POLAR AND ALPINE RESEARCH CONFERENCE 2026

ABSTRACT BOOK

České Budějovice

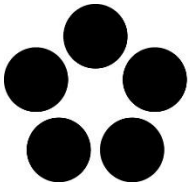
17-18 September 2026

Abstract book

Polar and Alpine Research Conference 2026

Edited by Jan Kavan

Conference is organized in cooperation with the University of South Bohemia and Masaryk University



Jihočeská univerzita
v Českých Budějovicích
University of South Bohemia
in České Budějovice

MASARYK
UNIVERSITY

PARC PROGRAMME

THURSDAY 17 SEPTEMBER

09:00-10:00 **REGISTRATION + COFFEE**

10:00-10:15 Introduction

10:15-10:45 **Iwo Wieczorek** (keynote) *Glacial lakes could be a future of Arctic landscape*

10:45-11:00 **Anton Puhovkin** *UAV Multispectral Mapping of Vegetation on Nelson Island, Maritime Antarctica, to Support Active Layer Monitoring*

11:00-11:15 **Tereza Mosočiová** *Tectonostratigraphic evolution of Late Permian evaporites in the East Greenland–mid-Norway rift system*

11:15-11:30 **Matěj Roman** *Exploring the palaeoenvironments of the last glaciation cycle in the James Ross Archipelago through new glaciolacustrine outcrops and glacial erratics*

11:30-11:45 **Filip Hrbáček** *Global trends of active layer thickness in the 21st century*

11:45-12:00 **Jan Kavan** Surge cycles and extreme meltwater events in Svalbard

12:00-13:30 **LUNCH**

13:30-14:00 **Stanislava Králová** (keynote) *From Frozen Dirt to Fancy Molecules*

14:00-14:15 **Katarína Brugošová** *Conserved and divergent RiPP pathways in Antarctic active-layer Streptomyces*

14:15-14:30 **Stanislav Jíra** *The secret life of limestone algae: Diversity, habitat shifts, and community assembly across an alpine elevational gradient*

14:30-14:45 **Alina Sadchenko** *Emerging Contaminants in Freshwater and Marine Systems of the Antarctic Peninsula: Preliminary Results of a Pilot Study*

14:45-15:00 **Jaroslav Semerád** *The Fate of Per- and Polyfluoroalkyl Substances in the Arctic Food Web: From Environmental Sources to Trophic Transfer*

15:00-15:30 **COFFEE BREAK**

15:30-15:45 **Divya Nautiyal** *Hoerbybreen forefield development after recent deglaciation*

15:45-16:00 **Simona Szymszová** *Effects of cloud cover and cloud genera variability on hortwave solar radiation at J.G. Mendel station, northern Antarctic Peninsula*

16:00-16:15 **David Tichopád** *Long-term variability and trends in Antarctic total ozone column based on LOTUS regression*

16:15-16:30 **Martina Sobotková** *Freezing-Thawing Cycles of Saturated Sand Sample*

16:30-16:45 **Pavla Waldhauserová** *Monitoring and networking activities in high latitude dust in the Arctic region*

16:45-17:00 **Magdalena Studená** *Polar ecology course 2026*

17:00-17:15 **IPY team** *International Polar Year 2032 – Czech Contribution*

17:15-18:00 **POSTER SESSION + COFFEE BREAK + DISCUSSIONS**

18:30 **ICEBREAKER**

FRIDAY 18 SEPTEMBER

09:00-09:15 **Jana Voříšková** *Responses of Arctic soil microbial communities to a changing climate*

09:15-09:30 **Pablo Cannestraci** *Stochasticity dominates microbial community assembly in Deception Island, Antarctica*

09:30-09:45 **Jiří Bárta** *Microbial Life Across Arctic Landscapes: Carbon Stability, Nutrient Limitation and Succession*

09:45-10:00 **Muhammad Waqas** *Permafrost degradation and SOC vulnerability: interplay of microbes, hydrology, and soil structure*

10:00-10:15 **Jason Bosch** *Using SIP-metagenomics to characterise the microbial taxa responsible for transforming carbon compounds in Arctic soil*

10:15-10:30 **Jiří Sekerák** *Light intensity downregulates photosynthetic performace of Antarctic lichens from James Ross Island during their thalli desiccation*

10:30-11:00 COFFEE BREAK

11:00-11:15 **Tereza Novotná Jaroměřská** *Chasing elements: interdisciplinary approaches for supraglacial microinvertebrates and why we need crazy ideas in polar ecology*

