Clouds represent nearly obligate ways to the deposition of micrometer-sized aerosols such as microorganisms. However, regarding the harsh conditions that a living cell has to face in clouds, they could act as selective environments to the atmospheric dispersion of microbes. In order to test this hypothesis, 5 bacterial or yeast strains isolated from cloud water and representative of the cultivable community generally observed (*Arthrobacter* sp.; *P. syringae*; *Sphingomonas* sp.; *Bullera armenica*) were subjected to conditions encountered in clouds and identified as probably selective for viable organisms: osmotic shocks, freeze-thaw cycles, presence of oxidants such as hydrogen peroxide, and solar radiation. The first results demonstrated that the microorganisms isolated from clouds were not particularly more resistant to these treatments than a strain of *E. coli* chosen as reference. These suggest that the sensitivity of microorganisms to those environmental factors only could not explain the composition of the viable community existing in clouds.

4 SEPT 10/5.00 - 5.20

Alpine lichen communities as evolutionary hot beds of stress-tolerant fungi

Muggia Lucia, Fleischhacker Antonia, Kopun Theodora, Hafellner Josef, Grube Martin

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Lichen symbioses are shaped and colonized by biologically and phylogenetically diverse fungi. Lichenicolous fungal species develop diagnostic structures and symptoms on the host lichen, whereas endolichenic fungi occur cryptically in the lichen thalli. Lichenicolous fungi exhibit varying degrees of host specificity, and occur as parasites or commensalists. We hypothesize that patterns of host specificity are insufficiently known because lichenicolous fungi could also occur cryptically in other than their known hosts. We test this hypothesis with a community-based approach using sequencing of the fungal ITS, fingerprint methods (SSCP) and pyrosequencing. Our study area is the Koralpe range in southern Austria, a particularly lichen-rich alpine area which remained free of ice during the last glaciation. We comprehensively sampled Alpine lichen communities in ten plots including uninfected thalli and those visibly infected by lichenicolous fungi. We present results demonstrating that lichens play a prime role as reservoirs of fungal diversity. We also provide phylogentic analyses of culture isolates of lichen-inhabiting fungal strains. The close relationships with fungi from other hostile habits indicate that lichens represent an evolutionary hot-bed of polyextremotoletant fungi. (The research is financed by the Austrian Science Foundation, FWF P24114-B16).

5 SEPT 10/5.20 - 5.40

Using historical Antarctic collections and next generation sequencing to unlock the past: Has polar cyanobacterial diversity changed over the last 100-years?

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Understanding of microbial diversity in Polar Regions, particularly at genotype level, is based on a few decades of polar research. Extending time scales into the past will assist in assessing resilience and change of microbial diversity to environmental and climatic change, especially important for key primary producers such as cyanobacteria in polar freshwater ecosystems. Cyanobacterial mats collected during R. F. Scott's Discovery Expedition (1901-4) from the McMurdo Ice Shelf and Ross Island allowed the comparison with present-day cyanobacterial communities from similar geographic regions in Antarctica to test whether cyanobacterial diversity has changed over the last 100-years since onset of human activity and climatic change. Here, we will present our cyanobacterial 16S rRNA gene 454-sequencing analyses that allowed to obtain in-depth community coverage of the historic cyanobacterial mat communities and determine how present-day cyanobacterial mats compare with past diversity in Antarctica. (Royal Society)

5 SEPT 10/5.40 - 6.00

Acidobacteria Communities in Arctic Tundra Soils

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Rutgers University, Finnish Forest Research Institute, University of Jyväskylä

Acidobacteria are among the most abundant bacterial phyla found in terrestrial ecosystems and are ubiquitous in acidic, organic-rich Arctic tundra soils. Nonetheless, the ecological role of the *Acidobacteria* remains elusive. To date, relatively few species have been characterized, and we thus know little about their function, nor how they respond and adapt to environmental change in Arctic soil environments. We are integrating a functional and ecological analysis of Arctic *Acidobacteria*, combining cultivation, genome analysis, microcosms and field studies to obtain an understanding of their regulatory and metabolic networks involved in biogeochemical cycling of carbon. Subdivision 1 *Acidobacteria* appear to be adapted to N-limited and acidic soils of low-productive tundra heaths, and are able to out-compete copiotrophic *Proteobacteria* and *Actinobacteria* that dominate in the more productive tundra with higher pH and N. *Acidobacteria* may also be able to out-compete other bacteria for limiting N resources. We have cultivated several representatives of subdivision 1 *Acidobacteria* from these soils. These new isolates belong to new species in the genera *Terriglobus* and *Granulicella*, with additional novel genera to be described. The wide taxonomic diversity of *Acidobacteria* in Arctic tundra soils is likely coupled to a functional diversity that reflects resource partitioning of different taxa. The selective pressure that allows *Acidobacteria* to be successful is likely a combination of their response to soil organic matter availability and their ability to survive through environmental perturbations. An understanding of the dynamics and activity of *Acidobacteria* communities and their response to changing environmental conditions will aid predictions of soil organic matter turnover and greenhouse gas flux from the terrestrial ecosystem.

6 SEPT 12/8.30 - 9.00 KEYNOTE LECTURE

Microbial Responses to Increased Nutrients in a Changing Environment

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The McMurdo Dry Valleys (MDV) are currently experiencing climate-induced changes including increased moisture and nutrient availability which are likely to intensify in the near future. We hypothesize that climate warming in the region will amplify connectivity among landscape units leading to enhanced coupling of nutrient cycles across landscapes, and increased biodiversity and productivity within the ecosystem. We tested the response of MDV microbial communities to increased nutrients by amending lake and soil samples with organic and inorganic sources of C, N, and P. In lakes, primary productivity and bacterial activity increased significantly in response to amendments. Respiration and extracellular enzyme activity was significantly increased with moisture and carbon addition. Changes in lake and soil microbial diversity varied with amendment, but significant differences in the community composition with most treatments were observed. Results from this experimental work suggest MDV lake and soil microbial communities may undergo rapid change in response to increased resources.

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6 SEPT 12/9.00 - 9.20

Microbial life in permafrost and cryptoendolith environments in a hyper-arid Antarctic Dry Valley

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University Valley (UV) is an Upper Dry Valley in Antarctica, and one of the coldest and driest places on Earth, with summer air temperature maxima never reaching above 0°C. At this site, ice in the ice-table exchanges with the atmosphere via water vapour diffusion rather than liquid water, thus this is a site of extremely low water activity. The potential for UV to support life at subzero temperatures is being investigated. Bacterial and fungal isolates are being cultured at cold and subzero temperatures, few bacteria have been isolated from permafrost (6 isolates) compared to the aerobic heterotrophs and phototrophs being cultured from UV cryptoendoliths (>50 isolates to date). Radiorespiration microbial activity assays were carried out on environmental permafrost samples at low and subzero temperatures, and are revealing a community that has none, or significantly lower activity than those measured from coastal Antarctic permafrost samples. 454 sequencing was used to examine the microbial diversity across all three domains of life in surface soil, permafrost, and cryptoendolithic samples and indicate high heterogeneity in permafrost microbial composition. Compared with the low biomass, few culturable isolates, and little/no measurable microbial activity observed at *in situ* temperatures in permafrost samples, the thriving cryptoendolithic communities are indicating that protection within rock is one habitable niche in an environment that is testing the cold-arid limits of life.

Work supported by the NASA ASTEP program, and CATP

6 SEPT 12/9.20 - 9.40

Pyrosequencing-based assessment of the fungal communities in the cryosphere and soil depths of the Damma glacier, Switzerland

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Global warming has been causing the retreat of most European glaciers. Newly exposed barren soils are rapidly colonized by microorganisms and plants governing soil formation. The occurrence of fungi and their functions in the colonization of deglaciated terrain are yet poorly known thus hindering a thorough understanding of the role of fungi in developing soils. This study aims to investigate the diversity and structure of the fungal community in snow, ice surface (cryosphere) and various soil ages and depths. Bioinformatic processing yielded 361,199 sequences of fungal pyortags classified in 2545 OTUs. The fungal community was dominated by *Ascomycota* (68%) and *Basidiomycota* (21%). In the cryosphere, the abundance of ITS2 rRNA gene copies and indices of α-diversity were low with *Leucosporidium* yeasts as most dominant species. Interestingly, *Leucosporidium* was also present in the surface of barren soils indicating re-colonization of new terrain by snow. Ergosterol and ITS2 rRNA frequencies were highest at the surface and in soils with increasing distance from the forefront due to higher carbon content while soil depth had no influence on community structure. Saprophytic fungi (e.g. *Phialophora* and *Dioszegia*) were most dominant in soils of the forefield independently on the distance from the forefront. In conclusion, yeast-like fungi dominate the cryosphere and may colonize barren soils triggering the decomposition of organic matter in initial soil formation. No shift of fungal community occurs within soil depths suggesting that fungal colonization is mainly driven by stochastic processes. We suggest that fungi play a crucial role in the establishment of first plants during soil formation, which in turn selects for plant-associated fungi.

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6 SEPT 12/9.40 - 10.00

Microbial communities in the snowpack of alpine meadows and glacier forefields

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In alpine regions, snowpack represents a heterogeneous oligotrophic habitat, which may influence nutrient and microbial flushes to the underlying soil during the winter-summer transition. We characterized the microbial communities in snow profiles of three alpine meadows of different altitudes and of a glacier forefield (Tiefen, canton Uri, Switzerland) at snowmelt (May-June). Snow trenches (approx..1m depth) were dug to visualize and sample the internal structure of the snow profile. At regular depth intervals, we measured physical (i.e. snow density, temperature, layering) and chemical (particulate and dissolved organic matter (POM and DOC), soluble ions) parameters of the snowpack. Assessment of microbial communities was performed through Terminal Restriction Fragment Length Polymorphism (T-RFLP) of the rRNA genes, flow cytometry and BIOLOG incubations. Chemistry of the snowpack was heterogeneous and varied strongly both vertically and horizontally. In general, our results suggest that POM (~0.02% at the surface) accumulates on the surface of the snowpack while DOC (~2.00 ppm) is rapidly flushed to the lower layers. Bacteria and Fungi, but not Archaea, were detected at all depths. We found higher microbial diversity and biomass in the top layers of the snowpack, and the presence of ubiquitous OTUs all through the snowpack. BIOLOG incubations showed growth at 0°C on polymers and complex substrates.Microbial diversity in the snowpack may reflect the physico-chemical heterogeneity of the snow system.

6 SEPT 12/10.40 - 11.00

Biogenic calcite structures in Green Lakes, James Ross Island, Antarctica

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In northern deglaciated part of James Ross Island (NE Antarctic Peninsula) special cyanobacteria-microalgae calcified structures were discovered in stable shallow lakes on higher-lying levelled surfaces. These lakes are among the oldest lakes in the studied region. Their periphytic community is dominated by the heterocytous cyanobacteria *Calothrix elsteri, Hassallia andreassenii* and green branched microalga *Hazenia broadyi*, which are currently considered to be endemic to the Antarctica. This community participate in formation of specific mosaic-like mucilaginous structures with limestone precipitations. Cyanobacterial and microalgae mats produce $CaCO_3$ through lithification. The process is thought to be driven by a metabolically-induced increase of the $CaCO_3$ saturation state in the microbial mat. This mat contains abnormal phospholipids with very-long-chain anteiso branched fatty acids (from C_{20} to C_{30}), and it is covered by thick layer of extracellular polymeric substances. Raman spectra obtained studying extracts from samples of the mat resemble the typical Raman features of scytonemin, an effective UV-protective pigment with major corroborative bands located at 1601, 1559, 1324 and 1173 cm^{-1}. Raman signal of pigments related to photosynthetic aparatus were registered with weaker intensity relative to scytonemin, with characteristic bands of carotenoids and chlorophyll. Macroscopic acicular $CaCO_3$ crystals were studied using scanning electron microscopy and geochemical methods. The EDAX and EBSD analyses have shown that each represents a rather pure calcite monocrystal, strongly elongated along the *c* crystallographic axis. This is the first record of such type of active microbial carbonates community in the shallow lakes in Antarctica.

6 SEPT 12/11.00 - 11.20

The imprint of glacial history on the biogeography of Antarctic lake-dwelling micro-organisms

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Radiometric and optically stimulated luminescence dating have revealed that coastal East Antarctic oases differ strongly in their Late Quaternary glaciation history. Some oases partially escaped glacial overriding, whereas others were completely ice-covered during the Last Glacial Maximum (LGM). Here we test the hypothesis that regional differences in glacial history are reflected in the current distribution and diversity of Antarctic lacustrine microbial communities. Surveys of contemporary communities were carried out using a combination of traditional survey techniques and next generation sequencing, complemented with paleolimnological evidence to reveal long-term community dynamics. Variance partition of biodiversity inventories of prokaryote and eukaryote phyla, including diatoms, green algae, cyanobacteria and other bacteria, revealed marked differences in the degree of bioregionalisation and environmental structuring of assemblages among different phylogenetic groups. This suggests that differences in dispersal capacity, physiological tolerance and perhaps rates of local adaptation between phylogenetic groups influence colonization-extinction dynamics and biogeographical structuring, although differences in taxonomic resolution may have led to an underestimation of bioregionalisation in some phyla. Paleo-ecological evidence based on fossil diatoms adds strong support to the hypothesis that glaciation history has long-lasting effects on microbial mat communities. Regions that escaped full glaciation harbor a more diverse diatom flora composed of true aquatic alpine-polar species complexes. The continuous presence of these species throughout the last glacial-interglacial cycle suggests that they might be relict elements from a widespread cold-adapted diatom flora in Antarctica. By contrast, regions that were fully ice-covered during the LGM are characterized by an impoverished, but largely endemic flora dominated by terrestrial taxa. Interestingly, many of these species appear to have undergone niche expansion compared to populations inhabiting regions that escaped glaciation, suggesting strong eco-evolutionary responses to regional ice sheet dynamics. Together, our results provide a strong case for the role of historical processes in microbial biogeography and add support to the need to enforce more stringent measures to prevent the human-mediated spread of microbes and the subsequent homogenization of microbial floras in East Antarctica.

6 SEPT 12/11.20 - 11.40

The Dynamic Arctic Snowpack Microbial Habitat

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Human-induced environmental changes are affecting cold ecosystems and predicted impacts include rapid warming, increased nitrogen and pollutant deposition, yet the effect of these on microbial communities and nutrient cycling is poorly understood. Much of the research concerning Arctic microbial community structure and function stems from soil and permafrost studies, however relatively little is known about the snowpack. Seasonal snow cover extends over a third of the Earth's land surface, covering up to 47 million km^2 and is also an important feature of the Arctic. Snow cover can be considered as a dynamic habitat of limited duration that acts as a medium and a mediator by transmitting and modifying interactions among microorganisms, plants, animals, nutrients, the atmosphere and soil. A growing body of evidence suggests that microbial communities play key roles in biogeochemical cycling in the snowpack, but little is known about the processes controlling their biogeographic distributions. We used metagenomic tools such as phylogenetic microarrays and high throughput sequencing to explore microbial community structure in samples collected from various Arctic snowpacks (North Pole, Greenland and Ny-Alesund) at different seasons (spring, summer, winter) and compared these to publicly available data from other ecosystems to evaluate the roles of niche-based processes vs spatial processes in explaining variations in community structure. The biogeography of Arctic microbial communities appears to be influenced by environmental factors, such as snow physics and chemistry relative to geographic distance. The results from this study offer insights into the mechanisms that generate and maintain diversity, such as speciation, extinction, dispersal and species interactions.

6 SEPT 12/11.40 - 12.00

Evaluation of Mixotroph Abundances in Polar Marine Environments by Quantitative PCR

Rebecca J Gast (Woods Hole Oceanographic Institution), Zaid McKie-Krisberg (Temple University) and Robert W. Sanders (Temple University)

Protists are traditionally described as either phototrophic or heterotrophic, but evidence has indicated that mixotrophic species could have significant impacts on prey populations. Estimates of abundances of mixotrophs are determined microscopically and are based upon the ingestion of fluorescent particles. We recently developed SYBR-based qPCR amplification strategies for several mixotrophic algae in our Antarctic protist culture collection (*Mantoniella antarctica, Pyramimonas tycotreta, Geminigera cryophila)*. Water samples collected in the Ross Sea, Antarctica in 2003, 2004, 2005 and 2011. All three were detected, and overall distributions were strongly influenced by season of collection, despite differences in sampling locations and years. Environmental variables that best explained variation in organism abundances were temperature, oxygen, fluorescence and latitude. When nutrients were included in the analysis, phosphate was identified as an additional explanatory variable.

This work was supported by NSF OPP 83895500.

6 SEPT 12/12.00 - 12.20

Extremophilic microorganisms in glacier forefields of the Larsemann Hills, East Antarctica

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Antarctic glacier forefields are extreme environments and pioneer sites for ecological succession. Increasing temperatures due to global warming lead to enhanced deglaciation processes in cold-affected habitats and new terrain is becoming exposed to soil formation and microbial colonization. In this study, using a combination of molecular and (bio)geochemical approach, we determine the structure and development of bacterial communities depending on soil parameters in two different glacier forefields on Larsemann Hills, East Antarctica. Furthermore, we have isolated and characterized new extremophilic microorganisms.

Our results demonstrate that deglaciation dependent habitat formation, resulting in a gradient in soil moisture, pH and conductivity, leads to an orderly bacterial succession for some groups, e.g. *Cyanobacteria*, *Bacteroidetes* and *Deltaproteobacteria* in a transect representing "classical" glacier forefields. A variable bacterial distribution and different composed communities were revealed according to soil heterogeneity in a slightly "matured" glacier forefield transect, where *Gemmatimonadetes*, *Flavobacteria*, *Gamma*- and *Deltaproteobacteria* occur depending on water availability and soil depth. *Actinobacteria* are dominant in both sites with dominance connected to certain trace elements in the glacier forefields.

Furthermore, we have characterized the new species *Chryseobacterium frigidisoli* PB4 and have examined the adaption of the cell membrane phospholipid fatty acid (PLFA) inventory of this strain in response to changing temperature. The PLFA pattern is dominated by saturated and unsaturated mainly branched fatty acids in the range between 15 and 18 carbon atoms. The ratios of iso/anteiso-C15:0 and iso/anteiso-hydroxy-C15:0 fatty acids show a decreasing trend with declining temperature. The relative proportion of an unknown fatty acid continuously increases from 20 °C to 0°C. Trends to more anteiso and unsaturated fatty acids are indications for a clear adaptation to colder ambient temperature conditions. The unknown fatty acid became the most abundant and dominant fatty acid (25.73 %) at 0°C. Thus, the unknown fatty acid plays an important role in the cell membrane temperature adaption of *C. frigidisoli*.

7 SEPT 12/1.50 - 2.20 KEYNOTE LECTURE

Ocean Worlds of the Outer Solar System

Dr. Kevin P. Hand, Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA, 91103.

At least five moons in the outer solar system may harbor liquid water oceans. These oceans have likely persisted for much of the history of the solar system and as a result they are highly compelling targets in our search for life beyond Earth. Jupiter's moon Europa, and Saturn's Enceladus, in particular, may have the right combination of chemistry and dynamics to sustain life as we know it.

Recently we have used ground based telescopes to show that Europa's surface contains salts, likely derived from the subsurface ocean, and hydrogen peroxide produced from the radiation bombardment of Europa's surface. I will discuss these and other recent results concerning the physics and chemistry of Europa and Enceladus. I will also discuss how the study of several extreme environments on Earth is helping to inform our search for habitable environments on distant worlds, while simultaneously providing new insights into Earth's complex ecosystems.

This work was supported in part by the NASA Astrobiology Institute "Icy Worlds" node at JPL, and the NASA Astrobiology Program Office.

7 SEPT 12/2.20 - 2.40

Microbial isolation from terrestrial 'icy worlds'

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Arctic thermokarst lakes on the coastal plain in the Northern Slope of Alaska are uncharted territory with regards to microbial diversity. To further characterize microorganisms involved in organic matter mineralization in these lake sediments, anaerobic enrichment cultures were established with samples collected in October 2011. Fragments of the SSU rRNA gene were sequenced using Sanger technology (~800 bp, Archaea and ~ 1200 bp, Bacteria). Archaeal clones were related to *Methanobacterium sp.*, *Methanosphaerula sp*, *Methanosarcina palustris* strains MS and MM (psychrotolerant methanogens), and uncultured Archaea clones found in other Arctic sediments. Bacterial clones were related to *Acetobacterium sp.* (the presence of which may affect CH_4 production and population dynamics by competition with hydrogenotrophic methanogens), to *Trichococcus sp*. KOPRI80183 from Svalbard, to uncultured bacterium clones from sub-glacial waters in Iceland, and to uncultured bacterium clones from anoxic bottom waters of a volcanic sub-glacial lake. Efforts to further isolate and characterize these microorganisms will be conducted. Our work will provide a framework to understand how microbial diversity of an environment that is highly sensitive to climate change may be affected. Additionally, new members will be added to a spectral database of microbes for studies under Europa-like conditions (*e.g.* high radiation and low temperature), as candidates for life in icy moons of our solar system.

NASA-NASA Astrobiology Institute "Icy Worlds"

7 SEPT 12/2.40 - 3.00

Cosmopolitan-to-Refugia Habitat Oscillations: Earth, Mars, Europa

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Positing that Mars has life, a curious mirror may exist with Earth:

(1) On Earth a cosmopolitan microbiota has prevailed for most of geologic time. Cosmopolitan microbiological community structures are the norm, encouraged by atmospheric and oceanic transport. Isolated refugia host a small fraction of the microbiota during most geologic periods and only dominate life during periods of exceptionally stressed (e.g., ice-bound) conditions. Earth has comparatively infrequent or sparse occurrences of global ice-equilibrated habitats where the biosphere is fragmented. Accelerated evolution, high turnover of life forms, and biological diversification occurs during recoveries from mass extinctions caused by infrequent large impacts, global ice ages, and large chemical excursions. During long warm, stable intervening periods, evolution of multicellular terrigenous life is driven in part by tectonic isolation and reintegration of landmasses. Aquatic life's evolution is accelerated by fluctuation, isolation, and reintegration of seas and lakes, which can be driven tectonically or climatically.

(2) On Mars cold and ice-bound (or desiccated) conditions have dominated most eras, when local, isolated, sparsely distributed, warm, wet niches occur deep within the crust. Global or regional warm, wet conditions have existed for only brief intervals, which served to wipe out diversity and to homogenize. Following the late impact cataclysm 3.8 Ga ago, large impacts probably were not a major driver of extinctions on Mars—since its life (if any) is mostly protected underground—but aided production of warm, wet regional crustal environments. Hence, impacts should have a big role in Martian evolution, but the role is different than on Earth. The martian atmosphere kills life and limits biological transport and integration. Crustal cooling also drives hydrospheric fragmentation and thus promotes isolation of physicochemically distinct habitats. Mass extinctions, reductions of biodiversity, and transitions to cosmopolitan communities occurred on Mars during brief, sporadic excursions to globally or regionally warm, wet environments.

Thermally, chemically, and physically isolated habitats—where extremophiles often rule (extreme only by comparison to the norm)—are rare on Earth but may be common on Mars. The biological evolution of Mars and Earth are each tied to their distinct geologic activity and climatic and geomorphologic process regime changes. Proximal hydrothermal and icy domains have special importance for habitats on Mars and Europa, the difference being in the dominance of refugia on Mars and of cosmopolitan biota on Europa. Thus Earth and Europa share the commonality of having a global ocean, which aids biological transport and eco-system integration.

7 SEPT 12/3.00- 3.20

Microbial life in the 18 to 27 m ice core section recovered from Lake Vida, Antarctica

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Lake Vida, one of the largest lakes in the McMurdo Dry Valleys, Antarctica, has a thick ice body that harbors liquid brine (salinity 188-210) that permeates the lake's perennial ice through channels and fissures 16 meters below the surface. Ice core retrieval from Lake Vida in 2010 reached nearly 27 m, 10.5 m below previous coring efforts. The 27 m ice core contains seven stratified sediment layers intercalating the ice layers below 21 m. This type of stratification has not been reported for other Antarctic lake sediments. Epifluorescence microscopy analyses from 18 ice/sediment segments from the lower portion of the lake-ice body (from 18 to 27 m) revealed the presence of microbial cells and diatom frustules throughout the core. To understand the dynamics and diversity of the microbial life in the Lake Vida deep ice, the microbial assemblage was profiled using next generation sequencing. Illumina technology targeting the V4 region of the 16S rRNA gene was applied to eight ice, five sediment, and five ice/sediment transition zones. The results showed that the major microbial assemblages detected across the core are affiliated with the genera *Marinobacter, Sulfurovum,* and *Gillisia*. Microbial populations that are potentially active were investigated in five sediment segments by targeting the ribosomal RNA. The bacterial assemblages with higher rRNA levels in the five segments analyzed are affiliated with the genus *Pseudoalteromonas.* Associations between predicted biogeochemical capacity of the identified taxa, chemical parameters and nutrients of each core-segment are being investigated.

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7 SEPT 12/4.00 - 4.20

Antarctic Basal Ice as an Analog for Icy Extraterrestrial Habitats

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The putative existence of water and ice throughout the solar system (e.g. Mars, Europa, and Enceladus) has raised considerable interest that these extraterrestrial worlds could plausibly harbor cryogenic habitats suitable for microbial life. As such, frozen environments on Earth such as glaciers, permafrost, and sea ice have been identified as ideal systems to investigate the survival and physiology of microorganisms under conditions analogous to those found on extraterrestrial worlds. Measurement of the concentration of gas species in air trapped in sediment-rich basal ice from Taylor Glacier, Antarctica revealed unusually high concentrations of CO_2 (60,000 to 325,000 ppmv) occurring simultaneously with decreased O_2 concentrations (4 to 18% of total gas volume). The high CO_2 and low O_2 concentrations occur concurrently with increased microbial cell abundance in the basal ice, suggesting that *in situ* microbial respiration altered the composition of the entrapped gas. Species of the genus *Paenisporosarcina* are a numerically abundant member of the microbial assemblage from the ice horizons with elevated CO_2 and depleted O_2 and were readily culturable from the basal ice samples examined. Metabolic experiments with *Paenisporosarcina* sp. TG14 revealed its ability to conduct macromolecular synthesis when frozen in basal ice melt-water at -15 °C. These results support the hypothesis that basal ice environments are microbial habitats harboring bacteria with the physiological capacity to remain metabolically active and cycle elements within the cryosphere.

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7 SEPT 12/4.20 - 4.40

Global-scale microbial dispersal characterized through genetic analysis of the fumarolic soils of Tramway Ridge, Mt Erebus, Victoria Land

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High-altitude, geothermally heated fumarolic fields in Antarctica are analogs for similar environments that may have supported pockets of life during "Snowball" periods in Earth's history or that exist today on icy terrestrial planets. These habitats provide a valuable resource for studying the evolution of mechanisms that enable global-scale dispersal between such sites and the resulting assembly of thermophilic microbial communities. At these locations, geothermal heat flux forms islands of warmth and liquid water in an otherwise extremely cold and dry environment. Our study has focused on Tramway Ridge (ASPA 130), a fumarolic field near the summit of Mt. Erebus, the southernmost active volcano on Earth. In order to better understand the composition, distribution and function of organisms within this community, we utilized amplicon and metagenomic sequencing of bulk environmental DNA. We found that surface-associated genetic signatures closely match signatures for thermophilic microbial mat taxa and mesophilic soil bacteria found widespread across Earth, whereas the subsurface is dominated by novel Archaea and members of poorly understood Bacterial candidate divisions that are closely related to those found in geothermal features at Yellowstone National Park (USA) and El Tatio Geyser Field (Chile). These distributions imply that aeolian processes readily disperse viable organisms to Antarctica and that several subsurface-associated thermophilic lineages possess currently unknown adaptations that enable planet-wide dispersal. An ongoing metagenomic effort has resulted in the reconstruction of over 20 partial to nearly complete draft genomes, which are being used to elucidate the general mechanisms by which these particular organisms survive desiccation and UV exposure during aeolian transport between geothermal habitats.

7 SEPT 12/4.40 - 5.00

L.I.F.E. Laser Induced Fluorescence Emission: Non-Invasive Tool to Detect Photosynthetic Pigments Applicable in Various Habitats of the Cryosphere

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Cryospheric ecosystems harbor microbial assemblages with sometimes surprising activities during periods with high water activity. Especially supraglacial environments can succeed rates of primary production rates known from temperate soils. However, models to extrapolate those rates to global assumptions often lack a good set of data in high resolution. The need for non-invasive techniques is hence given to ensure an enhanced coverage and to avoid a bias due to low representativeness.

Superficial primary production is requiring photosynthetic active pigments such as chlorophyll or phycoerythrine. Laser signals in specific wavelengths can produce a fluorescence signal which can be converted in a quantity of pigments per are. A prototype of a hand-held device called L.I.F.E. (Laser induced fluorescence emission) has been calibrated and tested in various ecosystems of the cryosphere such as glacial surfaces, cryoconite holes and englacial systems with artificial illumination.

For the first time, this system has been tested during a Mars simulation in the desert of Marocco (conducted by the Austrian Space Forum) to detect photosynthetic pigments of endolithic forms. After evaluation of data and applications in carious extreme environments, L.I.F.E. could possibly be applied also in systems accepted as analogues outside planet Earth.

SPA_132 TriPolar & SPA_147 CAVE.LIFE (bm.wf, Austria).

POSTER ABSTRACTS

EVENING POSTER SESSION

ODD NUMBERED POSTERS PRESENTING MONDAY EVENING
EVEN NUMBERED POSTERS PRESENTING TUESDAY EVENING

1 SURFICIAL GLACIAL ENVIRONMENTS

The Arctic snowpack microbial community highlighted by metagenomics and metatranscriptomics

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The Arctic seasonal snowpack can extend at times over a third of the Earth's land surface. This chemically dynamic environment interacts constantly with different environmental compartments such as the atmosphere, soil and snow meltwater, and thus, strongly influences the entire biosphere. However, the microbial community associated with this habitat and its potential role in biogeochemical cycling remains poorly understood. Previous studies based on 16S rRNA gene analysis revealed a high diversity of microorganisms within the snowpack. Here, we focused on both microbial community structure and function by applying a global approach using metagenomics and metatranscriptomics. From the 250 thousand sequence reads in all our snow metagenomes, the majority (between 58 and 88%) were unassigned to specific metabolic categories, which signals the lack of related functional data in sequence databases. However, snow metagenome analyses demonstrated major shifts in function distribution during the season indicating that the snowpack is a dynamic ecosystem. These changes seem to be related to fluctuations in environmental conditions as some chemical parameters, like mercury or methyl-mercury concentrations, were correlated with function abundance. Comparing snow metagenomes with publically available datasets from different ecosystems, we described the specific functional signature of snowpack microbial community. Some functions like oxidative stress response or lipopolysaccharides biosynthesis are more highly represented in snow metagenomes than in those from other ecosystems. These functions are probably related to how microorganisms cope with the harsh conditions (such as intense UV radiation and cold temperatures) characteristic of the Arctic snowpack. The extraction of mRNA from the Arctic snowpack for further metatranscriptomic analyses supports the hypothesis that microorganisms are metabolically active in the polar snow ecosystem. The expression pattern derived from the mRNA sequencing could lead to a better understanding of which microorganisms are the most active, what their dominant metabolic processes are, and how rapidly they respond to this highly fluctuating environment.

2 SURFICIAL GLACIAL ENVIRONMENTS

The Biogeography and phylogenetic structure of Red Snow Algae, *Chlamydomonas nivalis* and *Chloromonas nivalis*

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Red snow, caused by psychrophilic green algae such as *Chlamydomonas nivalis*, is a phenomenon in which the surface of snow turns red, and can be observed globally on mountain snowfields. Red snow captures greater solar radiation than pure white snow, resulting in the acceleration of snowmelt. Recently an expansion of red snow in global scale has been known, which might be caused by global warming. In this research, we aim to understand the mechanism determining the distribution of red snow algae by looking into their spatial genetic variation.

Red snow algae were detected and sampled in high mountain regions all over Japan, Greenland, Svalbard, and Alaska. Genetic markers (SSU rRNA genes and cpDNA genes) were sequenced and analyzed. A red snow alga species, *Chlamydomonas nivalis,* showed global distribution of close related clones, suggesting the strong dispersal ability. On the other hand, *Chloromonas spp.* showed locally structured distribution, suggesting the limited dispersal.

In conclusion, our results suggest that closely related taxa, *Chlamydomonas* and *Chloromonas,* have different dispersal abilities. The next step would be to identify key factors that make the difference between the two taxa and to analyze them at finer scale using Next-generation sequencing methods.

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3 SURFICIAL GLACIAL ENVIRONMENTS

Microbial diversity and ecophysiology of Cryoconite Sediments from the Dry Valleys, Antarctica

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Cryoconites are formed by windblown sediments that settle on a glacial surface to an equilibrium depth within the ice. Cryoconite holes provide an aqueous environment in the ice and contain biologically active aggregations of microbes associated with sediment granules. A detailed investigation of the microbial diversity, activity, and granule structure of an Antarctic cryoconite, from the Canada Glacier in the McMurdo Dry Valleys, showed that there are metabolically active microorganisms associated with sediment particles. Cryoconite granules were analyzed using scanning electron microscopy and powder x-ray diffraction, which showed that granule composition is relatively homogenous and primarily composed of silica oxides. Bulk organic matter content and composition were determined using step-wise thermogravimetric analysis. The organic matter was found to be 6.5% of the dry weight, with the greatest mass loss occurring between 200°C and 350°C, indicating that the majority of organic matter present is thermolabile. Confocal microscopy of individual sediment grains confirmed the association of microbial populations with sediment surfaces. Using fluorescent in situ hybridization the total bacterial cell abundance is 7.26×10^5 cells ml^{-1} of sediment slurry. *Bacteroidetes* comprise 78.2% of the bacterial population followed by *Alphaproteobacteria* 2.6%, and *Gammaproteobacteria* 0.3%. Carbon fixation and ammonia assimilation rates were determined at the single-cell level using Halogen In Situ Hybridization-Secondary Ion Mass Spectroscopy (HISH-nanoSIMS). Uptake rates of ^{13}C using HISH-nanoSIMS were determined for the dominant Cyanobacteria, an *Oscillatoriales* sp., which showed high enrichment of ^{13}C, indicative of carbon fixation. There was no evidence of carbon transfer and successive uptake of released exudates by heterotrophic bacteria. Nitrogen uptake rates of ^{15}N labeled ammonium were calculated in both the *Oscillatoriales* and *Bacteroidetes* populations. Cryoconite sediments are important reservoirs of organic carbon, nutrients and microbial activity on glacial surfaces, where resources are sparse. Cryoconites accumulate windblown sediment, which promotes the aggregation of microorganisms to granule surfaces providing a refuge for microbial life in these harsh environments.

4 SURFICIAL GLACIAL ENVIRONMENTS

Organic matter production and accumulation in simulated glacier surface environments: the cryoconite casserole experiment.

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Organic matter produced on the surfaces of glaciers is believed to be an important reservoir of nutrients that is periodically flushed into adjacent depauperate ecosystems, such as subglacial and other downstream environments. There is increasing evidence showing that supraglacial microbial communities are actively influencing biogeochemical cycles in the cryosphere and modifying nutrient export. In particular, cryoconite holes have been found to be 'hot spots' for supraglacial microbial activity and nutrient cycling. They are aquatic habitats, formed when cryoconite (solar-heated debris) melts into the surface ice of glaciers.

A novel laboratory experiment, the cryoconite casserole, was devised to simulate conditions in initially depauperate cryoconite holes over one summer season in Greenland. The main scope of the experiment was to test the microbial production, accumulation of organic matter and nutrient recycling in this nutrient-poor environment, within a closely monitored system. Additionally, the changes in the structure of the supraglacial microbial communities were studied in terms of dynamics, functionality and diversity. It was found that microbes, within certain nutrient and illumination settings, could fix significant amounts of organic carbon, provided that small, natural-level external inputs of nutrients stimulated the system (i.e. levels that mimicked aeolian debris deposition and nutrients released from ice melting). Starting from largely inert debris (90% combusted, to remove all organic matter, and 10% natural cryoconite material with an inoculum of representative microbes), these microorganisms could recreate typical glacial surface organic carbon concentrations (3-5%), using an exponential model applied to the lab results, in approximately 3.5 years. Analyses of phosphorous concentrations (inorganic and organic bound) indicate that there is an uptake of phosphorous from the sediment by microbes in the treatments where organic carbon fixation occurred. Furthermore, the organic carbon production was accompanied by a noteworthy decrease in the spectral reflection (proxy for albedo) within the samples. Thus, as long as certain favourable settings are met, the supraglacial microbes can be stimulated to produce enough organic carbon to accumulate in cryoconite holes and consequently change the albedo of glaciers.

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5 SURFICIAL GLACIAL ENVIRONMENTS

Spatial and temporal variation of the microbial community on the Greenland Ice Sheet

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The surface of the Greenland Ice Sheet (GrIS) is inhabited by a rich microbial community that plays a role in regional carbon cycling, nutrient export and also ice sheet melting via changing the albedo. Due to the large area of the ice sheet, considerable spatial and temporal gradients are present, affecting the microbes. We examine the changes in space and time of the microbial community structure, abundance, activity, and the proportion of the active microbes within the community in cryoconite on the surface of the western part of the GrIS, using co-extraction of DNA and RNA, quantitative PCR and pyrosequencing of DNA and cDNA along with *in situ* productivity measurements. We analyse the relationships between the physical, chemical and biological variables using multivariate statistical analysis, and identify the significant factors controlling the biological processes on the GrIS.

This research is supported by the Villum Foundation Young Investigator Programme Grant VKR023121 to MS.

6 SURFICIAL GLACIAL ENVIRONMENTS

EXPLORATION OF MICROBIAL BIODIVERSITY IN POLAR GLACIAL ICE

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The polar ice caps play a key part in providing an understanding of climate variability over the last eight glacial cycles and may give information about paleoenvironmental features and changes of microbial diversity in the past. Microbiological studies on polar ice cores are rare and focused so far on silty or accreted ice. Aim of our studies is to detect, characterize, and compare the prokaryotic diversity in different Arctic and Antarctic ice cores at different core depths in order to learn more about relations of past and recent communities and about alterations of ancient communities in relation to climatic changes. Critical points in ice core analytics are the strong contaminations of the outside of ice cores as well as the limited availability of sample material. Hence, preparation/decontamination protocols were tested and adapted with inoculated and artificially contaminated ice cores. Our work on real older glacial ice started with material from the uppermost 200m of the ice shield of Dronning Maud Land. We detected some pollen grains and a low abundance of bacteria cells by Sybr Green staining and solid phase cytometry in ice core meltwater. From 3 other ice core samples from about 130m depth, approximately 2150 years old, DNA could be extracted and amplified. DGGE-analyses of amplified DNA revealed a low bacterial diversity. Most of the DGGE-bands occurring in the inner ice core were also present in blanks and controls. One strong band however, was detected only in the inner part of two of the three ice cores analyzed. This band could be affiliated to the alpha-proteobacteria with a high similarity to *Bradyrhizobium japonicum*. Clone libraries and metagenomic studies supported the dominance of this bacteria type that might jointly be responsible for N_2O abnormalities in glacial ice cores.