11:15-11:30 **Linda Votrubová** *Change is the only constant: comparison of cryoconite communities across a dynamic Alpine glacier*

11:30-11:45 **Jiménez Santos Marco Antonio** *Small organisms, large ranges? Molecular diversity and biogeographic structure of bdelloid rotifers in cryoconite holes*

11:45-12:00 **Raquel Viso** *Strong spatial structuring of diatom communities across Antarctic cryoconite holes*

12:00-12:15 **Martin Lulák** *Coastal Evolution and Benthic Palaeoecology of Central Svalbard During the Early to Mid-Holocene*

12:15-13:30 LUNCH

13:30-14:00 IPA meeting

14:00-15:00 IPY-CZ meeting

Glacial lakes could be a future of Arctic landscape

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The Svalbard Archipelago, situated in the High Arctic and often dubbed the "Arctic Tropics," is experiencing a rate of warming approximately four times faster than the global average. One visible consequence of this rapid warming is the accelerated development and evolution of glacial lakes across the region, which in turn increases the likelihood of Glacial Lake Outburst Floods (GLOFs). While Svalbard's extremely low population density (approximately 0.044 people per square kilometre) means that these events rarely pose a direct threat to local communities or infrastructure, the growing number of scientific expeditions and increasing tourism highlight the need for a better understanding of the associated geohazards.

What is worth paying particular attention to is the rate of change associated with glacial lakes. It is generally accepted that the Little Ice Age reached its maximum extent in Svalbard in the early 20th century, around the 1920s–1930s. Since then, we have observed an uninterrupted process of deglaciation, accompanied by changes in the extent of permafrost and the development of geomorphological features such as glacial lakes.

In the 1930s, there were 126 glacial lakes in Svalbard, with a total area of 74.71 ± 1.78 km^2. By 2008–2012, this number had increased to 566 lakes, covering a total area of 146.14 ± 0.34 km^2. The most recent data, from 2020, indicate a decrease in the number of glacial lakes to 387, while their total area has simultaneously increased to 168.83 ± 4.22 km^2.

Nowadays, the number of locations where new glacial lakes can develop is already considerably limited. Most proglacial areas have already been occupied by lake waters; some of these lakes have subsequently drained, while the remaining areas do not provide suitable morphological conditions for the formation of these temporary lake basins.

Nevertheless, this process is important from the perspective of the gradual stabilization of these landforms within the landscape. The more unstable glacial lakes have already drained, meaning that the number of potential GLOF events in Arctic areas is gradually decreasing.

Larger lakes, on the other hand, have become sufficiently established within the landscape and have stabilized their basins to such an extent that we can begin to consider them as potential freshwater reservoirs in the Arctic. The increase in the volume of glacial lakes in Svalbard over the past century is estimated at approximately 1.5 km^3 of water.

Glacial lakes will therefore gradually lose their connection with the glaciers supplying them, becoming sediment traps while also accumulating heat. As a result, they will directly influence the active layer in the surrounding areas.

This study is a contribution to the National Science Centre project ‘GLOWS’ (Award No. 2023/49/N/ST10/01075) and Polish National Agency for Academic Exchange project ‘DKF GLOFS (Award No. BPN/BEK/2025/1/00084S’).

UAV Multispectral Mapping of Vegetation on Nelson Island, Maritime Antarctica, to Support Active Layer Monitoring

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Antarctic vegetation is closely linked to local environmental conditions, and its spatial distribution can reflect fine-scale environmental variability. However, the small size and spectral similarity of Antarctic moss communities make detailed vegetation classification challenging. This study evaluates UAV multispectral imagery combined with machine-learning methods for vegetation mapping on Nelson Island, South Shetland Islands, Maritime Antarctica, as a basis for integrated vegetation and active layer monitoring.

UAV surveys were conducted during three field seasons (2024-2026) within long-term monitoring polygons on Nelson Island. Multispectral imagery was acquired using a DJI Mavic 3M UAV at approximately 1-2 cm spatial resolution. Green, Red, Red Edge, NIR and RGB orthomosaics were produced using Pix4D. Eighteen spectral indices were calculated, and highly correlated indices ($r > 0.99$) were removed to reduce redundancy.