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7 SURFICIAL GLACIAL ENVIRONMENTS

Microbial succession in cryoconite holes

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We used Illumina sequencing of the 16S gene to study the composition of microbial communities in cryoconite holes on glaciers and ice sheets to gain a better understanding of their contribution to carbon cycling. Closer to the edge of ice sheets and glaciers, the proportion of heterotrophs in the community was relatively high, while in the interior of an ice-sheet, the microbial communities were dominated by cyanobacteria, which represented over 60% of sequences. The presence of significant numbers of Chloroflexi (about 10% of sequences in cryoconite holes in the ice-sheet interior) suggests that conditions in the lower layers of these holes may be anoxic. Eukaryal phototrophs (chloroplast sequences) remained a small proportion of the total phototrophic sequences in all locations. The data suggest a possible microbial succession, where cyanobacteria are particularly abundant and active in stable conditions, while heterotrophic populations are better adapted to the margins of the ice.

8 SURFICIAL GLACIAL ENVIRONMENTS

Variations in Sr and Nd isotopic ratios of cryoconite on glaciers in Asia, Alaska, and Greenland

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Cryoconite is biogenic surface dust on glaciers consisting of mineral particles and organic matter mainly derived from microbes living on glaciers. Since cryoconite is dark color, it can reduce surface albedo of glaciers and accelerate their melting. Thus, it is important to understand their sources and formation processes on glaciers. In this study, we analyzed Sr and Nd isotopic ratios of four mineral and organic fractions in cryoconite on Asian, Alaskan, and Greenlandic glaciers. Based on the isotopic ratios, we identified origins of minerals in cryoconite and mineral sources used as nutrients by microbes on the glaciers.

Sr and Nd isotopic ratios in the silicate mineral fractions, which are major components of mineral particles, vary significantly among geographical locations of the glaciers. Cryoconite on Asian glaciers showed higher Sr and lower Nd ratios in the north and also showed little variation within a glacier. On the other hand, those on Alaskan glacier showed lower Sr and large spatial variation in Nd on a glacier. Cryoconite on Greenlandic glaciers showed further high Sr and low Nd than the other glaciers. This result indicates that the isotopic ratios of minerals in cryoconites likely reflect those of the geology of the respective regions. Compared with the isotopic ratios of silicate minerals in moraine, desert, and loess reported over the regions, those in cryoconite on Asian, Alaskan, and Greenlandic glaciers were close to those in respective regions. This result indicates that silicate minerals in cryoconite were derived from surrounding the glaciers.

The Sr isotopic ratio of organic matter in the cryoconites was higher than those of saline and carbonate fractions, but lower than that of the phosphate fraction, suggesting that microbes on the glacier incorporate calcium of these three minerals as nutrients. However, the quantitative proportions of the minerals they used were different among the glaciers: the proportions of saline and carbonate minerals were higher in the Asian glaciers located in the mountains within desert areas than in other Asian, Alaskan and Greenlandic glaciers. This indicates that nutrient incorporation of the microbes is likely to be affected by the geology around the glaciers.

9 ANTARTIC & ARCTIC LAKES AND STREAMS

An “omics” approach to characterizing dissolved organic matter from microbially derived sources in Antarctica

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The complex mixture of organic compounds within aquatic systems, known as dissolved organic matter (DOM), comprises a significant pool of carbon on the planet. The ultimate source of DOM in many Antarctic systems is from microorganisms; however the processes leading to the release and subsequent alterations of these compounds are poorly understood. DOM is an integral component of the global carbon, nitrogen, and sulfur cycles, accounting for much of the total organic material flux in lakes, streams, and oceans. DOM also provides a carbon source for microbial activity, influencing biogeochemical and ecological processes. Despite the critical role of DOM in ecosystems, its properties and reactivity are not well defined.

An “omics” based approach was used to chemically characterize the interaction between DOM and the representative microbial species that transform it in an Antarctic ecosystem. To do this, a comparative analysis of environmental DOM from the microbially dominated Pony Lake and Cotton Glacier aquatic systems was undertaken using advanced mass spectrometry and spectroscopy techniques to generate an in depth molecular profile. Fundamental differences exist in the molecular profiles between the two microbially based sources of DOM. Complete proteomic and metabolic analysis using an approach coupling ultra performance liquid chromatography to a quadrupole time of flight mass spectrometer was undertaken for cultures of representative Antarctic *beta-Proteobacteria* (CG3) grown on a minimal media supplemented with DOM from Antarctic and terrestrial locations as a carbon source. This study represents the first untargeted metabolomic profile performed on an Antarctic microorganism, making available a direct indicator of cellular activity in response to the various carbon sources. Using cutting-edge analytical techniques we can follow how DOM is produced and transformed by microbes in this extreme environment. *NSF-PLR 1141978*

10 ANTARTIC & ARCTIC LAKES AND STREAMS

Segregation of geochemical and biological constituents during progressive freezing in polar lakes

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Habitability of icy systems on Earth is influenced by the freezing process and the resultant segregation of biological and chemical constituents between the liquid and solid phases. As water molecules freeze, they create a crystalline ice lattice that repels solutes and particulate matter in a predictable pattern, but little is known about the responses of microorganisms to the freezing process.
We used a comparison between perennially and seasonally ice covered lakes to address questions regarding the response of microorganisms to progressive ice freezing. To address the overarching question of whether or not there is a biological response to ice formation, we conducted a series of controlled freezing experiments from perennially (Lake Fryxell, Antarctica) and seasonally (Lake Sukok, Barrow, AK) ice covered lakes. In nature, perennial and seasonal ice cover subjects the lakes to contrasting freezing regimes.
We hypothesized that microorganisms are adapted to the freezing process and will exhibit a biological response to freezing, which will differ from the predictable chemical response to the freezing process.
We expected evidence for a biological response as differential partitioning of microorganisms compared to chemical species during freezing of the seasonally ice covered lakes.
Our results showed that lakes from Antarctica and the Arctic strongly excluded F^- and SO_4^{2+} from the ice phase; however, Mg^{2+} and K^+ were the first ions incorporated into the ice. The pattern of solute exclusion from ice was similar to other experimental studies of water freezing.
Preliminary biological results from seasonally ice covered lakes indicate the microorganisms showed an affinity to be incorporated into upper portion of the ice cover. In contrast to the seasonally ice covered lakes, microorganisms from perennially ice covered lakes were excluded from the ice and behaved similar to the geochemical constituents.
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1 ANTARTIC & ARCTIC LAKES AND STREAMS

Bacterial Biodiversity of McMurdo Dry Valley Streams, Antarctica

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The ephemeral streams of the McMurdo Dry Valleys (MDV), Antarctica are biological hotspots and are central to the cycling of nutrients and solutes throughout the ecosystem. This study surveys the biodiversity of bacterial communities in 12 streams throughout the MDV, looking at sediment and microbial mat samples collected during the peak of the stream flow season. Using 454 pyrosequencing techniques we examined the bacterial community composition and structure in regards to stream location and analyzed the taxonomic dispersal and abundance within stream microenvironments and across individual streams. Our results indicate that MDV streams host over 45 bacterial phyla, with ~24,000 operational taxonomic units (<97% similarity) identified. Community composition was most related to substrate type and geographical location.

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12 ANTARTIC & ARCTIC LAKES AND STREAMS

Characteriziation of a Novel Psychrophilic *Marinobacter* Strain Isolated from Blood Falls, Antarctica

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More than 80% of the Earth’s biosphere is below 5°C. These cold environments include sea ice, permafrost, and subglacial ecosystems. There has been an increase in the number of psychrophilic isolates – bacteria, archaea, eukaryotes, and viruses – from these systems in recent years, significantly increasing the number of cultured representatives for study of psychrophilic physiology. Physiological adaptation in psychrophiles such as enzymes with lowered activation energy, increased membrane fluidity, and ice-binding proteins has enabled the survival and growth of these organisms in low temperature and freezing conditions as well as offer novel biotechnological applications. Few samples have been collected directly from Antarctic subglacial environments, due to the difficulty in accessing samples below thick ice covers. Here we present the characterization of strain BF05_4 in the *Marinobacter* genus, which describes rod-shaped, gram-negative, aerobic bacteria with a high tolerance for salt (up to 20% (w/v) NaCl). Strain BF05_4 was isolated from a subglacial outflow of the Taylor Glacier, McMurdo Dry Valleys, Antarctica. The outflow is known as Blood Falls, and is hypersaline (1,440 mM Cl^-) and rich in ferrous iron (3.8 mM total Fe). Strain BF05_4 grew fastest at 10°C with limited growth at 30°C, indicating it is a true psychrophile. Predominant cell membrane fatty acids of BF05_4 were unsaturated 18:2 ω6,9c, 18:0 ante, 18:1 ω 9c, and 18:1 ω7c, which would promote cell membrane fluidity at low temperatures. Preliminary results indicate BF05_4 can utilize fructose, mannitol, lactose, mannose, sorbitol, sucrose, serine, trehalose, alanine, and benzoate as carbon sources. The complete description of isolates, such as strain BF05_4, from subglacial

13 ANTARTIC & ARCTIC LAKES AND STREAMS

Influence of Photosynthetic protist diversity on the community composition of enrichment cultures from an Antarctic lake.

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Microbial mats are repositories of diversity in ecosystems that are exposed to extreme environmental conditions, including those resembling habitable environments on other worlds in our solar system. In the McMurdo Dry Valleys of Antarctica, microbial mats develop as dense interacting communities of cyanobacteria, algae, heterotrophic and chemolithoautotrophic bacteria, predatory protists, and microscopic invertebrates. These communities represent hot spots of biodiversity and production in this harsh polar desert environment. One of the current frontiers in the ecology of these microbial habitats is to describe the interactions within microbial mat communities. We approached this problem by inoculating microbial mats collected from two distinct sampling sites located on the surface ice of an Antarctic lake (Lake Fryxell) into a series of growth media that differentially selected for various photosynthetic microorganisms. We then followed the succession of bacterial and eukaryote communities across the enrichment cultures by isolating total environmental DNA from a collection of 18 cultures and sequencing 16S and 18S rRNA. Our enrichment cultures produced a series of unique microbial ecosystems that harbored heterotrophic bacteria, cyanobacteria, unicellular algae, predatory protists as well as microscopic invertebrates (tardigrades, nematodes, and rotifers). Furthermore, our results show that microbial diversity was influenced by both the origin of the original inoculum as well as the type of growth media used in the enrichment. Last, this enrichment scheme of using photosynthetic microorganisms to capture specific bacterial species may also provide an avenue for cultivating a broader range of bacteria from the “uncultivable” biosphere.

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14 ANTARTIC & ARCTIC LAKES AND STREAMS

Photooxidative stress response in mesophilic versus psychrophilic *Chlamydomonas* spp.

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Chlamydomonas raudensis UWO241 is model psychrophilic alga. *C. raudensis* SAG49.72 is the sister mesophilic strain. UWO241 was isolated from the ice-covered Lake Bonney (McMurdo Dry Valleys, Antarctica) and is adapted to low temperatures (T_{opt}=8°C), low light and high salinity (700mM NaCl), while SAG49.72 was isolated from a temperate lake in Europe, is salinity-sensitive and adapted to moderate temperature and light conditions. These two organisms present a unique opportunity to compare environmental adaptation between two closely related organisms isolated from divergent habitats. In this study we explored the ability of UWO241 vs. SAG49.72 to resist temperature- and light-induced oxidative stress. Photooxidative damage was monitored as the loss of photochemical efficiency (F_V/F_M) in cultures exposed to varying light and temperature stress. Under high light, the psychrophilic UWO241 exhibited a rapid decline in F_V/F_M which was independent of incubation temperature. In contrast the mesophile SAG49.72 exhibited maximal losses in F_V/F_M at incubation temperatures at or below 8°C. To explore the molecular mechanisms governing photooxidative sensitivity in the psychrophile, we sequenced the first transcriptome from UWO241. Assembly of the raw reads produced 11,500 contigs, of which >80% could be annotated. The annotated psychrophile transcriptome yielded many homologs for key enzymes involved in stress responses, including several putative antioxidant enzymes (AOEs). Several AOEs were cloned and sequenced from UWO241 mRNA, and AOE expression was quantified in cells exposed to photooxidative stress using real time quantitative PCR (qPCR). These results as well as standardization of qPCR data in UWO241 using housekeeping genes will be discussed.

This work was supported by NSF Office of Polar Programs (0631659 and 1056396)

15 ANTARTIC & ARCTIC LAKES AND STREAMS

Carbon fixation in cold environments: RubisCO enzyme activity of microbial communities in McMurdo Dry Valley lakes, Antarctica

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Photosynthetic microorganisms drive fixation of inorganic carbon in the vast majority of aquatic ecosystems on earth, including those at low temperature. Low temperature aquatic food webs are dependent upon energy and carbon derived from autotrophic organisms which primarily rely on light-driven photosynthetic reactions catalyzed by cold-adapted photosynthetic microorganisms (or photopsychrophiles). The microbially dominated McMurdo Dry Valley (MDV) lakes provide a unique opportunity for understanding carbon cycling and food web dynamics in aquatic systems. Not only are the food webs relatively simple, but the physically and chemically stratified lakes allow correlations to be made between food web function and environmental parameters. Here we present work on the enzyme Ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO), which catalyzes the first step in fixation of inorganic carbon into simple sugars. We report catalytic rates of RubisCO through the water column of three chemically distinct MDV lakes (Bonney, Fryxell, Vanda), as well as the distribution of autotrophic microorganisms based on distribution of the RubisCO large subunit gene. Our results show that the majority of carbon fixation is carried out by haptophytes, stramenopiles and cryptophytes. These results will be placed in the context of major environmental factors in order to understand how abiotic drivers influence the distribution of autotrophic microorganisms. This work was supported by NSF Office of Polar Programs (0631659 and 1056396).

16 ANTARTIC & ARCTIC LAKES AND STREAMS

Molecular and Morphological Characterization of Microbial Eukaryotes (Protists) Residing in Ice-covered Antarctic Lakes

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The McMurdo Dry Valleys (MDV) of Southern Victoria Land, Antarctica, is considered as one of the best earth analogues for habitability of icy worlds in our solar system, due to its geological and extreme climate characteristics. The MDV harbors numerous permanently ice-covered lakes, which provide unique aquatic oases to support the food webs that are completely dominated by the microbial loop. A better understanding of MDV microbial community dynamics will contribute to answering the open, fundamental questions in microbial ecology, and also provide information on possible survival strategies in other icy worlds. Lake Bonney is one of several lakes that are part of a Long Term Ecological Research site (McMurdo LTER). Protists are the dominant eukaryotes in this lake, and they play important trophic roles from primary producers to the top predators in this simple food web. Past studies have reported that chlorophytes, haptophytes and a stramenopile are key primary producers in Lake Bonney, while ciliates were reported to be a major predator. However, to date, a thorough morphological description of the microbial eukaryotes residing in this lake has been lacking due to the low biomass and difficulties in sample preservation for microscopy. During our most recent field season (October – December 2012), we applied a tangential flow filtration approach to concentrate protistan biomass in the water samples, and morphological and physiological characteristics were surveyed by light, fluorescence, and electron microscopy methods. Furthermore, distinct protistan morphological features were linked to taxonomic data. Last, we will present a new MDV food web model that incorporates our morphological and taxonomic data as well as protistan nutritional modes.

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17 ANTARTIC & ARCTIC LAKES AND STREAMS

Impact of Mimicked Summer Flood Event (Nutrient Amendment) on Microbial Communities residing in two Chemically Stratified Antarctic Lakes

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The McMurdo Dry Valley (MDV) lakes in the Taylor Valley of Antarctica are characterized by permanent ice cover, low stream inputs, and a strong vertical nutrient gradient. This stable water column has a simple food web dominated by microbial eukaryotes (protists) and bacteria. Nitrogen and phosphorus are often the primary limiting nutrients within these lake systems, thus limiting biomass and overall productivity. It is predicted that MDV lakes will be impacted by climate change by higher summer floods and increased input into the ecosystems. This could lead to changes in nutrient availability, particularly in the surface microbial populations and has the potential to significantly alter community structure and dynamics. Thus, predicting the influence of altered nutrient availability on microbial community structure is an important factor in understanding the impact of climate change on the MDV lake ecosystems. In the current study, the influence of inorganic nitrogen (N) and phosphorus (P) amendment was examined on shallow communities in two chemically distinct MDV lakes (Lakes Bonney and Fryxell) which differ in their N:P stoichiometry. In P-amended treatments phosphorus was rapidly removed by Lake Bonney but not Fryxell microbial communities. Spectral chlorophyll fluorescence revealed minor changes in the distribution of major algal classes, including an enrichment of cyanobacteria in all Lake Bonney treatments. We used quantitative PCR to monitor the effect of N- and P-amendment on the abundance (DNA) and expression (mRNA) of phylogenetic (16S and 18S rRNA) and functional (*rbcL, psbA*) genes. Lake Bonney bacterial abundance (16S rDNA) was moderately stimulated under all treatments, while in Fryxell communities, P-amendment had a strong impact on 16S rRNA levels. Conversely, all treatments exhibited a loss of eukaryote (18S rDNA) abundance in Lake Bonney, while 18S rDNA levels remained relatively low across all Lake Fryxell treatments. Lake- and treatment-specific patterns at the level of functional gene abundance will be discussed.

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18 ANTARTIC & ARCTIC LAKES AND STREAMS

Temporal changes in the microbial communities form the Lemon Creek glacier, AK: relations to isotope composition and hydrological residence times.

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The composition of glacial out flow from the sub-glacial hydrological network depends on three major parameters; water residence time, microbial population and bedrock geology. We investigated these parameters using a multi disciplinary approach: (1) analyzing chemical and isotopic compositions (Fe, Sr and O systems) of glacial outflow and sediment, (2) sequencing ribosomal RNA genes found in the sediment, and (3) thermodynamic calculations to investigate mineral saturation states in the dissolved load. Our results suggest that interstitial microbial weathering supports diverse microbial communities that are distinct from samples taken from the runoff lake, waters mixed with snowfall and under glacier waters. Proteobacteria were the most abundant phylum regardless of sampling site or time and consist of organisms recognized for metal redox cycling abilities. These results show interstitial communities are unique from those exposed to surface and are linked with geochemical measurements.

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19 ANTARTIC & ARCTIC LAKES AND STREAMS

Microbial Composition and Growth of Lake Vanda Microbialites

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Benthic microbial mats in the perennially ice-covered Lake Vanda in Antarctica form pinnacled structures that are distributed from just below the ice to greater than 40m depth. Investigation of the physiology and growth of these modern microbial mats will inform an understanding of ancient microbial communities. Here we present a model for pinnacle growth, and an investigation of the microbial communities present within the Lake Vanda benthic mat.

Pinnacle size and density were measured *in situ* and individual pinnacles were collected for Pulse Amplitude Modulated (PAM) fluorometry, cyanobacterial 16s rRNA gene analysis, and examination via microscopy of cyanobacterial morphotypes.