Seven classes were distinguished: high- and low-vitality forms of *Sanionia georgicouncinata* and *Warnstorfia sarmentosa*, *Bryum pseudotriquetrum*, bare ground/rock, and biological soil crust. Vegetation classes were identified in the field, and samples collected from the monitoring polygons were further verified in the laboratory. The verified vegetation areas were used to generate pixel-level training data. Five machine-learning models were evaluated: Random Forest, Extra Trees, XGBoost, LightGBM and CatBoost. Spatial GroupKFold cross-validation was used for model comparison based on overall accuracy (OA), macro-F1 score and Cohen's kappa.

All models achieved high classification accuracy, although the best-performing model differed between monitoring polygons. In the "Green Valley" polygon, CatBoost achieved the highest performance, with an OA of 97.36 ± 1.02%, macro-F1 of 96.67 ± 1.18% and kappa of 0.967 ± 0.013. In the "Lakes" polygon, Extra Trees performed best, reaching an OA of 92.5 ± 1.4%, macro-F1 of 88.1 ± 2.5% and kappa of 0.900 ± 0.019. Most classes showed high

agreement, with limited confusion between vegetation classes. The main errors occurred between spectrally similar moss communities, while rock and biological soil crust showed high spectral separability.

The resulting georeferenced vegetation maps provide a spatial baseline for repeated monitoring on Nelson Island. Vegetation distributions were also examined in relation to surface-moisture measurements within the monitoring polygons. Combining repeated UAV surveys with surface-moisture and active-layer observations can provide a basis for tracking vegetation and ground-condition changes. Continued multi-year observations and field validation will help clarify these relationships.

Tectonostratigraphic evolution of Late Permian evaporites in the East Greenland–mid-Norway rift system

Tereza Mosociova

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Upper Permian evaporites are well documented from East Greenland but remain less constrained offshore mid-Norway despite growing evidence for their regional distribution. This study integrates observations from a 2026 field campaign in Greenland with subsurface data from mid-Norway to investigate the origin, distribution and tectonic significance of these evaporites within the East Greenland–mid-Norway rift system. We propose that the evaporites formed during the initial stages of the Late Permian transgression, when fault-controlled rift basins along the eastern and western margins became flooded from the Boreal Ocean while remaining restricted to the south. The resulting shallow, hypersaline embayments promoted gypsum precipitation under sabkha, salina and restricted lagoonal conditions.

In East Greenland, the Karstryggen Formation records this evolution through successions of limestones and evaporites deposited in subtidal to supratidal environments. Laminated and nodular gypsum accumulated in isolated tectonically controlled depocentres surrounded by algal laminated limestones and oolitic shoals, reflecting repeated fluctuations between hypersaline and more dilute conditions. Deposition terminated with extensive subaerial exposure, karstification and dissolution, producing deep sinkholes and debris-filled valleys that demonstrate prolonged emergence before renewed sedimentation.

Equivalent evaporites are recognised offshore mid-Norway as the "Anhydrite Unit", drilled in the marginal Sula Basin and interpreted as reworked sabkha deposits containing replacive anhydrite, enterolithic fabrics and desiccation surfaces. Although more siliciclastic than the Karstryggen Formation, the unit records the same transition from shallow-marine deposition to hypersaline restriction. Seismic and structural observations further suggest that equivalent evaporites extend beyond the drilled occurrences into the Kåvik and Froan basins. In the Kåvik Basin, numerous Ladinian listric faults detach into an undrilled high-velocity interval interpreted as Permian evaporites, whereas geochemical signatures associated with the Triassic Silfari volcanic succession provide indirect evidence for their presence in the Froan Basin. Although large-scale karstification comparable to East Greenland has not yet been demonstrated offshore mid-Norway, localized evidence exists on the Nordland Ridge, where wells penetrated carbonate collapse breccias interpreted to have formed by subaerial karstification of Upper Permian carbonates.

Our results indicate that the distribution of Late Permian evaporites was primarily controlled by syn-rift topography and marine restriction during the Late Permian transgression. Their preservation exerted a fundamental influence on subsequent Mesozoic deformation by providing mechanically weak detachment horizons that localized thin-skinned faulting and controlled later basin evolution. Karst-related collapse breccias in mid-Norway further suggest that parts of the carbonate–evaporite sequence experienced subaerial exposure, supporting a close palaeogeographic and stratigraphic affinity with the Karstryggen Formation.

Exploring the palaeoenvironments of the last glaciation cycle in the James Ross Archipelago through new glaciolacustrine outcrops and glacial erratics

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The polar regions exert a key influence on the abrupt changes in the Earth's geosystem, as their amplifying feedbacks frequently drive the crossing of critical tipping points and initiate cascading global impacts, evident both in the geological record and the contemporary, rapidly transforming environment. This contribution highlights recent progress in understanding the timing and pattern of ice retreat in the James Ross Archipelago on the eastern Antarctic Peninsula. Building (also) on the recent morphostratigraphic reconstructions and ~50 ka chronology by Romero et al. (2026), we targeted newly revealed sedimentary records preserved by former glacier-dammed water bodies. Specifically, we sampled a thinly laminated glaciolacustrine sediment outcrop, one of nine new stratigraphic exposures, near the outlet of the southern Lachman Lake for OSL and ^{14}C dating. This initial work paves the way for high-resolution, multi-proxy sampling in future campaigns to reconstruct environmental conditions at the onset of the Holocene (~11.2 ka BP) and possibly in the Pleistocene. Because deeper parts of the exposure remain frozen in permafrost, future microbiological or environmental DNA sampling represents a highly promising avenue.

Additionally, we will provide an update from last year's expedition to the J.G. Mendel station regarding the geomorphological mapping and surface exposure dating of glacigenic sediments, particularly granitoid erratic boulders. This sampling was conducted alongside landslide dating of the local tablelands, taking advantage of our access to uplands and steeper locations near past ice divides or overflowing saddles. Together, this combined geomorphological approach aims to disentangle the complex interplay of glacial, gravitational, marine, atmospheric and solid-Earth processes in the region.

References:

Romero, M, Strelin J.A., Kaplan M.R., et al. (2026). Glacier and Sea-Level Fluctuations on James Ross Island, Antarctica, during the Last ~50,000 Years. *Quaternary Science Reviews* 390: 110133. https://doi.org/10.1016/j.quascirev.2026.110133.

Surge cycles and extreme meltwater events in Svalbard

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The widespread retreat of Svalbard glaciers has been frequently interrupted by short-lived surge advances. In the case of calving glaciers this is often expressed in the remodelling of coastal zones. Here, we analyzed the coastal zone changes in front of the recently surging Recherchebreen and Penckbreen. Both glaciers advanced more than 1000 m during ca two years surge. Recherchebreen surged from 2018 and suddenly stopped in June 2020 followed by the rapid formation of a delta system in front of its subglacial meltwater outlet. The delta advanced by ca 450 m with probably the fastest progradation rate ever detected in the Arctic

region (ca 7 m/day). The synchroneity of the final slow-down of the glacier with the delta building indicates that this event records the release of stored water and sediments from beneath the glacier and thus provides direct evidence of drainage reorganisation at the termination of a surge. Similar situation was observed in case of Penckbreen where we identified 4 surge cycles with timing very similar to that of neighboring Recherchebreen. The surge activity resulted in formation of massive push moraine (served as a proglacial lake dam) around 1830, which was later eroded and remodelled during consequent surges accompanied by massive and repeated glacier lake outburst floods. Such extreme geomorphic dynamics is likely common among Svalbard surging glaciers documenting the importance of extreme events for current Arctic landscape transformation.

References

Kavan, J., Strzelecki, M.C., Benn, D.I. et al. Glacier surge as a trigger for the fastest delta growth in the Arctic. Commun Earth Environ 5, 700 (2024). https://doi.org/10.1038/s43247-024-01877-8

Kavan, J., Lulák, M., Lindhorst, S., van der Bilt, W., Wieczorek, I., Emmer, A., Farnsworth, W., Hein, C.K., Osika, A., Strzelecki, M. Surge cycles and extreme meltwater events drives long term proglacial landscape transformation at Penckbreen, Svalbard. Land Degradation and Development (in Review)

From Frozen Dirt to Fancy Molecules

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Antarctic environments impose strong selective pressures through persistent cold, oligotrophy, desiccation, radiation and pronounced seasonal fluctuations. The microorganisms inhabiting these ecosystems are expected to harbour unusual adaptations, yet remain strongly underrepresented in culture collections and genomic databases.