Pinnacle distribution is consistent with random initiation, and morphology varies with size. Larger pinnacles show more complex morphology. Smaller pinnacles dominated shallow waters, while maximum pinnacle size increased with water depth. Smaller, shallow water pinnacles were interpreted to be younger in age due recent lake level rise. Analysis of cross sections of individual pinnacles revealed internal laminations that varied in pigmentation. The 16s rRNA gene analysis of these layers revealed that the pinnacles are dominated by the order Oscilatoriales, with *Leptolyngbya* and *Phormidium* being the most common genera. The majority of sequences from the outer layers of the pinnacles belonged to *Leptolyngbya*, while inner layers consisted of both *Leptolyngbya* and *Phormidium*. PAM fluorometry suggested that the subsurface green and pink layers are at least as photosynthetically active as the outer layers. This photosynthetic potential indicates that the pinnacles have increased biomass accumulations internally, as opposed to growth from the outer laminae or the pinnacle tips. Pinnacle distribution data suggest that pinnacle initiation is random, and furthermore competition for nutrients is not a factor in pinnacle spacing.

This work was supported by the NASA Astrobiology grants NNX08AO19G and NN13AI60G and the New Zealand Foundation for Research, Science and Technology grant CO1X0306.

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20 ANTARTIC & ARCTIC LAKES AND STREAMS

Preliminary results of chemical and metagenomic analyses of Lake Vostok water refrozen in borehole 5G-1 following the unsealing of the lake

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One year after the subglacial Lake Vostok was unsealed, the first samples of refrozen lake water have become available for research due to redrilling of the deep borehole at Vostok Station in the 2012-2013 austral season.

The top of the refrozen material was represented by a foam-like hydrate compound which was preliminarily identified as a mixed clathrate hydrate of lake gases and hydrofluorocarbon densifier. The secondary ice had a heterogeneous, radial-beam texture, with the concentration of gaseous and liquid inclusions increasing towards the borehole axis.

A few horizontal thick sections of the secondary water ice were analysed using ion chromatography and GC-MS with focus on the modified organic species of drilling fluid that may give additional information on the properties of the lake water.

Comparative metagenomic analyses (16S rRNA gene identification, 454 pyrosequencing) of selected water ice samples are now in progress.

This study is supported by a grant from the Russian Foundation for Basic Research (RFBR, 12-05-0085).

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21 ANTARTIC & ARCTIC LAKES AND STREAMS

Ecology of a winter diatom bloom in a montane-desert river

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Primary production and standing stocks of biomass are often assumed to be at their minimum in the winter due to abiotic constraints (low temperatures and irradiances). However, notable winter blooms of diatoms have been observed and documented in some river systems (.e.g the Truckee River, CA-NV, USA). Longitudinal accrual rates, specific growth rates, community metabolism have been documented in the Truckee River to evaluate the relative magnitude of the blooms and associated rate processes to better evaluate potential ramifications in regards to ecosystem energetics and material cycling. Standing stocks generally increased downstream (up to 60 μg chlorophyll *a* cm^{-2}) in conjunction with specific growth rates (up to 0.15 divisions day^{-1}). Photosynthesis always exceeded respiration in epilithic communities, indicating a continual net gain in energy (both spatially and temporally) throughout the winter bloom. Net autotrophy at the ecosystem-scale was also demonstrated in a high biomass reach and emphasized the potential significance of the winter bloom in regard to the annual primary production. Seasonal estimates indicate that the winter months (November to January) contribute approximately 37% of the yearly net gain in energy in the Truckee River, thus underscoring the importance of evaluating ecological processes during winter to truly understand the complete energetics and mass-balance of aquatic systems.

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22 SELECTED ENVIRONMENTS

IDENTIFICATION OF MICROBIAL COMMUNITIES FROM ANTARCTIC: TAXONOMY AND MOLECULAR APPROACHES BASED ON DGGE FINGERPRINTING AND 454 SEQUENCING

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Microorganisms are the dominant inhabitants in extreme environments. Understanding the taxonomy, distribution, and diversity of extremophiles could give us important guidelines to harvest their potential.

This study focused on the identification and diversity determination of the microorganisms obtained from thirteen soil samples taken from the Greenwich Island in the Antarctic continent during summer of 2010, 2011, and 2012. Molecular techniques based on PCR, Sanger sequencing, DGGE and 454 sequencing of semi-conserved regions were used to determine the principal groups of bacteria and fungi present in the samples. Likewise, cultured microorganisms were submitted to taxonomic analyses to confirm identities.

The main fungi identified were *Mortierella pulchella, M. fymbricystis, M. parvispora, Antarctomyces psychrotrophicus*, *Geomyces spp., Variscosporium elodeae*, and yeast *Cryptoccocus gasrticus, C. gilvescens* and *Rhodotorula glacialis*; whereas the main bacteria were from the family *Lactobacillaceae, Xanthomonadaceae, Chlorobiaceae, Comamonadaceae, Rhodobacteraceae, Pseudomonadaceae, Micrococcaceae, Moraxellaceae, Oxalobacteraceae* among others.

DGGE analysis showed significant differences between sample locations in terms of diversity based on Shannon-Wiener index (H); highest diversity was found in soil with bird guano (H: 258.11), whereas the lowest diversity was from the zone of melting glacier (H: 146.61). Results were confirmed by 454 sequencing data.

Principal Component Analysis (PCA) was run on the 454 sequencing data; samples were grouped by year of sampling. The operational taxonomic units (OTUs) contributing to the PCA grouping were *Psychromonas* and *Microcoleus* as well as OTUs from the *Rhodobacteraceae* and *Chthoniobacteraceae* families. Other uncharacterized microorganisms were also responsible of the PCA grouping. Special sampling sites showing biofilm formation and hydrocarbons (HC) contamination formed a separated group in the PCA. The main OTUs in HC sample were *Acidimicrobiales* and *Actinobacteriales*. In the biofilm sample most of the OTUs found belong to class *Acidobacteria*. There is also a high percent of non-characterized families, indicating the big potential for discovering new taxonomic groups that could be of interest for bioprospecting.

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23 SELECTED ENVIRONMENTS

Phylogenetic Characterization of an Antarctic Ice Cave Microbiome

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Microbial ecosystems of polar and alpine regions have recently attracted attention due to the potential metabolic properties of their inhabitants and their possible role in carbon cycling and climate changes. Ice caves represent one of the least studied ecosystems for particularly cold-adapted microorganisms. The aim of this project was to describe the microbial community of an ice cave located near the Vanishing Creek at King George Island, Antarctica. Triplicate soil samples were aseptically collected inside the cave and kept frozen in -20 °C until the laboratory in Brazil. Real Time PCR (qPCR) and 454 Pyrosequencing of the 16S rRNA gene were applied to quantify and analyze the microbial composition, respectively. Total microbial DNA was extracted from ~5 g of soil using PowerSoil DNA kit (Mo Bio, USA), and then amplified with barcoded primers U519F and U1068R that corresponds to the V4-V6 regions of *E. coli* 16S rRNA gene. Amplicons were sequenced in 454 GS FLX Pyrosequencing and resulted in 9,170 sequences of varied length (~90-570 bp). High quality (Phred score > 20) and non-chimeric sequences were analyzed on RDP “Classifier”, showing high abundances of Bacteria (99.9%) over Archaea (0.1%). Dominant bacterial Phyla were Proteobacteria (40.4%) and Actinobacteria (30.7%). The remaining sequences were classified into Bacteroidetes (7.3%), Acidobacteria (3.9%), Verrucomicrobia (2.6%), Chloroflexi (2%), Gemmatimonadetes (1.5%), Firmicutes (1.4%), Cyanobacteria (1.3%), and other 13 different Phyla (total of 1.8%) or Unclassified (7.1%). Dominant genera included *Nocardioides*, *Conexibacter*, *Perlucidibaca*, *Albidiferax*, *Polaromonas*, *Sphingomonas*, GP4, *Gemmatimonas*, *Solirubrobacter* and *Novosphingobium*, comprising around 28% of the sequences. The abundances of major microbial groups, as determined by qPCR, were reported as DNA copy numbers of 16S rRNA genes per g of soil. Bacterial 16S rRNA genes were dominant (99.74%) over Archaea (0.26%), in agreement with 454 results. Ice caves are considered a distinctive refuge for microorganisms in cold ecosystems and identifying the species is an important step for biotechnological and astrobiological studies.

Acknowledgments: FAPESP, CNPq-PROANTAR.

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24 SELECTED ENVIRONMENTS

Microbial Biogeochemistry in Arctic Subglacial Sediments

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Subglacial sediments, whether under Arctic and Alpine glaciers or the Greenland and Antarctic ice sheets, play host to extensive and active microbial communities. Due to the relative inaccessibility of this ecosystem, however, fundamental ecological questions remain unanswered, such as how productive the microbes are, or which are the most important interactions with different mineral substrates taking place?

Analysis of subglacial upwellings has provided compelling evidence for a microbial role in the mineral weathering processes and redox reactions that dominate water chemistry in this environment. Determining ecological processes from outflow chemistry is limited, however, by difficulty in separating biotic and abiotic processes under the glacier. The work being carried out for my PhD takes a laboratory approach, in which subglacial sediments, removed from a number of glaciers in Svalbard, Greenland and South Georgia, are being utilised in microcosm experiments that investigate microbial diversity, activity and importance in geochemical processes. It is hoped that the integration of lab-based microcosms into future field studies, can strengthen the conclusions drawn about subglacial ecosystems from geochemical analysis of outflow.

Sediment microbial composition was investigated using fluorescence in situ hybridisation to target bacteria, archaea and eukaryotic domains as well as some bacterial subgroups. A radio label approach has been used to measure bacterial and primary production in the sediments under laboratory conditions, assessing the linkages between metabolism and geochemistry as well as the relative influence of heterotrophy and chemoautotrophy in these dark, cold ecosystems. On-going batch and flow-though microcosm experiments investigating the microbial influence to mineral weathering processes and hydrogeochemistry at an ecosystem scale will also be presented.

25 SELECTED ENVIRONMENTS

Comparative evaluation of the indigenous microbial diversity versus drilling fluid contaminants in the NEEM Greenland ice core

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Validating microbiological results from non-aseptically drilled deep ice cores is challenging because exogenous microbial cells could compromise the intrinsic microbial populations. The NEEM Greenland ice core project provided a first-time opportunity to address this contamination problem during and soon after the drilling process. We applied both metagenomic and cultivation approaches to perform parallel microbiological analyses of five decontaminated freshly drilled ice core samples from different depth/age (100m to 2051m/ 300 – 80,000 years BP), the two original components of the drilling fluid (Estisol 240 and Coasol), drilling fluid and chips (DF+ice) collected during drilling. We found that the ice deposited during colder climate had relatively higher microbial abundance (106/ml), which corresponded to higher in-situ ion content. The drilling fluid contained lower load of microbial cells (104-105/ml) but had significantly higher culturability. Comparative analyses showed variable diversity and different proportional representation of major phylogenetic groups in the samples. In result of multiple plating experiments we created a collection of 46 isolates from decontaminated ice, 83 bacterial and fungal contaminants originating from the drilling fluid and its components and 63 isolates from chips, which were taxonomically identified and characterized. Combined phylogenetic and genomic analyses and strain by strain comparisons helped distinguish exogenous contaminants and intrinsic glacial ice microorganisms. Betaproteobacteria related to *Massilia* and *Variovorax* were recovered only from the ice, as well as a gammaproteobacterium *Enhydrobacter* and some isolates from Actinobacteria genera *Oerskovia*, *Arthrobacter*, *Kytococcus* and *Humicoccus* with closest relatives originating from cold and frozen habitats. Among those was a novel isolate from a 634 m ice sample, affiliated with alphaproteobacteria, with the closest validated relative *Hansschlegelia plantiphila* (utilizing methanol) at a distance of 90.7%. Conversely, isolates belonging to *Aerococcus*, *Citrococcus*, *Gordonia*, *Lysinibacillus*, *Rummeliibacillus*, *Sporosarcina*, *Geobacillus*, *Methylobacterium*, *Paracoccus*, *Sphingomonas* and *Pseudomonas* originating only from the drilling fluid were considered contaminants. Categorization of other mixed clusters of drilling fluid and ice isolates *Acinetobacter*, *Staphylococcus*, *Paenibacillus*, *Bacillus*, most fungi and some Actinobacteria (*Micrococcus*, *Frigoribacterium*, *Streptomyces*) was based on several criteria, including ERIC-PCR fingerprinting, morphological and physiological characteristics, presence in chips and/or ice. This study provides a database of potential contaminants useful for future studies of NEEM cores that will help establish better criteria for validation of microbiological results.

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26 SELECTED ENVIRONMENTS

hima: a meta-database for genomes, metagenomes, and isolate phenotypes from cold environments

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One hundred years after Beijerinck proclaimed "everything is everywhere," the modern flood of sequencing data has revolutionized the classically data-poor field of environmental microbiology. And yet, connecting this information with traditional phenotypic observations like those made by Baas Becking (of "but the environment selects" fame) has lagged behind the digital deluge. You want that data? Go look it up in *Bergey's* – no online database allows one, for example, to list all bacterial isolates known to grow below 10˚C, much less to take the next step and link that trait to available phylogenomic data.

Cold-active microorganisms --- including Bacteria, Archaea, Eukarya, and viruses --- play important roles in both natural and built environments, by mediating biogeochemical cycles in the deep and polar oceans, sea ice, permafrost, and glaciers, as well as affecting food safety and as sources of novel biotechnology. Using these microbes as a testbed, I have used text-mining and manual curation to collate a queryable, open-access MySQL database, as a step towards a future where phenotypic, genomic, and phylogenetic information can be readily accessed for use in comparative genomics and predictive biology. Some parameters include sampling environment and location, type strain identification, optimal temperature and growth range, electron acceptors used, growth substrates used, genome sequences, gene clusters, mapped metagenomic reads, and many other traits. Currently, the database covers >10 cold-active genera, >50 complete genome sequences and >400 metagenomes and microbiomes, including a number of transcriptomes and viromes, all collected between 79˚N and 77˚S.

hima (http://reric.org/work/hima**)** is navigable via a phylogenetic tree interface and will be updated into the future, as it is further expanded to include more analytical resources for use by researchers interested in the ecology and evolution of cold-loving microbes.

27 SELECTED ENVIRONMENTS

Physiological characteristics of polar and alpine bacteria according to the taxonomy, habitat, and geographical origin

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Polar and alpine areas may have harsh environments with low temperature and low nutrient concentration. Microorganisms in these areas survive and grow by their unique characteristics such as cold-adapted enzyme productions. Extracellular enzymes secreted by cold-adapted microorganisms may play important ecological roles in the cycling of organic matters. In this study we performed broad scale screening of the physiological characteristics such as temperature response and extracellular enzyme production of bacteria according the taxonomy, habitat, and geographical origin. Three hundred forty seven bacterial strains of Polar and Alpine Microbial Collection (PAMC) with various taxonomic information which were originated from a variety of habitats of polar areas were selected. Bacterial strains were included in *Gammaproteobacteria* (48.4%)*,* *Bacteroidetes* (20.2%)*,* *Actinobacteria* (13.5%)*,* *Alphaproteobacteria* (7.5%)*,* *Firmicutes* (6.1%)*,* *Betaproteobacteria* (4.0%) and *Deinococcus-Thermus* (0.3%) and they were originated from biotic (lichen, moss, algae and animal) and abiotic (terrestrial soil, marine sediment, sea water, fresh water, cryoconite, debris, ice, snow and biofilm) samples of Arctic (Svalbard, Khuvsgul, Kara Sea, and Barents sea), Antarctic (Adelie Island, Barton Peninsula, King George Island, Weaver Peninsula), Innsbruck and Russia. Most strains grew ranging from 4℃ to 30℃ (optimal 10℃), while the number of strains could grow at higher than 30℃ decreased. The number of bacterial strains from biotic samples could better grow than that from abiotic samples. By phylum, strains included in *Bacteroidetes, Gammaproteobacteria* and *Alphaproteobacteria* were more psychrophilic than others. Bacteria from arctic were psychrophilic and strains from Innsbruck and Russia showed mesophilic patterns. One hundred thirteen strains showed hydrolytic enzymes activity. According to habitat, strains from algae, animal, biofilm, cryoconite, ice/snow, sea water and terrestrial soil had all extracellular enzyme (protease, lipase, cellulase) activities examined. Five strains from algae showed the highest activity of all enzymes. Eight strains from lichen/moss and cryoconite showed high protease activity and 24 strains from biofilm showed high cellulose activity. Bacteria from Innsbruck and Russia showed the highest enzymatic activity. [This research supported by Korea Polar Research Institute (Grant PE13030)]

28 SELECTED ENVIRONMENTS

Bioprospecting of Antarctic microorganisms and their enzymes.

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Bioprospecting of microorganisms from Antarctic zones has significantly grown in the last years mainly because of the potential of finding novel low-temperature active enzymes. The objective of this study was to evaluate the presence of low-temperature-active enzymes in microbial isolates from the Antarctic continent. Mineral media containing starch, pectin, casein, gelatin, cellulose, or urea were used to assay the presence of microbial amylases, pectinases, proteases, gelatinases, cellulases, or ureases respectively. The enzymatic activity of each isolate was determined at 16 ˚C for eight days by measuring the halo formed on the media. Microbial identification was carried out by sequencing part of the 16S region of bacterial isolates and the ITS1, 5.8S, and ITS2 regions of fungi. Of the 167 isolates assayed (137 bacteria and 30 fungi), 104 were positive for at least one of the enzymes tested (74 bacteria and 30 fungi). The most common bacterial isolates found were the genres *Pseudomonas sp.*, *Arthrobacter sp., Rhodococcus sp.,* and *Pantoea sp.* whereas the fungal most common isolates identified are *Mortierella pulchella, Mortierella fymbricystis, Mortierella parvispora, Antarctomyces psychrotrophicus, Geomyces violaceum,* and *Variscosporum elodeae*. The isolate (C27) identified as *Arthrobacter* sp. showed the largest amylase halo (0.9 cm) and the isolate (C101) identified as *Pseudomonas* sp. showed the highest gelatinase activity (1.2 cm). Others isolates such *Rhodococcus sp. (*C22) showed the largest urease halo (1.0 cm) whereas isolated from *Pseudomonas sp.* present high digestibility of casein. No bacterial isolate showed either cellulose or pectinase activity but 20 fungal isolates including *Geomyces violaceum* showed cellulase or pectinase activity. Protease activity was not observed in any fungal species tested. Characterization of purified enzymes is currently going on to determine optimum operation conditions of each enzyme.

29 SELECTED ENVIRONMENTS

West Antarctic Ice Sheet (WAIS) Divide Ice Core: A microbially derived reservoir of organic carbon

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John C. Priscu, Dept. Land Resources and Environmental Science, Montana State University, Bozeman, Montana, USA, 59717.

WAIS Divide is a collaborative, multi-investigator US deep ice coring project focused on developing interrelated climate, ice dynamics, geochemical, and biological records at high resolution. Once thought devoid of life, glacial ice is now recognized as a habitat for microorganisms and a potentially significant reservoir for a new, uncharacterized reservoir of organic material. Our data indicate that the WAIS Divide ice contains a temporal record of organic carbon. We measured temporal trends in the quantity and quality of dissolved organic matter (DOM) from early Holocene ice (1300-1700m) and the late Glacial ice (1700-2100m) extending back to the Last Glacial Maximum (2100-2700m) of the WAIS Divide core using a flow-through dissolved organic carbon analyzer and excitation emission matrix fluorescence spectroscopy (EEMS). Despite dissolved organic carbon concentrations in the WAIS Divide ice core that are typically less than 50 ppb, sufficient fluorescing material was present to characterize the different fluorophores present in the ice core DOM. Approximately 90% of the DOM in these ice cores was dominated by the presence of both tyrosine-like and tryptophan-like protein fluorescence signatures. Proteinaceous fluorophores are believed to reflect the production of amino acids during microbial metabolism and are typically more labile than DOM with significant humic signatures. Less than 2% of all EEMS displayed fluorescence intensities in terrestrial or marine humic-like fluorescent regions, characteristic of higher plant inputs or chemically altered biomolecules to highly conjugated aromatic refractory humic substances. Humic-like fluorescent components were detected by EEMS in regions of the ice core thought to correspond to terrestrial inputs and volcanic activity. However, fluorescence in those regions was far less prevalent than the protein-like fluorescent contributions. Our results imply that microbially derived organic matter within this ice is the largest contributor to the fluorescent chemical nature of the DOM.

This research was funded by NSF-OPP grant 0839075

30 SELECTED ENVIRONMENTS

Microbial Abundance in the WAIS divide ice core between the Last Glacial Maximum and the Early Holocene

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The Quaternary period is unique in Earth's history due to human habitation and the rapid and high magnitude climatic and environmental changes. Proxies and evidence for Quaternary environmental conditions are more abundant, of higher resolution, and better preserved than those from any other period. Additionally, biological proxies and geological features are more similar to extant species and current features than those from other periods.

Microorganisms that are preserved in ice and living on glaciers have been studied in recent decades and have been successfully used to date and estimate the net mass balance from firn/ice cores in temperate glaciers. Bacteria respond quickly to environmental changes due to short generation time (hours, days and months) and play important roles in ecosystems as key drivers of elemental cycles. Consequently, measurements of their abundance can complement and expand paleoclimatic and paleoenvironmental information from ice cores.

We used the West Antarctic Ice Sheet (WAIS) ice core to reconstruct bacterial abundance throughout the Last Glacial Maximum (LGM) and the Early Holocene (6000 - 27000 Years BF 1950). An overarching goal of our work was to reconstruct and interpret the abundance of bacteria and use this information to infer environmental patterns. We used flow cytometry and epifluorescence microscopy of DNA stained cells to quantify bacterial concentrations from small sample volumes in the WAIS ice core. Time series analysis and Generalized Additive Models (GAM) will be used to describe the cycles, periodicity, trend and time scales on which the bacterial record responds.

Funding: NSF-OPP0839075

31 SELECTED ENVIRONMENTS

Field Test of a Thermal Melt Probe for Access to Subglacial Environments

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Subglacial observation is currently severely limited by practical limitations on deploying instruments beneath hundreds to thousands of meters of ice. This situation can be improved greatly through modernization of thermal melt probes, which melt their way vertically down through ice at speeds of meters per hour. An electrical wire, which spools out from the vehicle as it travels, connects to a modest power-plant and telemetry transceiver on the ice surface. Water above the vehicle refreezes, so the transit is one-way downward – which precludes sample return but is useful for instrumented measurements beneath or within the ice. Modern electronics and materials now enable robust and sophisticated measurements with relatively small, and thus logistically light, melt probes.

We have developed a 7 cm-diameter thermal melt probe system for instrument deployment beneath ice up to 1 km thick (total system mass including the power plant is ca. 500 kg). Here we report on initial field tests in the ablation zone of the Greenland Ice Sheet during July 2013. We reached approximately 65 m depth during approximately 20 hours of operation, limited only by time available after initial testing and modification of our electronic systems.

Acknowledgements: This work is supported by the Major Research Instrumentation program of the US NSF.

Figure 1. Elam and Winebrenner with the thermal melt probe and launch system, 68 N,49 W (1000 m elevation), July 2013

32 SELECTED ENVIRONMENTS

Ectomycorrhizal community composition and function across a forest-heath ecotone in northern Sweden

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Shrubs and trees are expanding into the tundra circumpolarly as the Arctic warms. There is growing evidence that while this vegetation shift increases ecosystem productivity and consequently biomass, it also leads to soil carbon depletion in treeline systems, resulting in a net loss of carbon. Little is known of the mechanisms causing loss of soil carbon, but it is likely that ectomycorrhizal fungi (ECMF) are a key component of the process and respond significantly to increasing abundance of woody plants. To explore how fungal species as well as their enzymatic capabilities change as the ecosystem becomes woodier, we investigated ECMF community composition and function across a forest-heath ecotone near Abisko, Sweden. With the onset of an autumnal moth (*Epirrita autumnata*) defoliation outbreak, our study also compared ECMF communities between foliated and defoliated mountain birches (*Betula pubescens*) to assess if ECMF degradative capacity changes with the resulting loss of carbon source from trees followed by defoliation. Organic soil samples were collected from heath, shrub, and forest sites along ecotone transects. To characterize ECMF communities, we isolated ECM root tips from soil cores, ran enzyme assays to detect degradative capabilities, analyzed species composition through molecular techniques, and examined ECMF morphology. Additionally, soil CN and nutrient content, pH, and moisture were recorded. We observed a 25-30% decrease in hydrolytic enzyme activity and a 50-75% decrease in oxidative enzyme activity from ECMF associated with defoliated compared to foliated birch. Furthermore, enzymatic activity decreased from heath to forest sites, suggesting that woody encroachment may significantly alter ECMF function.

This research was supported through the Northern Ecosystems Research for Undergraduates program (NSF REU site EAR#1063037).

33 SELECTED ENVIRONMENTS

Three Domains of Life: Adenylate Pool Regulation and its Role in Cold Temperature Adaptation

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Permanently cold (≤5°C) temperatures are a defining feature of a major portion of Earth's biosphere. Despite inherent biochemical and physiological constraints imposed on biological systems as temperatures decline, numerous organisms, both prokaryotic and eukaryotic, have adapted to and thrive in these frigid environments. Due to conceivable applications with regard to cell/organ storage and viability, therapeutic hypothermia, and cold-active enzyme biotechnology, cold-adaptive strategies are a subject of intense study. Of particular interest is the ability of psychrophiles (cold-adapted organisms) to maintain energy levels sufficient to sustain biological functions under conditions that drastically reduce enzymatic reaction rates and molecular diffusion. To date, many essential components of cold adaptation have been identified, the most important of which are energy-dependent processes (e.g., ion balance, membrane pumps), suggesting that the ability to maintain sufficient energy supply may indeed be a critical and perhaps limiting factor for cold tolerance. Previous work in our lab has established that disparate psychrophilic organisms maintain relatively high intracellular ATP levels (compared to non-psychrophilic counterparts), and we have proposed that increased [ATP] serves to offset cold-induced reductions in molecular motion and enzyme kinetics. Furthermore, the observation that this phenomenon occurs in diverse genera in two domains (Bacteria, Eukaryota) suggests that changes in adenylate pool regulation may be a requisite adaptation to psychrophily. To test our hypotheses, we performed genetic manipulations of adenylate regulatory enzymes in the mesophilic bacterium, *Escherichia coli,* to reflect a psychrophilic bacterium profile. Single mutation strains showed 30% higher intracellular [ATP] and 5-fold greater cold tolerance, and double mutation strains displayed ~10-fold greater cold tolerance and 70% faster growth (at 15°C), compared to wild type. Current investigations employ a different biological system that will enable us to test both the efficacy and universality of our proposed cold tolerance-ATP link, *Haloferax volcanii*, a genetically tractable mesophile from the third domain of life: Archaea.

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34 SELECTED ENVIRONMENTS

Comprehensive study on Bacterial Community Structures in terrestrial ecosystems of Barton Peninsula of King George Island, Antarctica

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In recent years, applications of molecular methods to study microbial ecology have allowed the extension of our knowledge that Antarctica contains unexpected high diversity of bacteria and their complex of community. We conduct a comprehensive analysis of bacterial communities in soil samples from Barton Peninsular in Antarctica. Total 288 samples were collected from December of 2010 to February of 2012. Among these samples, we here presented the preliminary results with 42 samples. On the basis of the 16S rRNA genes amplicon using next generation sequencing, total 85,078 sequence reads were obtained and 5,924 OTUs were defined using 97% similarity cutoff. The bacterial community structures confirmed habitat specific with significant patterns that the predominant phylum is *Bacteroidetes* (45%) in coastal soil, *Proteobacteria* (24%) in upper layer soil and *Actinobacteria* (26%) in lower layer soil. These findings may be inferred that the bacterial specific adaptation to these terrestrial environments was affected by the underlying soil parameters.

This work is supported by Korea Polar Research Institute (Grant PE13030).

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35 SELECTED ENVIRONMENTS

Bacterial communities of sea ice, melt pools, and surface water in the Central Arctic Ocean during summer 2011

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Currently the Arctic is severely affected by global warming. Summer minimum sea ice extent is shrinking and estimates of sea ice thickness also indicate a rapid decrease. Whether such changing sea ice conditions affect biodiversity and functioning of bacterial communities from sea ice, melt pools, and surface water was studied during a summer expedition in 2011 in comparison to earlier studies in 1997 and 1999. The route of the 2011 cruise lead to the Central Arctic Ocean thus samples of Atlantic as well as Pacific influenced water could be taken. In the Atlantic influenced area higher secondary production rates, determined by means of thymidine incorporation, were obtained in comparison to the Pacific influenced area. Bacterial activities of the sea ice samples in the Atlantic section exceeded in most cases those of melt pools while in the Pacific section melt pools and upper ice samples were more active than the deeper ice layers. However, especially in the Atlantic influenced area, a high percentage of the melt pools were covered by big yellow/orange aggregates. Such amounts of visible organic matter were not observed during the cruises in 1997 and 1999. The differences in bacterial activites were found to be reflected in the phylogenetic bacterial community compositions that were analysed based on 16S rRNA-gene clone libraries and amplicon sequencing as well as CARD-FISH. In the Atlantic influenced area *gammaproteobacteria* were found dominating while in the Pacific influenced area *betaproteobacteria* or *alphaproteobacteria* were abundant. Further, differences between the bacterial communities in 2011 and 1997 were tried to reveal by means of temperature adaptation studies.

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36 ARCTIC AND ANTARCTIC MARINE

Characterization of Growing Microbial Populations in McMurdo Dry Valley Soils through Stable Isotope Probing with ^{18}O-water.

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For decades the soils of the McMurdo Dry Valleys, Antarctica were thought to be essentially aseptic. We now know that this is an ecosystem that is dominated by microorganisms, but early cultivation efforts failed to detect the apparent high diversity of the region's poorly weathered, low organic-matter soils. Initial surveys of microbial diversity using 16S rRNA gene sequencing revealed a surprising bacterial richness, including representatives from at least ten different phyla, and a high proportion of unique and rare sequences. However, given the low rates of microbial activity and decomposition rates, the question of whether this richness represents functioning vs. dormant members of the community was raised. We set out to determine if microbial populations grow in the McMurdo Dry Valley soils by characterizing the growing microbial community through stable isotope probing (SIP) with ^{18}O-water. In $H_2{}^{18}O$-SIP, an environmental sample is incubated with ^{18}O-water. Microorganisms that grow and replicate their DNA incorporate ^{18}O into their nucleic acids resulting in DNA with higher densities than non-labeled DNA. The labeled DNA may be separated from non-labeled DNA along a cesium chloride gradient generated in an ultra-centrifuge. We show that DNA of microbial populations in the McMurdo Dry Valley was indeed labeled with ^{18}O water indicating these microorganisms grew in the McMurdo Dry Valley soils. During our incubations, especially members of the Proteobacteria phylum proliferated.

This research was supported by award 1142096 from the National Science Foundation, division of polar programs.

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37 ARCTIC AND ANTARCTIC MARINE

Characterizations of cold-active bacteriophages on *Pseudoaltermonas* spp. from Arctic deep-sea sediments

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Cold-active bacteriophages are generally defined as bacterial viruses that are capable of infection and production at low temperature (≤4°C). Several studies of cold-active bacteriophages isolated from aquatic environments have been reported. However, characteristics of cold-active bacteriophage-host systems in deep-sea sediments are still poorly understood, despite high viral abundance maintain in persistently low temperature. To establish cold-active bacteriophage-host systems, we made an attempt to isolate host bacteria and their bacteriophages from 3 deep-sea sediment cores taken from the Mendeleev Ridge in the western Arctic Ocean. Nearly half of 55 bacterial strains (44%) obtained by a conventional plate method belonged to the genus *Pseudoalteromonas*. Using plaque assays with 55 bacterial strains, seven bacteriophages specific to 4 *Pseudoalteromonas* spp. were isolated. The *Pseudoalteromonas* bacteriophages turned out to exhibit successive propagations at low temperature of 1°C, indicating that they are cold-active ones. Morphology and physiological characteristics of the 7 sediment bacteriophages will be provided in a poster presentation.

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38 ARCTIC AND ANTARCTIC MARINE

Prevalence of horizontal gene transfer among cold-adapted microbes and implications for crude oil bioremediation in the polar environment

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Low temperature environments often contain water ice, a medium that presents certain opportunities and challenges to microbial life. Among the opportunities, it has been suggested that ice can enhance microbial evolution through horizontal gene transfer (HGT), by concentrating bacterial communities and elevating the contact rates between bacteria, and between bacteria and bacteriophages. Previous studies have identified several likely HGT events within cold adapted bacteria, including a gene encoding for an ice-binding protein and genes for compatible solute acquisition and catabolism. As part of an evaluation of the distribution of potential crude oil degradation genes within 32 cold adapted (psychrotrophic and psychrophilic) prokaryotic genomes, we quantified the number of possible horizontally transferred open reading frames (ORFs) as identified by GC anomaly, following a de-novo annotation of those genomes. We find the number of ORFs within these genomes with anomalous GC content to be significantly higher than in a population of 20 randomly selected prokaryotic genomes (Students T-test: $p = 0.0174$, $t = 2.485$). To further explore these HGT candidates we employed a network visualization of blastn results against the NCBI nt database. This analysis revealed numerous homologous ORFs shared between surprisingly divergent taxonomies, including 93 open reading frames shared between the domains Eukaryota and Bacteria (when searched to a depth of 1,000 hits with $E < 1e^{-20}$). Here we present further details of this analysis and of the ecological implications of enhanced microbial evolution in ice, with an emphasis on crude oil bioremediation processes. This work is supported by an EPA STAR Fellowship to JSB and the Walters Endowed Professorship to JWD.

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39 ARCTIC AND ANTARCTIC MARINE

Seasonality in coastal Beaufort Sea microbial community

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Coastal Arctic ecosystems receive large quantities of terrestrial organic matter (OM) through river discharge and shoreline erosion, the magnitude of which changes both seasonally and as a result of climate warming. The dynamic interplay between contributions of this terrestrial OM and phytoplankton-derived OM to the marine carbon pool likely impacts the composition of and metabolisms employed by the microbial community. We addressed seasonality of microbial communities and their gene content in coastal lagoons and nearshore, open ocean sites in the eastern Beaufort Sea over two years, sampling in April (ice-covered), June (ice break-up), and August (open water). Microbial communities exhibited distinct seasonal patterns in community structure. Seasonal differences overwhelm inter-lagoon differences in seawater microbial communities, while marine sediment communities show much greater geographic variation with little seasonal variability. In the water column, community differences are influenced by runoff (e.g. [DOC], SUVA$_{254}$) and the degree of exchange between lagoons and the open ocean, which varies seasonally with ice thickness and barrier island migration. June bacterial communities bear the strongest resemblance to riverine communities (higher relative abundances of *Betaproteobacteria* and *Acidobacteria)*, with the presence of river-derived microbes decreasing throughout the summer and winter. Wintertime communities were characterized by higher relative abundances of SAR406, *Pelagibacteraceae*, and *Oceanspirillales*. Given the clear seasonal differences in bacterial communities, in available carbon sources and in net community metabolisms, seasonality in gene content and metabolic pathways used to process the available carbon sources are expected and will be examined using metagenomic analysis.

This research is supported by NSF award 1023465 to Byron Crump.

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40 ARCTIC AND ANTARCTIC MARINE

Microbial diversity in snow on North Pole ice floes

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Sea ice of the Arctic is a vanishing environment. Despite the extent and vulnerability of this habitat, little is known about the biodiversity in snow on Arctic ice floes. With use of 454 pyrosequencing a total of 291,331 16S rRNA gene sequences were obtained from snow on ice floes at three sites near the North Pole. qPCR results showed gene abundances of 43-250 copies per mL of melted snow. Pyrosequencing data was analysed using Qiime resulting in 1887 OTUs. Two samples were dominated by *Cyanobacteria* including a large fraction of chloroplasts. The third sample consisted of 95 % *Proteobacteria* and a number of marine *Genera* not found in the other two samples. Chloroplast sequences that could be mapped to known organisms belonged to either marine or halophilic algae or to higher plants such as *Fragaria sp.* (strawberry), *Castanea mollissima* (chinese chestnut), liverworts, cycads and other

41 ARCTIC AND ANTARCTIC MARINE

A vertical profile analysis of the structure of bacterial communities from Arctic multi-year ice

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The Arctic sea ice is a vast habitat with a microbial community that is active year-round and plays a key role in the biogeochemical cycles and energy flux of the Arctic Ocean. Until recently, the Arctic was dominated by multi-year ice, however, MYI levels have dwindled to just 45% of the total ice cover due to climate change. Furthermore several studies predict a MYI free arctic by the end of the century. Therefore studying the microbial communities that inhabit MYI is crucial to our understanding of the challenges that the Arctic Ocean ecosystem faces. MYI flows typically have gradient of conditions from top to bottom, including temperature, salinity, organics and other dissolved materials. Therefore Microbes that inhabit MYI flows have to deal with a diverse array of environmental conditions, dependent on their vertical position in the ice. Here, we contend that these differences in abiotic conditions will select for unique microbial communities along the depth of MYI sheets. To test this hypothesis we collected ice samples from MYI flows off the shore of Northern Ellesmere Island, NU, Canada, during May 2011. The samples were then sub-sectioned in 30cm intervals, melted and filtered for subsequent DNA extraction. Assessment of microbial community structure was performed by identifying variable sequences (V1-V3 region) of the 16s rRNA gene using 454 pyrosequencing platform. Our results show a general trend of top to bottom increase in the richness and diversity of the communities. Furthermore, hierarchal clustering based on dissimilarity matrix generated by both Unifrac and θYC dissimilarity index, grouped the microbial communities to three distinct groups($p<0.001$ Unifrac, $p<0.005$ θYC): top, which corresponds to the top 30cm of the ice; middle, which corresponds to sections 60cm-150cm; and bottom, which corresponds to the bottom 90cm of the ice. Our results also indicate a shift from a community dominated by Flavo and Actino bacteria at the top portion of the ice, to a community mainly dominated by α-Proteobacteria in the middle and bottom sections.