At Masaryk University, we are developing a platform for microbial natural product discovery that builds on environmental and ecological knowledge and connects cultivation, (meta)genomics, metabolomics and experimental characterization. Targeted cultivation of Antarctic microorganisms has provided access to diverse slow-growing and oligotrophic bacteria, many representing putative new species or taxa previously known only from environmental sequencing. Their genomes reveal extensive biosynthetic potential, but for much of this diversity neither the encoded chemistry nor its biological function is known. Specialized metabolites may contribute to adaptation through metal acquisition, redox homeostasis, signalling, competition or protection from environmental stress, while also providing starting points for biomedical, agricultural or biotechnological applications. Connecting environmental origin and microbial physiology with biosynthetic genes and chemical products is therefore key both to natural product discovery and to understanding microbial survival in the cold.

Kineochelins, a cryptic family of metal-binding metabolites discovered from a rare Antarctic actinomycete through cultivation, genome mining and metabolomics, illustrate this approach. They show how cultured Antarctic microorganisms can provide an accessible bridge between unexplored phylogenetic diversity, ecological adaptation and new chemistry, helping us understand how specialized metabolites contribute to survival in extreme environments while also revealing molecules with biotechnological potential.

Funding: This work was supported by MUNI/SC/1946/2024. Antarctic fieldwork was supported by Czech Antarctic Research Programme (VAN 2025).

Conserved and divergent RiPP pathways in Antarctic active-layer *Streptomyces*

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Antarctica has been geographically isolated for millions of years, resulting in distinctive microbial ecosystems shaped by persistent cold, nutrient limitation, freeze–thaw cycles and other environmental stresses. Yet polar extremophiles remain strongly underrepresented in genomic databases, and their biosynthetic potential is still poorly explored.

Here, we investigate approximately 300 bacterial isolates collected in Antarctica between 2013 and 2025, predominantly from active-layer soils. The collection spans broad taxonomic diversity and is dominated by Actinomycetota, alongside Pseudomonadota, Bacillota and Bacteroidota, including slow-growing, oligotrophic and psychrophilic taxa. Importantly, it includes nearly 100 Antarctic *Streptomyces* genomes, providing a phylogenetically diverse framework for investigating RiPP evolution.

Genome mining revealed extensive potential for ribosomally synthesized and post-translationally modified peptides (RiPPs), including lanthipeptides, thiopeptides and other less-characterized systems. Across Antarctic *Streptomyces*, RiPP pathways ranged from highly conserved biosynthetic systems shared across multiple lineages to strongly divergent clusters with unusual precursor organization, tailoring-enzyme composition and pathway architecture. Several multi-precursor systems were also identified, potentially generating cocktails of structurally related products. Comparison with non-polar homologues further distinguished broadly conserved RiPP families from divergent Antarctic-associated variants.

Selected pathways are being prioritized for cultivation-based activation, metabolomics and heterologous or cell-free expression, providing a genome-guided route towards accessing unexplored Antarctic peptide chemistry.

This work was supported by GA25-17343S and internal fundings MUNI/SC/1946/2024, FNBr 65269705. Antarctic fieldwork was supported by Czech Antarctic Research Programme VAN 2025.

The secret life of limestone algae: Diversity, habitat shifts, and community assembly across an alpine elevational gradient

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Mountain ecosystems are characterised by strong environmental gradients and increasingly stressful conditions with elevation. These environments provide natural laboratories for studying how microbial communities respond to environmental filtering and habitat constraints. Lithobiontic phototrophic microorganisms are important primary producers and ecosystem engineers in these systems, yet their diversity, distribution, and ecological responses to alpine conditions remain poorly understood.

We investigated the diversity, habitat distribution, and ecological patterns of lithobiontic green algae along an elevational gradient in the Northern Calcareous Alps, Austria (Dachstein Massif, Hochkönig Massif, and Selbhorn peak), spanning 800–2,655 m a.s.l. We combined field sampling at 52 sites with isolation and molecular characterisation of laboratory strains, measurements of photosynthetic performance using rapid light curves, and environmental sequencing based on ITS2 rDNA metabarcoding.

The distribution of lithobiontic growth forms changed markedly with elevation. Epilithic growth decreased from up to 70% at lower elevations to approximately 10% at the highest sites, while endolithic growth increased from less than 10% to almost 50%. Hypolithic growth remained relatively stable at around 25% across the gradient. Environmental sequencing revealed 620 chlorophyte OTUs, with the highest diversity in the forest zone (800–1,700 m a.s.l.) and a pronounced decline towards the alpine zone (>2,200 m a.s.l.). Community composition differed significantly among elevational zones, and numerous taxa were restricted to particular parts of the gradient, suggesting strong environmental filtering and habitat-specific distributions. Trebouxiophyceae dominated the dataset, while photosynthetic measurements of isolated strains revealed substantial variability but no significant difference between strains originating from shaded and open habitats.