This work was supported by NSERC discovery grant (BDL), Alberta Innovates Technology Future grant (CH) and the Canadian Circumpolar Institute research grants (IH)

42 ARCTIC AND ANTARCTIC MARINE

Bacterial survival in sea ice brines: salinity shifts and the cellular fate of compatible solutes

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In exploring the temperature and salinity tolerances of bacteria in sea ice, we hypothesized a seasonal synergy between bacteria and algae, based on bacterial uptake and metabolism of compatible solutes. In this model, algae release choline into the brine pockets of new sea ice, which can then be converted to compatible solutes by bacteria as a means to resist the osmotic stress of inhabiting brines that will become colder and more saline (> 210 ppt) in winter. In spring, as the ice warms and brine salinities (and osmotic stress) decrease, bacteria will metabolize these compatible solutes as nitrogen-rich carbon sources, potentially recycling ammonia to the algae. For initial testing of this hypothesis, samples of sea ice, brines and seawater were collected from Nuuk, Greenland, in spring 2013. Sample treatments included incubation at –1°C and at salinities higher than, similar to or lower than original conditions after amendment with ^{14}C-choline. The proportions of respired choline (implying metabolism) versus retained choline (implying conversion to compatible solute for osmotic protection) were compared between treatments. Samples exposed to lower salinities respired a greater fraction of the total ^{14}C-choline transported into cells (51–103% converted to $^{14}CO_2$) compared to samples exposed to higher salinities (3–28% respired), validating key aspects of the proposed model. Ongoing work involves similar experiments with model organisms and plans to study more natural samples obtained from coastal Greenland at different times in the lifecycle of sea ice.

This work was supported by NSF award ARC-1203267.

43 ARCTIC AND ANTARCTIC MARINE

Survival of sea-ice bacteria under fluctuating T/S regimes

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Sea-ice bacteria experience fluctuations in temperature and salinity that depend on degree of exposure to atmospheric conditions. Records of Winter and Spring sea ice temperature and inferred brine salinity (Barrow, Alaska), for example, showed significantly more energetic fluctuations at the snow-atmosphere interface than 10 cm into the ice. To evaluate bacterial survival under these regimes, we compared cell losses for two Arctic isolates, psychrophile *Colwellia psychrerythraea* strain 34H (*Cp*34H) and new psychrotolerant *Psychrobacter sp.* strain 7E (*P*7E), when subjected to constant or fluctuating freezing conditions. Hypothesizing salinity shifts as more challenging than temperature shifts, we examined melting protocols and effects of compatible solutes. Samples melted directly (osmotic shock) lost significantly more cells than those melted into brine (minimal shock). Freezing *Cp*34H under fluctuating conditions resulted in cell losses of ~ 50 %, higher than observed at a constant –20 °C ($p < 0.01$, ANOVA). Compatible solutes, whether glycine betaine, proline or the precursor choline, had a protective effect, reducing (though not preventing) *Cp*34H cell loss under fluctuating conditions ($p < 0.01$, ANOVA). In contrast, freezing *P*7E under either regime led to increased cell numbers in six of nine experiments ($p < 0.01$, ANOVA), explained by cell miniaturization and fragmentation. Stronger fluctuating regimes at the ice surface could favor bacterial communities distinct from those in the ice column, while overall community composition may depend on the presence of compatible solutes in the brine.

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44 ARCTIC AND ANTARCTIC MARINE

Biogeochemical characteristics of sub-Ross Ice Shelf waters near McMurdo Sound, Antarctica

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The McMurdo Ice Shelf lies off of the Victoria Coast of Antarctica, and comprises the northwest corner of the Ross Ice Shelf. The underlying water is mainly sourced from McMurdo Sound via a channel to the Ross Sea. In December 2012, we penetrated the McMurdo Ice Shelf (56 m) with a hot water drill. Water samples were collected with Niskin bottles deployed to 30 m and 850 m below the ice water interface and an *in situ* water filtration unit deployed to 850 m was used to collect samples for DNA extraction. Physical characteristics of the water column (depth=917 mbsl) were profiled with a CTD. Samples from both depths contained $\sim 10^5$ cells mL^{-1} and 2 – 3 □g chl-*a* L^{-1}. DNA was successfully extracted from the 850 m sample for microbial community characterization. DOC concentrations were greater at 30 m than at 850 m, but heterotrophic activity was higher at 850 m than at 30 m, while dark incorporation of ^{14}C-bicarbonate was similar at both depths. Fluorescence analysis of dissolved organic matter revealed DOM of mainly microbial origin, consistent with expected limited allochthonous inputs to the ice-shelf cavity. These data provide new insights into an under-sampled oceanic environment.

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45 ARCTIC AND ANTARCTIC MARINE

Bacterial community structure of the surface water along the latitudinal gradient in the Southern Ocean

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Prokaryotes represent an important component of the marine plankton, comprising up to 70% of the total biomass in surface waters. They play significant roles in the biogeochemical cycles and their structures are known to be influenced by environmental conditions. In this study, we investigated the structures of bacterial community of surface sea water along the latitudinal gradient, from the Dunedin, New Zealand (48°S, 170°E) to the Australian-Antarctic Ridge (AAR, 63°S, 156°E). Surface water samples were collected from 25 stations during the ARAON cruise in March 2011. Pyrosequencing of 16S rRNA genes was applied to reveal spatial variation of operational taxonomic units (OTUs) and relationships between bacterial community and environmental conditions were analyzed. The temperature of sea water dropped from 12.9 to 2.8˚C, salinity decreased from 34.2 to 33.8 psu, and concentrations of inorganic nutrients increased toward higher latitudes. Environmental conditions such as temperature and salinity changed dramatically at 55°S, the approximate latitude to the Polar Fronts (PF) of Antarctic Circumpolar Current (ACC). Seventeen phyla were recovered from 25 samples and the major phyla included *Bacteroidetes* (25.4-50.5%), *Alphaproteobacteria* (28.3-44.3%), *Gammaproteobacteria* (14.2-36.7%), *Cyanobacteria* (0.3-8.4%), *Verrucomicrobia* (<6.8%), *Betaproteobacteria* (<3.7%), SAR406 (<3.2%), *Actinobacteria* (<1.5%), *Epsilonbacteria* (<0.8%), and *Deltaproteobacteria* (<0.7%). *Bacteroidetes* increased from 29% to 50% toward higher latitude while *Cyanobacteria* (from 8.4% to 0.3%), *Verrucomicrobia* (from 6.8% to 0.0%), and *Actinobacteria* (from 1.3% to 0.0%) decreased. OTUs of genus *Fluviicola* and *Prochlorococcus,* family *Halomonadaceae, Phyllobacteriaceae*, and *Verrucomicrobiaceae,* and order *Rickettsiales* showed significant decrease in the composition toward higher latitude. Conversely, OTUs of family *Rhodobacteraceae, Flavobacteriaceae, Halomonadaceae, Alteromonadaceae*, and *Oceanospirillaceae* significantly increased. Overall, bacterial community analysis with the physicochemical data shows the clear differences of bacterial structure across the PF and supports the PF as a strong biogeographic boundary which shapes the bacterial communities in the Southern Ocean. (Grant: PP11040 and PP13040)

46 ARCTIC AND ANTARCTIC MARINE

Microbial mat morphology correlates with microbial community composition and lake chemistry in Lake Fryxell, Antarctica

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Benthic, mat-forming microorganisms are important contributors to nutrient cycling and primary productivity in many polar lacustrine environments, including Lake Fryxell (Taylor Valley, South Victoria Land, Antarctica), a stratified, perennially ice-covered lake with high biologic productivity. Microbial community membership often varies along environmental gradients, and, in Lake Fryxell, steep nutrient, oxygen concentration, and photosynthetically active radiation (PAR) gradients occur with depth.

In 2012, we found that macroscopic mat morphology co-varied with several aspects of water chemistry. Topographical features including ridges, peaks, webs, pinnacles, and pits and pigmentation, including brown, green, and purple coloration, varied with depth in both spatially discrete mats and layers of individual mat samples. Brown-peaked and brown-ridged mats were prevalent in shallower waters, green-ridged and green-flat mats at intermediate depths, and gold-flat and grey-flocculent mats in deeper waters. Dissection of purple-ridged mats retrieved near, but above, the oxycline revealed that within mats, lamination was a consistent feature; superficial and intermediate laminae were purple, and deeper laminae were beige.

The metagenomes of five dissected layers of purple-ridged mats appear to reflect variation in mat pigmentation and macroscopic morphology. Results to date suggest that the distribution of microbial taxa and their functional capacity in the benthic microbial mats in Lake Fryxell spatially vary by both mat layer and larger-scale physical structure throughout the lake, and are ultimately controlled by physical and chemical gradients in the water column at both scales.

The samples and field data were collected under the auspices of McMurdo Dry Valleys Long Term Ecological Research program grant OPP ANT-1115245 and their analysis is supported by NASA Astrobiology grant NN13AI60G.

47 ARCTIC AND ANTARCTIC MARINE

Microbial mat morphology as a record of environmental change in perennially ice-covered Lake Joyce, Antarctica

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Microbial mats with diverse macroscopic growth forms are abundant in perennially ice-covered Lake Joyce in the McMurdo Dry Valleys of Antarctica. Lake levels rose by over 7 m between 1973 and 2010, and benthic cyanobacterial communities presently have depth-associated distributions. In 2010 mats at <12m depth contained abundant *Phormidium autumnale, Leptolyngbya antarctica, L. fragilis,* and *Pseudanabaena frigida* morphotypes, whereas deeper mats lacked *P. autumnale*. Microscopy data indicate that different relative abundances of cyanobacterial morphotypes are associated with specific mat morphologies, and this is supported by preliminary 16S rRNA PCR analyses. Mats dominated by *P. autumnale* morphotypes had little topographic relief, whereas mats lacking *P. autumnale* commonly contained small peaks and branch-like bundles of filaments growing away from the mat surface. At 20-22 m depth, mats lack measureable photosynthetic activity and form dm-scale columnar stromatolites interpreted as having grown when lake levels were lower and thus illumination was higher.

Calcite that precipitated within these stromatolites preserves variations in growth form with time from smooth prolate columns to branched and irregular columns. Crystals also contain cylindrical molds, which have diameters similar to the trichome widths of cyanobacteria living in Lake Joyce. Preserved community composition and stromatolite morphology co-vary. *P. autumnale*-sized molds are abundant in calcite forming the oldest smooth stromatolite layers, but are absent from younger layers with branched and irregular growth. This suggests that *P. autumnale* was present early in stromatolite growth, but disappeared from the community through time. Observations of both active mats and columnar stromatolites thus suggest that changes in microbial community composition influence growth forms and preserve a record of microbe-environment interactions consistent with longer-term environmental change in Lake Joyce.

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48 ALPINE

A lichen species-complex to study evolution of organisms in symbiosis.

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We compiled a worldwide study on the *Tephromela atra,* a widespread, crust-forming lichen species complex, which exhibits a high degree of morphological heterogeneity. The long lasting debate about the recognition of intraspecific taxa did not treat the question whether the adaptation to habitats (spanning from the Mediterranean to the arctic and alpine regions) or substrates (calcareous and siliceous rocks, bark) correlates with the preference to certain algal partners. The multilocus phylogenetic hypothesis reconstructed for the mycobionts recovered 13 monophyletic clades, the majority of them well supported by morphological, chemical or ecological traits. We found that lichen mycobionts can associate with photobionts belonging to nine strains of *Trebouxia*. In the Alps and other cold habitats *Trebouxia simplex* and three new photobiont strains were recovered, whereas lichen thalli from the Mediterranean and temperate region consort with different algal strains retaining in the thalli multiple photobionts. *T. atra* represents an interesting model to study in a geographic scale adaptation and evolution of organisms in symbiosis. (The research is financed by the Austrian Science Foundation, FWF T481-B20).

49 ARCTIC AND ANTARCTIC MARINE

Transcriptome comparison of two *Aureobasidium pullulans* varieties: *subglaciale* versus *pullulans*

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Aureobasidium pullulans (Dothideales, Ascomycota) is a ubiquitous saprophytic black yeast-like fungus. It thrives in many different environmental conditions, even in extreme environments such as hypersaline water and Arctic glaciers. It tolerates a variety of environmental stresses and can be considered polyextremotolerant. *A. pullulans* is of great biotechnological interest because of its production of extracellular polysaccharide pullulan, antimycotic aureobasidin A and various extracellular enzymes. It is used as a biocontrol agent in agriculture and is also a well known pathogen, which can cause a variety of localized and even rare systemic infections.

We performed pyrosequencing and analysis of transcriptomes of the *A. pullulans* var. *subglaciale* isolated from subglacial ice and *A. pullulans* var. *pullulans* from hypersaline water. Since the environments of these two varieties contain high salt concentrations, but differ substantially in some other parameters, we compared the salinity induced differencial transcription of genes of both varieties. The differences between varieties will be discussed in light of their salt stress tolerance and preferences for different habitats and conditions.

50 ARCTIC AND ANTARCTIC MARINE

Recent changes in physical, chemical, and biological conditions on the bare ice surface of Tyndall Glacier of the Patagonia

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Melting and shrinkage of glaciers have been recently reported in the many part of the world. The shrinkage is not caused only by global warming but also by surface reflectivity reduction due to surface dust on glaciers (cryoconite). In this study, we analyzed surface reflectivity, cryoconite amounts and snow and ice algae collected on Tyndall Glacier in 2012 and these results were compared with those from studies in 1999. Moreover, a satellite image was analyzed to estimate of recent variations in surface albedo in entire surface of the bare ice area.

The surface reflectivity and amounts of cryoconite were measured at the 3 site on the bare ice surface on Tyndall glacier in 2012, and then were compared with the result of same measurements in 1999. However, there was statistically no significant difference between the two years, indicating that surface reflectivity and the amounts of cryoconite did not significantly change in the last decade. The analysis of community structure of snow algae on glacier surface showed that there were various snow algae on the ice surface in 2012, however there were statistically no significant differences in their biomass and community structure between in 2012 and 1999. These results suggest that there was no significant physical and biological change on the ice surface of the glacier in the last decade. The analysis of Landsat-7/ETM+ satellite image of the Tyndall Glacier reveals that there was no significant change in surface albedo between 2001 and 2010. Thus, the entire bare ice surface of the Tyndall glacier did not significantly changed in the last decade.

Recent years, the bare ice surface of the Greenland ice sheet has been darkened probably due to increase of cryoconite on the surface, however, our studies showed that of Patagonia Icefield has not changed significantly. The shrinking on Patagonia Icefield is unlikely due to surface darkening, but to calving effect of glacier margin by marine and lake water.

51 ARCTIC AND ANTARCTIC MARINE

Census of bacteria associated with glacier invertebrates

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In glaciers, cold-adapted invertebrates and microbes form specific ecosystems. However, our knowledge on their ecology, physiology, and evolution is still limited. Particularly, there has been no report on microbial communities associated with invertebrates in glaciers. In the present study, we performed a census of bacteria associated with the ice worm *Mesenchytraeus solifugus*, the glacier stonefly *Andiperla willinki*, and the glacier midge *Diamesa* sp. DNA was extracted from the entire body or gut of each specimen, and 16S rRNA genes were amplified by PCR, cloned, and sequenced. We found that the majority of the obtained sequences were affiliated with known psychrophilic bacterial genera. This implies that the bacterial gut microbiota might have been replaced by bacteria indigenous in the glacier during the course of evolution. On the other hand, several 16S phylotypes were phylogenetically related to known symbiotic (i.e. gut-wall-associated or endosymbiotic) bacteria, which have never been detected from glaciers. These results suggest that some symbiotic bacterial lineages have kept association with the host invertebrates despite the drastic change of the host habitat. Our results provide the insight into the adaptive evolution of animals and their associated bacteria.

52 ALPINE

Polar and Alpine Microbial Collection (PAMC): a culture collection dedicated to polar and alpine microorganisms

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Microorganisms in polar areas may have important ecological roles in biogeochemical cycles and the food chain. Culture collections for polar and alpine microorganisms can provide research resources for ecological and physiological studies. The Polar and Alpine Microbial Collection (PAMC) is a specialized culture collection for maintenance and distribution of polar and alpine microorganisms. A database system was developed to share important data fields with DarwinCore2 and OBIS database schemas. Approximately 1,500 out of 5,500 strains maintained in PAMC have been identified and belonged primarily to the phyla *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria*. Many of the microbial strains can grow at low temperature and produce proteases, lipases, and/or exopolysaccharides. PAMC provides search tools based on keywords such as taxonomy, geographical origin, habitat and physiological characteristics. Biological materials and information provided by PAMC will be important resources for ecological and physiological studies on polar and alpine microorganisms. (Grant: PE13240 and E413060)

53 ALPINE

Combination of culture- dependent and culture-independent approaches for the isolation of microbial populations from glacier forefields

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Microbes in unvegetated habitats are strongly related to their geological background. It is still unclear, however, if and how specific physico-chemical properties of the bedrock determine the establishment of endemic microbial populations. The majority of microorganisms in such environments have not been cultivated yet, and this limits the possibilities of direct investigations of microbial adaptation. In oligotrophic environments, the choice of appropriate growth conditions may be crucial for the isolation of specific populations and to avoid the overgrowth of opportunistic microorganisms. We tested a strategy based on different enrichment media to isolate specific microbial groups from an oligotrophic carbonatic glacier forefield (Wildstrubel, Switzerland). Soil samples were taken along two transects parallel to the glacier front and analysed in terms of their soluble nutrient and DOC contents. In parallel, we cultivated the local microbial communities from each transect into different enrichment media based on local soil extract. The efficiency of the enrichments in selecting different populations was compared with terminal restriction fragment length polymorphism (T-RFLP) profiles of the bacterial 16S rRNA gene. FISH, DAPI staining and flow cytometry were performed to visualize the biomass and diversity in the enrichments. In addition, physiological profiles of the enrichments were estimated through incubations (+4°C) in Biolog Ecoplates. T-RFLP evidenced that less than 50% of the estimated diversity could be retrieved through culturing, and that different microbial populations could be enriched with the different growth media. The culturable fraction of the microbial community included opportunistic microorganisms related to several species of beta-Proteobacteria (e.g. *Polaromonas* sp.), and to typical components of oligotrophic cold environments such as Cyanobacteria, cyst-forming (e.g. *Ramlibacter* sp.) and pigmented (e.g. *Flavobacterium* sp., *Deinococcus* sp.) bacteria. Differences could be observed also in the physiological profiles, which generally showed high utilization of easily-degradable carboxylic acids and carbohydrates, as well as of phenolic compounds and polymers. From the flow cytometry output we could select different microbial clusters from which we sorted cells in 96-well plates containing growth media. The isolates will represent a useful tool to test adaptation to different substrate chemistries and environmental conditions. Our study showed that calcareous glacier forefields might be dominated by heterotrophic opportunistic microorganisms able to readily grow on a wide variety of substrates; cell sorting from local oligotrophic enrichment cultures may represent a strategy to obtain pure cultures of less abundant taxa from extreme environmental samples.

54 ALPINE

The physical and chemical factor of snow coverage related to breeding of snow algae during the thaw season in Japan.

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It is known that the phototrophic microorganism called snow algae breed on the surface of the snow coverage in thawing season. When snow algae breed, the reflectance of a snow surface decreases and melting snow coverage is promoted. Therefore, it is important to reveal factors of their breeding in order to predict melting of snow coverage. However, it is not revealed what the most direct related factor of breeding is. Therefore, in this study, it aimed at revealing factors of snow algae breeding. In the melting snow coverage of Tohkamachi Experimental Station, Forestry and Forest Products Research Institute in Niigata-ken in Japan, the seasonal variation of snow algae was quantitatively revealed using the chlorophyll-a in snow coverage, and the chlorophyll-a was compared with the weather, snow coverage, and snow physics model data.

When the chlorophyll-a concentration was compared with result of the snow coverage conditions is calculated by the snow physics model, it was suggested that all layers of the snow coverage change granular snow and snow coverage is melting four days or more through day and night is the conditions on which snow algae starts breeding. It is considered that to change granular snow is conditions for snow algae in the ground under snow coverage swim to the snow surface. It is considered that melting of snow coverage period four days or more through day and night is the conditions for snow algae which arrived at the snow surface breed stably.

When increment of the chlorophyll-a concentration was compared with the melting period through day and night, it was considered that the amount of snow algae breeding increased rapidly only by the case melting of snow coverage period over four days through day and night. In case of melting of snow coverage period four days or more through day and night, Chlorophyll-a concentration increased 15 [μg / m^2] or more. However, in case of melting of snow coverage period three days or less through day and night, the value of Chlorophyll-a concentration is not more than 15 [μg / m^2]. These results indicate that steady breeding of snow algae in snow surface may require four days or more periods, as mentioned above.

55 ALPINE

Mid-latitude "cold traps" as possible refugia for cold-adapted microbes

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Mid-latitude "cold traps" are found at the base of steep north-facing slopes with extensive talus fields that collect cold winter air from a large area and have limited sun exposure. Therefore, cold trap soils remain cold year round (below 10ºC in this case) and may serve as refugia for cold-adapted microbes. Mid-latitude cold refugia can inform ecological models and have implications for cold-adapted species in other areas (alpine, Arctic, *etc.*). Cold refugia may be particularly relevant to northern polar latitudes where temperatures are rapidly increasing causing habitat fragmentation.

We sampled soils in and around the Colerain ice caves of the Rothrock State Forest, PA over 2.5 years to document the diversity of bacteria present via t-RFLP analysis and the potential for cold-adaptation within populations via plate counts, freeze/thaw experiments, and molecular analyses. Initial data from plate counts indicate that cold trap soils are dominated by bacteria capable of growth at 0 and 10°C; while nearby soils are dominated by bacteria capable of growth at 10 and 22°C. Ongoing analyses are determining the diversity of microorganisms present and their degree of cold adaptation in these cold trap and nearby soils.

56 ALPINE

Activity of Autotrophic Organisms (Lampenflora) in an Englacial System

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Autotrophic organisms are normally absent in anthropogenic undisturbed dark habitats like caves or englacial systems. If artificial light sources get installed, e.g. to open those habitats to tourism, algal communities known as Lampenflora, develop. Here, we investigate the microbial community within the so called "Natur Eis Palast" crevasse in the Hintertuxer glacier (Tirol, Austria). Production rates of englacial autotrophic and heterotrophic microbes were assessed using radiotracers ($NaH^{14}CO_3$ and ^{3}H-Leucin, respectively). The effects of the light spectrum on the growth of the lampenflora were also estimated, as well as the penetration depth of light in the ice allowing lampenflora to grow. An experiment using different lamps with various wavelengths was conducted over 10 weeks to investigate how long microbial communities would need to establish and which organisms are the first to inoculate the ice. Original and sterile glacier ice was exposed under in situ conditions (the same lamps and conditions). Our results showed high activity of photoautotrophic organisms and algal communities under different spectral conditions. Light spectra influenced greatly the structure of the lampenflora communities present. This study provides additional information about the establishment of in situ activities and microbial processes in englacial systems also under the aspect of touristic usage.

57 ALPINE

Influence of climate change and anthropogenic activity on bacteria in a Tibetan ice core

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The Tibetan Plateau, which contains the largest area of glacial ice outside of the polar regions, is experiencing rapid temperature increase and direct anthropogenic pressure. We used ice cores to obtain continuous bacterial abundance records for the past 46 years and DNA-based community composition records for the past 16 years from the Noijin Kangsang Glacier located on the southern Tibetan Plateau. A quasi-Poisson log-link generalized additive model was used to examine the relationships between selected climatic and anthropogenic factors, and bacterial abundance in ice core. Bacterial abundance increased linearly from 1960-1989 (446 cells mL yr^{-1}), then increased more rapidly from 1989 to 2002 (2951 cells mL yr^{-1}) before leveling off from 2002-2006. Black soot in the ice core showed a significant linear relationship with bacterial abundance and was the most important predictor in the model. Calcium, a proxy for dust, had a significant non-linear relationship with bacterial abundance. Temperature showed a nearly linear increase over time, but it did not directly explain the observed variability in bacterial abundance once time, soot and calcium was accounted for. Results from our statistical model infer that the variation we observed in bacteria abundance is not influenced by temperature directly. We tracked the potential sources of the glacial bacterial phylotypes in the ice core with pyrosequencing of the 16S rRNA gene. Bacterial diversity showed a shift from deposition dominated by local lake sediment to deposition dominated by soil-associated bacteria between 1963 and 1973. This shift may result from the dramatic increase in the frequency of glacial outburst floods and associated runoff during this period. Our results from the Noijin Kangsang Glacier show that (i) bacterial abundance has increased over time since 1960, (ii) this increase is related directly to the deposition of black soot and calcium, and (iii) changes in bacterial community composition in the ice core are related to climate change on the Tibetan Plateau.

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58 ALPINE

Potential for unusual viral life strategies in cold environments

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Microbial communities on the surface of glaciers play an important role in the cycling of carbon and other elements within the cryosphere. In cryoconite holes viruses are numerically dominant and likely to be the main cause of bacterial mortality. In this study we addressed the control that viruses play in these highly truncated ecosystems. Assuming only lytic infection strategies, the viral induced bacterial mortality was calculated to be more than capable of accounting for the mortality of all bacterial production, suggesting that viruses are responsible for the release and recycling of carbon and nutrients in supraglacial ecosystems. However, infection strategies in cryoconites exhibit unusual characteristics. Investigations using Transmission Electron Microscopy (TEM) found a high frequency of bacteria displaying visible virus infection (mean 23%) and a low burst size (mean 2.4 per cell) which was found to be amongst the lowest recorded in the literature. As visible infection occurs for only a fraction of the latent period this suggests the majority of bacteria in cryoconites are infected by viruses. There is growing evidence that this strategy appears to be a characteristic of Polar regions, however its function remains unclear. The measured virus production, assuming such a low burst size, implies a rate of bacterial mortality an order of magnitude greater than was observed in this study. Therefore we provide evidence at the community level that alternative infection strategies may be at work in glacial ecosystems, specifically we hypothesise supraglacial bacteria may be exploiting chronic, in addition to lytic infection strategies.

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59 ALPINE

The Influences of the Snow Alga *Chlamydomonas nivalis* on Fungal Community Structure

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Late season snows are inhabited by diverse sets of microorganisms, and we sought to understand how photosynthetic algae influence fungal diversity under extreme conditions with limited resources. Snow inhabiting fungal communities associated with *Chlamydomonas nivalis* (Division Chlorophyta), a psychrophilic snow-borne alga, and with matched adjacent non algal-colonized snow were Illumina (MiSeq) sequenced from North America (Washington and Colorado) in 2011 and 2012. We found that OTU richness is higher in algal-colonized snow patches than matched non-colonized sites but diversity and evenness were unchanged. Ordination analyses suggest that fungal communities are distinct between algae-associated snow and uncolonized snow and several OTUs are enriched in algal snow samples (representing putatively parasitic or saprobic OTUs). Additionally, we see a diverse and heterogeneous fungal community that is remarkably site-specific (little interannual variation) dominated by few OTUs. Communities were composed largely of Basidiomycetous yeasts and Chytridiomyceteous parasites and pathogens. The algal community specific drivers were outweighed by the spatial variability on large scale as indicated by the marked differences in fungal communities between the sites in Colorado and Washington.

60 ALPINE

Effects of alpine nitrogen deposition on mycorrhizae-sedge relationships

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Plant and mycorrhizae responses to nitrogen fertilization have been described separately, but a new challenge is to integrate the responses of the below and aboveground organisms. Mycorrhizal responses to nitrogen fertilization vary, but biomass and species richness commonly decrease, coupled with species turnover. Understanding the mechanisms by which microbes influence plant sensitivity to nitrogen deposition should help explain the differential responses of plant species.

Alpine ecosystems near industrial and agricultural sources receive high inputs of reactive nitrogen because of high precipitation due to orographic lifting. Niwot Ridge (Colorado, USA) receives ambient nitrogen deposition high enough to trigger abundance changes of nitrogen-sensitive plant species (~4 kg N/ha/yr). *Kobresia myosuroides,* a dominant plant in dry meadows, decreases with N fertilization while *Carex rupestris* increases at current rates of nitrogen deposition. Shifting abundances of these two species will likely feedback to community-level changes in composition and function if they occupy different niches.

I hypothesized that identity and strength of mycorrhizae relationships can explain *K. myosuroides* and *C. rupestris*' opposing responses to increased nitrogen.

In order to test whether mycorrhizal responses to nitrogen deposition are linked to host plant response, I compared root colonization rates and mycorrhizal identity on sedges in plots that received 0, 20, 40, and 60 kg N/ha/yr each growing season since 1997. Since *K. myosuroides* harbors ectomycorrhizae (involved in nitrogen uptake) whereas *C. rupestris* is non-mycorrhizal, I predicted that increased nitrogen deposition would reduce micorrhizal colonization and promote shifts in taxa because the disabled mutualism could reduce *K. myosuroides*' competitive ability.

The main focus of this research is to learn how mycorrhizae mediate plant species responses in order to predict species shifts and community level change.

We acknowledge the EBIO department at the University of Colorado and the Indian Peaks Wilderness Alliance for small grants supporting this work.

61 ALPINE

Identification of biomass utilizing bacteria in a carbon depleted glacier forefield soil by the use of ^{13}C-DNA-stable isotope probing

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As Alpine glaciers are retreating rapidly, bare soils with low C and N contents are becoming exposed. Availability of C is a key factor regulating microbial diversity in these soils. The aim of this study was to investigate how bacterial activity and community structure are influenced by C availability. Bare soils were supplied with ^{13}C-labelled fungal (*Pencillium* sp.) and green algal (*Chlorella* sp.) biomass. These organisms have been isolated near the glacier terminus. CO_2 evolution from soil and its $\delta^{13}C$ signature were monitored up to 60 days. DNA-SIP followed by T-RFLP profiling was employed to identify bacteria able to assimilate C from these amendments.

The C resource clearly influenced the composition of the soil bacterial communities and the ^{13}C-labelled biomass were differently incorporated. *Flavobacterium* sp. within the *Bacteroidetes* predominantly incorporated fungal-derived C whereas the algal-derived C was mainly incorporated by *Acidobacteria* and *Proteobacteria*. Higher respiration and higher bacterial activity indicated a more efficient utilization of algal cells than fungal cells.

This study emphasizes the important role of both fungal as well as algal cell fragments in increasing the available C pool in recently deglaciated bare soils. We found that only 20% of C was respired as CO_2 after 60 days, and the rest, we presume, remained in the soil, increasing the soil organic matter content.

62 ARCTIC AND ANTARTIC PERMAFROST

Viable Methanogens in the McMurdo Dry Valleys Permafrost

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Despite of wide distribution of the methanogenic archaea in cold environments, there was no evidence for presence of viable methanogens in Antarctic permafrost until now. The permafrost sediments with (Ant1) and without (Ant2) biogenic methane were collected in McMurdo Dry Valleys, Antarctica, and were evaluated for methanogenic activity. Methane production in anoxic microcosms was observed only in Ant1 samples after one-year long incubation period at room temperature and purging of CO_2/H_2 as carbon and energy source. Total genomic DNA was extracted from both Ant1 and Ant2 enrichments and metagenome sequencing was conducted using the Illumina HiSeq 2000 platform generating 2x100 bp paired end reads with an insert size of ~250 bp. The raw reads as well as the assembled datasets were submitted to the MG-RAST server for automated annotation. Following analysis revealed a significant dominance of Archaea in enrichment Ant1. Up to 90% of hits spanning *Archaea* were affiliated with *Methanosarcina* spp. In contrast, no methanogens were observed in Ant2 permafrost enrichment where *Alphaproteobacteria* formed a core of the microbial community.
The presented data demonstrate a preservation of the viable methanogens at harsh conditions of the Antarctic Dry Valleys permafrost.

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63 ARCTIC AND ANTARTIC PERMAFROST

Unusual fungal diversity in soil and historic wood at Deception Island, Antarctica

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Deception Island, an active volcano with heated soils and rare flora in the South Shetland Islands has remarkable fungal diversity that differs from other Antarctic sites. Activities from whaling, scientific research and military bases over the past decades left an abundance of wood and other artifacts on the island. A diverse group of wood associated fungi were identified and wood decay types were characterized. *Cadophora* species were the most prominent ascomycetes found, including several new species that caused soft rot in the wood. In addition, DSE species (dark septate endophyte) were also abundant. Filamentous basidiomycetes, including *Hypochniciellum*, *Pholitoa* and others, not commonly found degrading wood in Polar Regions, were identified and shown to cause a brown or white rot type of degradation. Isolations and phylogenetic analysis of fungi from heated soils (as high as 60°C) show several undescribed species including a likely new species in the *Lecthophora*/*Coniochaeta* complex.

64 ARCTIC AND ANTARTIC PERMAFROST

Microbial diversity in permafrost and marine sediment from the King George Island, Antarctica, revealed by 16S rRNA gene pyrosequencing.

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Microbial responses to environmental changes are still uncertain, mainly because little is known about the species that inhabit climatic sensitive regions such as the Antarctic Peninsula. To evaluate the effects of environmental changes on microbial communities, permafrost samples were aseptically collected near the Russian Antarctic Station "Bellinsgauzen". Five samples were selected from a borehole drilled 4 to 9 meters below the surface (P13=4.6 m; P14=5.8 m; P15=6.9 m; P16=8.1 m; P17=9.2 m). Initial analysis indicated they represent Antarctic marine sediments frozen between ~2,500 to 7,500 years ago. A "modern" marine sediment from Maxwell Bay (sample B2) was collected to compare the past and present microbial communities. Total DNA was extracted, amplified with barcoded primers for the 16S rRNA gene and run in a 454 GS FLX Pyrosequencer (Roche), resulting in 63,610 sequences. A high abundance of Unclassified sequences (49% in average) was found, similarly to other studies using massive sequencing approaches on permafrost from Canada and Asia. The remaining sequences were assigned to 19 different Bacteria phyla. The modern marine sediment B2 was dominated by Proteobacteria (73%), Bacteroidetes (13%) and Verrucomicrobia (6.3%). Sample P13 revealed Proteobacteria (49.9%), Actinobacteria (20.7%) and Firmicutes (17.1%) as dominant phyla. Except for Proteobacteria, different taxa were found to be dominant in depth below 5.8 m. P14 and P15 showed high abundances of Proteobacteria (respectively 88.7% and 55%), Firmicutes (6.4% and 20.3%) and Actionobacteria (2.3% and 13.7%), while P16 showed high abundance of Proteobacteria (98.9%) and a few Firmicutes (0.46%) and Cyanobacteria (0.42%). The oldest permafrost P17 showed Proteobacteria (56.9%), Firmicutes (20.1%), Cyanobacteria (14%) and Chloroflexi (5%) as dominants. The results revealed differences in the microbial community which could be related to past environmental changes in the Antarctic Peninsula over the past 7,500 years.
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65 ARCTIC AND ANTARTIC PERMAFROST

A Metagenetic Study of Microeukaryotes in Antarctic Soils

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Microeukaryotes are important but poorly understood components of Antarctic soil ecosystems. The relatively simple Antarctic soil ecosystems serve as a model for understanding both biotic and abiotic drivers of ecosystem structure and functioning. Equally important are the mechanisms that microeukaryotes have evolved to survive in these extreme conditions and the potential parallels that can be drawn between this terrestrial environment and similar extraterrestrial environments. To shed some light on both of these topics, I will report on a metagenetic exploration of the species diversity of microbial eukaryotes in representative samples of the McMurdo Dry Valleys. Although some work has been done on the community structure of the prokaryotes and the metazoan members of the Dry Valley ecosystems, very little exploration has been done of the microbial eukaryotes. Previous studies have demonstrated not only their presence, but also their probable importance in the overall structure and functioning of Dry valley ecosystems. A more thorough characterization of their diversity and survival tactics will benefit both our understanding of Antarctic soil ecology and the abiotic parameters that are required for life both on planet earth and elsewhere.

NSF LTER grant

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66 ARCTIC AND ANTARTIC PERMAFROST

Bacterial Diversity and Function in Taylor Valley Soils, McMurdo Dry Valleys, Antarctica

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While bacterial life is known to be active during the austral summer in the McMurdo Dry Valleys (MDV) of Antarctica, little is known about what activities these microbes are performing. This project investigates soil bacterial activity during austral summer in the MDV using metatranscriptomes sequenced on the Illumina platform. The total mRNA transcripts of soil bacterial communities from Taylor Valley soils of the MDV were sequenced to identify microbial diversity and function of the dominant active members.

This project also considers future impacts of climate change to the region by investigating community responses to carbon and/or water additions. Comparisons of the controls and each addition will be discussed, as well as microbial richness and function with respect to ecosystem function in this unique polar desert environment.

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67 ARCTIC AND ANTARTIC PERMAFROST

Climatic Forcing of Biological Activity in Snow and Ice-bound Ecosystems on Signy Island, Maritime Antarctica

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Microbial abundance on the surface of glacier ice is estimated to be 10^{14}-10^{17} cells per km^{-3} making it the largest freshwater reservoir of microorganisms on Earth. Yet snow and ice remain among the most poorly understood habitats globally. Ice covers 99.7% of the Antarctic landscape, but the biology of these snow and ice-bound ecosystems has so far been largely overlooked compared to other Antarctic terrestrial and freshwater habitats. It is known that microorganisms living on the surface of glaciers and ice sheets are active throughout the melting season, and can readily transform inorganic nutrients and CO_2 from the atmosphere into organic biomass. Part of the organic matter produced is then transported to the surrounding terrestrial or marine ecosystems in meltwater. Due to the recent rapid regional warming in West Antarctica and around the Antarctic Peninsula in particular, large masses of ice and snow have been lost into the surrounding ocean (~180 Gt of ice $year^{-1}$). With this ice, around 16 Gg of organic carbon are also released every year and transferred into the ocean, but the ecological implications of this for the marine ecosystem remain unclear. Furthermore, iron lost from melting glaciers has been recently shown to stimulate phytoplankton production in the Southern Ocean, which can potentially partially offset the negative effect of the warming in the region by leading to enhanced uptake of atmospheric CO_2.

We aimed to assess climate forcing on biogeochemical activity in snow and ice-bound ecosystems in the maritime Antarctic and to estimate nutrient and biomass export by glacier meltwater into terrestrial habitats and coastal waters. We studied internal production and biogeochemistry of snow and ice habitats at Signy Island (South Orkney Islands, 60°S) in the maritime Antarctic. Microbiology, nutrient economy and productivity of snow and ice surface habitats were assessed at two major glaciers. These sites represent the broad range of melting and nutrient gradients found along much of the Antarctic Peninsula's west coast and associated archipelagos. Microbial community structure and biomass changes were studied in snowpack, slush and superimposed ice between November 2012 and March 2013 using molecular techniques, phospholipid fatty acid analysis and flow cytometry. Fluxes of carbon, nitrogen, phosphorus and iron were also monitored throughout the season within snowpacks and the runoff they produced. Net ecosystem production, respiration and photosynthesis of the Signy ice-bound ecosystems were evaluated using radioisotope labelling (^{14}C and ^{3}H) and CO_2 flux measurements. Meltwater runoff was monitored continuously in order to estimate microbial and nutrient loss from glaciated areas into the ocean.

This is a first systematic study of internal biological production and biogeochemistry of snow and ice-bound ecosystems in maritime Antarctica. We will present a conceptual model depicting how snow and ice-bound ecosystems are dynamically coupled to Signy Island's coastal ecosystems once the summer commences.