Our results demonstrate that elevation strongly influences both the habitat structure and community composition of lithobiontic green algae. The shift from predominantly epilithic to increasingly endolithic growth, together with declining diversity and distinct community assemblages at higher elevations, suggests that alpine environmental conditions impose strong ecological constraints on lithobiontic microbial communities.

Beyond ice: cryosphere-adjacent rocks as reservoirs of cold-adapted green algae

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Snow and glacier ice algae are well documented components of cryospheric ecosystems, particularly during snowmelt periods, yet their persistence outside the snowpack and glacier ice remains poorly understood. At the same time, lithobiontic green algae are widespread in mountain environments but remain comparatively understudied. Alpine terrestrial habitats may therefore represent potential refugia or transitional habitats for lineages associated with cold cryospheric environments.

We investigated the diversity and community composition of lithobiontic green algae along elevational gradients in the Northern Calcareous Alps (800–2,655 m a.s.l.) and the Higher Tauern (900–2,600 m a.s.l.), focusing on the occurrence of taxa previously associated with alpine, polar, periglacial, snow, or glacier-influenced habitats. The two mountain regions differ markedly in their geological history and bedrock composition, allowing comparison of algal communities inhabiting contrasting substrates. Algal diversity and community composition were assessed using ITS2 rDNA metabarcoding.

Algal diversity declined significantly with increasing elevation, consistent with increasing environmental filtering under harsher alpine conditions. Communities were dominated by aerophytic and lithobiontic lineages, with most dominant taxa being characteristic of terrestrial rock habitats. A substantial proportion of taxa were associated in previous studies with alpine, polar, or periglacial terrestrial environments, while a smaller subset of taxa had previously documented associations with snow or glacier-influenced habitats *sensu stricto*.

Results indicate that exposed rocks can potentially host diverse communities partly overlapping with cryosphere-adjacent habitats and serving as potential reservoirs for these taxa in temperate regions.

Emerging Contaminants in Freshwater and Marine Systems of the Antarctic Peninsula: Preliminary Results of a Pilot Study

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Antarctic environments are generally considered remote from direct anthropogenic impacts; however, research stations, temporary field camps, and long-range atmospheric and oceanic transport may contribute to the introduction of contaminants into polar ecosystems. Information on contemporary pharmaceuticals, pesticides, per- and polyfluoroalkyl substances (PFAS), and industrial chemicals in Antarctic waters remains limited.

As part of a pilot study, water samples were collected using Polar Organic Chemical Integrative Samplers (POCIS), passive samplers that accumulate dissolved organic contaminants over time. Unlike conventional grab sampling, POCIS provide a time-integrated measure of contaminant exposure and may improve the detection of compounds occurring at low or variable concentrations. POCIS were deployed for approximately two weeks at two Antarctic locations: near the Akademik Vernadsky Research Station (Argentine Islands) and on Nelson Island. Sampling included freshwater sites upstream and downstream of human infrastructure, glacier/snowmelt-fed waters, a freshwater lake, and coastal seawater near the station and pier. Field blanks were included for quality control.

Samples were analysed by liquid chromatography–mass spectrometry (LC-MS) for a broad range of pharmaceuticals, pesticides, PFAS, and industrial chemicals. Targeted analysis using analytical standards has been completed; the results presented here represent the first preliminary assessment. No pharmaceuticals or pesticides were detected. Only a small

number of industrial and other anthropogenic compounds were observed, generally at low levels.

Trace signals of benzotriazole-related compounds, including 1-methyl-1H-benzotriazole, were observed in a freshwater stream. In seawater from a bay near the station pier, where yachts and other vessels are present, DADMAC-C10 (didecyldimethylammonium C10), a quaternary ammonium compound used in surfactant and disinfectant formulations, was detected at a low level, only slightly above the detection range. Similar quaternary ammonium compounds were observed in some other samples, but at concentrations close to the detection range.

The relatively short two-week POCIS exposure may have limited contaminant accumulation and therefore the sensitivity of this pilot study. Longer deployments could provide stronger integrated signals, particularly for compounds present at very low or intermittent concentrations. Further non-target screening will be conducted to investigate additional compounds outside the targeted analytical list.

Overall, these preliminary results provide an initial chemical snapshot of Antarctic freshwater and coastal environments and demonstrate the potential of passive sampling combined with LC-MS for investigating emerging contaminants in polar waters.