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Bioprospecting of Antarctic Yeasts

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Research on microbial bioprospecting from extreme environments has been rapidly increasing mostly due to the potential use of extremophiles in biotechnological applications. This study focused on the molecular identification and bioprospecting of yeasts isolated from the Antarctic continent. Soil samples were collected from areas of high plant diversity, presence of nesting birds, and thawing in two Antarctic islands: Torres and Greenwich. Samples were plated on Trypticase Soy Agar, Potato Dextrose Agar, Sabouraud Dextrose Agar, and Yeast Extract agar, and yeast colonies were identified by macro and micromorphology followed by PCR amplification and sequencing of the ribosomal ITS1, 5.8s, and ITS2 DNA regions. Bioprospecting was carried out by incubating each yeast at 20 °C on mineral media enriched with urea, casein/gluten, starch, or fat to test for ureases, peptidases, amylases or lipases respectively. Fermentation of sugars was tested using a Duncan tube and various substrates including sucrose, fructose, glucose, maltose, lactose, or glycerol. Various fermentation temperatures were tested including 5, 10, 15, 25 and 30°C. Twenty six yeasts isolates from Greenwich and two from Torres Island were obtained. The highest identity percentages (98% identity or above) from BLAST analyses were achieved with *Cryptococcus gastricus*, *Cryptococcus sp*, *Candida sp*, *Candida sake*, *Rhodotorula glacialis*. A potential new yeast specie (CIBE 1b.1) was found with only a maximum of 76% similarity of the ITS1, 5.8s, and ITS2 DNA regions and significant variations in the distribution of the internal organelles when compared to the closest yeast (*Rhodotorula* spp.). Three strains -*Candida sake*, *Candida sp*., and CIBE 12-, were positive for urease; only *Candida sp*., was positive for proteases when gluten was used as substrate. *Candida* species were positive for amylase using both cassava or corn starch substrates; lipase activity was not observed in any isolate and only *Candida sake* fermented sucrose, fructose, glucose and maltose sugars with an optimum fermentation temperature of 24°C. The highest fermentation yield (240 µL CO_2/day) was reached when glucose and fructose were used as substrate.

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Spatial Distribution of Bacterial Community Structure in Tundra Soil, Alaska

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Bacteria are the most abundant, diverse and ubiquitous in environments including soils, however, their spatial distributions are limited by environmental variables. Environmental heterogeneity is one of the major factors affecting bacterial distribution, but their relative importance is poorly understood. Here, we assessed the bacterial community structure with environmental factors to identify the similarity of bacterial communities within or between sampling sites in a local scale (tens of meter). We collected 70 soil samples (36 of upper layer and 34 of lower layer) from a tundra region in Council, Alaska. Soil bacteria were determined through DNA extraction and pyrosequencing for 16S rRNA gene identification, and several soil physicochemical properties (moisture content, carbon and nitrogen contents, pH, etc.) were analyzed. Dominant bacterial groups in the upper layer and lower layer soils were Alphaproteobacteira and Acidobacteria, respectively. Among several soil properties, pH showed the highest correlation ($r=0.41$, $p<0.001$) with some bacterial groups in both upper and lower layer soils. However, the other soil properties that were correlated with bacterial groups between two depths were different as showing total nitrogen content ($r=0.38$, $p<0.001$) and ammonium ion concentration ($r=0.25$, $p<0.05$) for the upper layer soils and carbon/nitrogen ratio ($r=0.20$, $p<0.05$) and moisture content ($r=0.23$, $p<0.05$) for the lower layer soils. The distance decay analysis showed that there was no significant correlation between the distances among sampling sites and bacterial community composition. These results indicated that the research site of the tundra area in Council, Alaska is homogenous, and local bacterial composition was affected by soil physicochemical properties. This study was supported by the National Research Foundation of Korea Grant funded by the Korean Government (MSIP) (NRF-2011-0021067) (PN13082, KOPRI).

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Microbial Contributions and Responses to Climate Change in Zakenberg Greenland

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Microbial contributions and responses to climate change vastly exceed previous expectations and appear to be substantially impacting both climate change rates and ecosystem responses, yet remain poorly understood. This microbial "black box" needs to be exposed and examined to provide more accurate climate models. Specifically, this study aims to address the microbial community composition and community function observed in permafrost and the correlation to greenhouse gas emissions measured along a methane production gradient in the permafrost active zone in Zakenberg, Greenland. Microbial community composition data from deep 16S cDNA sequencing was interpreted in the context of biogeochemical data, greenhouse gas flux measurements, and other physicochemical data. Generally, as methane production increases, microbial organisms associated with both methane production and consumption become more common in the microbial community. Understanding this pattern will help to develop better predictions as to how microbial communities shift in changing environments in the arctic.

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Microbial fingerprinting and greenhouse gas production from thawing permafrost layers in Northeast Greenland

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Thawing permafrost and the resulting mineralization of previously frozen organic carbon (C) and nitrogen (N) is considered an important future feedback from terrestrial ecosystems to the atmosphere. Within the framework of the newly funded Center for Permafrost (CENPERM), we have characterized two contrasting permafrost cores as well as 21 top permafrost cores from Zackenberg in High-Arctic Greenland which is a site characterized by progressive permafrost melting of more than 1 cm y^{-1} since 1996. Samples have been analysed for total C and N content, dissolved C and N as well as the potential production of carbon dioxide, methane and nitrous oxide in an incubation experiment. The same samples have been characterized by fingerprinting to assess microbial diversity. In this way the role of microbial community composition in C and N cycling in the current active layer and top permafrost is explored. Rates of CH_4, CO_2 and N_2O release rates from selected soils are discussed in relation to the presence of functional genes in the same soils.

Keywords: Permafrost, Carbon dioxide, Methane Production, Arctic, Microbes, Greenland

hosted by Carsten Jacobsen

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Isolation and characterization of anaerobic, fermentative and respiratory microbes from permafrost soil

Romy Chakraborty, Angelica Pettenato, Neslihan Tas, Susan Hubbard, Janet Jansson

The Arctic is characterized by vast amounts of carbon stored in permafrost and thus an important focal point for the study of climate change. Increasing temperature potentially accelerates microbially mediated release of carbon stored in permafrost as CO_2 and CH_4. Yet very little is known about the vulnerability and response of resident microorganisms to their changing environment. As part of the U.S. DOE Next Generation Ecosystem Experiment (NGEE) in the Arctic, we collected permafrost cores in an effort to isolate resident microbes. The cores were from the Barrow Environmental Observatory (BEO), located at the northern most location on the Alaskan Arctic Coastal Plain, and up to 3m in depth. In this location, permafrost starts from 0.5m in depth. Enrichments from different permafrost depths for heterotrophs were initiated at 4°C and 1°C in several different media types, under both aerobic and anaerobic conditions. Positive enrichments were identified, and after incubation period ranging from three to five weeks, individual colonies were obtained. Several strains were isolated that include Firmicutes such as *Bacillus, Clostridium, Sporosarcina,* and *Paenibacillus* and Iron-reducing Betaproteobacteria such as *Rhodoferax*. In addition, methanogenic enrichments continue to grow and produce methane at 2°C. In this study, we present the characterization, pH, temperature and osmotic tolerance, as well as the effect of increasing climate change parameters on the growth rate and respiratory gas production from these permafrost isolates.

The NGEE Arctic project is supported by the Office of Biological and Environmental Research in the DOE Office of Science.

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Metagenomics and microbial community profiling across an Arctic polygon transect

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Permafrost soils store almost as much organic carbon as is found in the rest of the world's soils. With increasing global temperatures, thawing permafrost is becoming a potential source of greenhouse gas (GHG) emissions. Because of widespread permafrost thaw much of this soil organic matter may be vulnerable to rapid mineralization by microorganisms in the soil. Yet little is known about the vulnerability of permafrost and the potential response of soil microorganisms to availability of new carbon sources. On the Alaskan North Slope the collapse and rise of soil due to formation of ice wedges and permafrost thaw create distinct features called polygons. As part of the U.S. Department of Energy (DOE) Next Generation Ecosystem Experiment (NGEE) in the Arctic, we aimed to determine the horizontal and vertical distribution of microbial populations across a range of polygon features and to correlate the microbial data to GHG flux data. We collected seasonally thawed active layer soil samples along a 450 m transect of polygons (Site 0), including high-centered, transitional and low-centered polygons. In addition, two deep cores (1m and 3m depth) were taken from a transitional polygon in the same transect. Prior to sectioning, the cores were CT-scanned to determine the physical heterogeneity throughout the cores. Illumina HiSeq technology was used to sequence 16SrRNA genes and metagenomes from the samples. The sequence data was correlated to GHG flux measurements and to environmental data from the site, including geophysical and geochemical soil characteristics. Both the microbial communities and the flux measurements varied with horizontal and vertical distance along the polygon transect. Functional genes involved in methanogenesis and CH_4-flux measurements were higher in low centered and wetter polygons than high centered drier polygons. On the edges of polygons the microbial community compositions and flux data were indicative of CO_2 production. There were also dramatic shifts in community compositions and functional genes with depth based on profiles obtained from 1m and 3m cores. Methanogen sequences were abundant in some of the deeper permafrost samples. The metagenome sequence data suggested that nitrate was utilized as a nitrogen source, but not lost through denitrification. The long-term goal is to use information gleaned from omics datasets to better inform climate models.

This study is supported by The Next-Generation Ecosystem Experiments (NGEE Arctic) project is supported by the Office of Biological and Environmental Research in the DOE Office of Science.

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Microbial Community Changes in Thawing Permafrost and its Potential Impact on Global Climate Change

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Results and discussion from the following experiment will be presented:

Permafrost covers 25% of the Northern Hemisphere land area and contains enormous amounts of carbon and nutrients bound in organic material. Global climate change will increase the temperature, especially in the colder regions of the world, and thus thaw much of the permafrost. This makes the stored carbon and nutrients of the permafrost available for microbes, which eventually will transform some of the nutrients to potent greenhouse gasses. In this way a self-reinforcing feedback mechanism will, most likely, establish. Despite this feedback mechanism could have huge impact on future climate, knowledge of how the microbial community develop in thawing permafrost are sparse.

This study will investigate how the microbial communities develop in thawing permafrost and to what extend greenhouse gasses are released from it. This will be done in aerobic and anaerobic conditions because, depending on the landscape, the water released from the thawing permafrost will either accumulate on top of the remaining permafrost or be removed – thus creating local differences in oxygen levels.

A permafrost sample, collected in NE-Greenland, is incubated at 2ºC for two weeks in aerobic- and anaerobic conditions. The release of greenhouse gasses (CO_2, CH_4 and N_2O) are monitored throughout the incubation and sub-samples of the incubated permafrost are regularly collected for subsequent DNA and RNA (cDNA) extraction. The extracted DNA and cDNA are then 454-pyrosequenced and specific functionally genes involved in the production and transformation of greenhouse gasses are quantified using real-time PCR (qPCR).

The results from this study could give detailed knowledge of how the microbial communities develop in thawing permafrost. Also, the results can give knowledge about which part of the microbial community we can expect to become active in thawing permafrost and how, and to what extent, the stored carbon and nutrients of permafrost will be transformed into greenhouse gasses by microbes.

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Seasonal variation in the microbial community in the active layer of permafrost in Svalbard

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Thawing permafrost may result in an increased release of greenhouse gases due to microbial degradation of the large permafrost organic matter pool. Despite this, there is limited knowledge of active microbial community changes within permafrost soil systems. We studied the microbial community changes by co-extracting DNA and RNA from 12 active layer permafrost cores from Svalbard collected over the period of a year. 16S rRNA genes at the DNA and RNA levels were sequenced using Illumina and analysed with QIIME. Multivariate statistical analysis of the microbial diversity data indicated that there were seasonal changes in the community, especially in the active part of the community: for example, the June sample was dominated by *Cyanobacteria*. Statistical analysis of the microbial community structure and the measured physico-chemical parameters showed also that the variations observed in the community structure were significantly correlated with total organic carbon (TOC), total organic nitrogen (TON), pH and season at the DNA level. The diversity of the active community was significantly correlated with TOC and nitrate concentrations. In conclusion, the structure of the microbial community in a Svalbard permafrost active layer showed a strong seasonal variation and was controlled by pH and nutrient contents.

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Biohopanoids in *Acidobacteria* from Arctic Tundra Soils: a role in tolerance to extreme conditions

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Hopanoids are a diverse group of pentacyclic triterpenoid lipids that are preserved as `molecular fossils' or geohopanoids in both modern and ancient sediments and soils, serving as diagnostic biomarkers of their precursor bacterial metabolites. Biohopanoids are also referred to as `sterol surrogates' owing to their structural similarity to eukaryotic sterols, thus congregating their functional role in modulating membrane fluidity and permeability. However, the vast structural diversity of hopanoid compounds indicates additional physiological roles under certain extreme conditions particularly in bacterial strains with high G+C (>50 mol%) found to occupy stressful ecological habitats. *Acidobacteria* species constitute a dominant bacterial community that is resilient to conditions of extreme frost, freeze-thaw and nutrient limitation in Arctic tundra soils. However, relatively little is known about their diversity, distribution and most critically, their function/s under these extreme conditions. Genetic and metabolic analysis of cultivable novel *Acidobacteria* isolates that thrive in these environments will provide clues to their successful colonization and survival in acidic tundra heaths. Towards such efforts, we analyzed the genomes of three novel cold-adapted strains of subdivision 1 *Acidobacteria*, *Granulicella mallensis* strain MP5ACTX8, *Granulicella tundricola* strain MP5ACTX9 and *Terriglobus saanensis* strain SP1PR4 isolated from Arctic tundra soils. We identified gene/gene clusters encoding for enzymes of the hopanoid (*Hpn*) biosynthetic pathway. Further, C_{30} and extended C_{35} functionalized hopanoids were analyzed by GC-MS and LC-MS in lipid extracts of steady state grown cultures of the three strains of *Acidobacteria* from Arctic tundra soils. These results imply that *Acidobacteria* synthesize hopanoids that may likely play a role in membrane stability and may have additional biological functions for survival under extreme cold and nutrient limited conditions in Arctic tundra soils.

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Proteomic changes during subzero growth in the halophilic cryophile *Planococcus halocryophilus*

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Polar cryoenviroments, such as subzero saline springs, permafrost and cryptoendoliths, are home to active, complex and unique microbial communities that are critical to our understanding of life in cold habitats and for increasing our knowledge of microbial activity, ecology and diversity. We have recently identified a halo- cryophilic bacteria, *Planococcus halocryophilus*, from Arctic permafrost, capable of growth at the lowest temperature recorded to date (-15 °C). Current research with *P. halocryophilus* is aimed at identifying the proteins and molecular mechanisms active during subzero growth. Cell surface proteomics, achieved by proteolytic treatment (trypsin and proteinase-k) of intact bacterial cells, will be used to identify surface exposed proteins that may be involved in the striking morphological changes observed during growth at -15°C. Whole cell proteomics, achieved through proteomic analysis of whole cell lysates, is being used to identify the molecular pathways that are active during subzero growth. In all cases, peptides will be identified using LC-MS/MS, followed by bioinformatics analysis to analyze the sequences and compare between growth conditions (RT, -15°C and 18% salt). Peptide analysis of surface exposed proteins cleaved from *P. halocryophilus* grown at RT has identified 39 peptides. Bioinformatics analysis of the identified peptides is currently underway, as is proteomic analysis of the remaining samples. Gaining greater insight into the cold and salt adaptations of *P. halocryophilus* and other cryophiles will help us better understand the cold limits of life, both here on Earth, and possibly Mars and other planetary bodies. This research is funded through the NSERC CREATE Canadian Astrobiology Training Program.

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Decimation of Cold-Adapted Bacteria by Ultraviolet Light

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Because DNA strongly absorbs, and is photolyzed by, light in broad wavelength bands around 220nm and 260 nm, 200-300nm-wavelength light (UVC) is very effective in decimating viable organisms. For icy environments, however, data are lacking on how UVC doses vary with depth in pertinent types of ice, and on whether UVC susceptibilities of organisms in ice (as measured by their dose-response curves) differ from those under other conditions.

Here we report novel data on UVC-decimation of viability of glacial- and sea ice bacterial isolates, in comparison to the well-known, UV-susceptible strain *E.coli*. Specifically, we report UVC dose-response curves for glacial isolates *Psychrobacer cryohalentis, Psychrobacter arcticus, marine Colwellia psychrorerythraea str. 34H,* and a cryoconite derived bacterial isolate str. CS117 (closely related to *Cryobacterium psychrophilum*), all for this initial work in liquid water. We irradiate these organisms with light from a Mercury-Xenon arc lamp narrowly filtered around 254 nm wavelength. We find a range of susceptibilities relative to *E.coli*: *Colwellia psychrorythraea str. 34H,* for example, is approximately 4 times as susceptible as *E.coli*, whereas *P. cryohalolentis*, is approximately only 1/3 as susceptible. These results in liquid culture provide a basis for experiments in which these organisms are irradiated while immured in fresh and saline ice, for which we will also report initial results.

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Enzymatic activity of Ectomycorrhizal Fungi in a Defoliated *Betula pubescens* Forest near Abisko, Sweden

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Carbon limitation can significantly affect ectomycorrhizal fungi (ECM) species presence and function. In the Arctic, where climate change is expected to result in increased insect outbreaks, insect-caused defoliation reduces the ECM-host supply of carbon. The mutualistic association of ECM fungi with woody plant species, in which ECM fungi transfer nutrients to the host species in exchange for carbon, is essential to plant fitness in the shallow, nutrient-limited soils of the Arctic. Carbon limitation may induce ECM fungi to shift their functional role towards saprotrophic behavior and work to decompose roots; additionally, ECM may actively 'mine' nutrients from soil organic matter. We examined ECM community composition and function in the context of a natural defoliation event by the autumnal moth (Epirrata autumnata) and subsequent carbon limitation in a birch (Betula pubescens)-dominated forest near Abisko, Sweden. Through DNA extraction and enzyme assays of ECM root tips, we compared ECM species composition and enzyme activity between a foliated and defoliated stand. Preliminary results suggest that cellulase, chitinase, and peroxidase enzymes increased in the defoliation treatment, whereas amino peptidase and phosphatase enzymes were unaffected. DNA sequencing (in progress) will be utilized to determine if defoliation effects on enzymes of ECM fungi at the community scale are due to changes in species composition.

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Simultaneous Co-consumption of N_2O and CH_4 in Arctic Polar Desert Soils

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Investigations of patterns of greenhouse gas (GHG) production, consumption, and movement within the soil profile of polar deserts on Ellesmere Island, Canada discovered some soils apparently consuming both N_2O and CH_4 simultaneously. Known conditions for the oxidation of CH_4 and the reduction of N_2O are mostly incompatible: N_2O-reduction is associated with oxygen-limited aerobic conditions, typically in soils with high water content, while these soils are very dry and well aerated from surface to the permafrost layer. Other reports of co-consumption are from environments highly different from the cold, dry, nutrient-poor polar deserts.

The techniques used to identify regions of co-consumption rely on an averaging procedure for estimating net production for each gas that often obscures the relationships between gases. In contrast to previous survey efforts, in 2013 soils identified as putative co-consumers are isolated in microcosms and incubated under conditions similar to those found in-situ. Measurements of GHG net production from these microcosms allows more precise characterization of these relationships, and soil samples will be examined in detail in the laboratory in late 2013, with the goal of identifing major functional groups of microorganisms responsible for observed patterns.