The Fate of Per- and Polyfluoroalkyl Substances in the Arctic Food Web: From Environmental Sources to Trophic Transfer

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Per- and polyfluoroalkyl substances (PFAS) represent a large group of highly persistent anthropogenic chemicals that have become contaminants of global concern. Despite limited industrial activity in the Arctic, PFAS are present in Arctic ecosystems as a consequence of long-range atmospheric and oceanic transport, while local anthropogenic activities may constitute additional sources. The Svalbard Archipelago provides a unique environment for studying the relative importance of local and global PFAS sources and their subsequent transfer through Arctic food webs.

The ongoing project The Fate of Poly- and Perfluoroalkyl Substances in the Arctic Food Chain investigates the occurrence, sources, environmental fate, and trophic transfer of PFAS in terrestrial, freshwater, and marine ecosystems of Svalbard. The study focuses particularly on the Longyearbyen and Adventfjorden area, where potential local sources include firefighting activities at the airport, untreated municipal wastewater, harbour activities, and historical coal mining. These impacted environments are compared with remote areas of Svalbard with substantially lower direct anthropogenic influence.

A comprehensive sampling strategy integrates abiotic matrices, including snow, surface water, seawater, sediments, and soils, with biota representing different trophic levels. Aquatic and terrestrial food webs are investigated using samples of plankton, benthic organisms, fish, birds, and mammals. Particular attention is paid to differences between resident and migratory species, providing a basis for distinguishing the contributions of local contamination and long-range pollutant transport.

PFAS are characterized using a combination of targeted and non-targeted analytical approaches. Targeted LC-MS/MS and GC-MS/MS analyses are complemented by high-resolution mass spectrometry, total oxidizable precursor analysis, and combustion ion

chromatography to provide broader information on PFAS contamination, including precursors and emerging compounds. Passive sampling techniques are also evaluated for monitoring PFAS in Arctic aquatic environments. Stable carbon and nitrogen isotope analyses are used to establish trophic positions and assess PFAS biomagnification across food webs. Additional isotope-based approaches and atmospheric transport modelling support the identification and differentiation of potential contaminant sources.

By integrating environmental and analytical chemistry, isotope geochemistry, ecology, and atmospheric modelling, the project provides a comprehensive framework for understanding the processes controlling PFAS distribution and accumulation in Arctic ecosystems and for assessing the vulnerability of polar environments to contaminants originating from both local and global sources.

Paraglacial landscape transformation in the forefield of Hørbyebreen, Petuniabukta, Svalbard (2009–2024)

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Arctic glacier forefields represent some of the most rapidly evolving landscapes on Earth, yet the partitioning of deglaciated terrain between competing paraglacial landform systems remains poorly quantified at high temporal resolution. This study documents geomorphological change across the forefield of Hørbyebreen, a polythermal valley glacier in Petuniabukta, central Svalbard, between 2009 and 2024, using a georeferenced Evans et al. (2012) geomorphological map as a baseline and a UAV-derived orthophoto and digital elevation model (DEM) as the 2024 endpoint.

Glacier terminus retreat was quantified along 16 equally-spaced transects, yielding a mean retreat of 592.3 ± 268.6 m (39.5 ± 17.9 m/yr) over the study period, with a maximum rate of 78.3 m/yr recorded at the central outlet, substantially exceeding the historically documented rate of 30 m/yr for the Hørbye flow unit. The spatial heterogeneity of retreat (SD = 45% of mean) reflects contrasting dynamics between fast retreating central terminus and stagnant, debris-mantled lateral margins.

Within study frame, the ice-free fraction of the forefield expanded as glacier area declined, with deglaciated terrain redistributed unequally across three landform systems. The glacifluvial plain recorded the largest absolute gain (+60.7%), driven by concentrated meltwater reworking of newly exposed till (+10.9%). The ice-cored latero-frontal moraine showed negligible planform change (+1.4%, within mapping uncertainty), with surface lowering in the DEM indicating ongoing downwasting of buried dead ice rather than lateral expansion.

Proglacial kettle lake area declined by 49.9% (from 95,943 m^2 to 48,069 m^2), with 24 of 65 lakes draining completely. This pattern of catastrophic drainage, concentrated among small and mid-sized kettles, contrasts with the broader Svalbard-wide trend of glacial lake expansion and suggests that buried ice in the Hørbyebreen latero-frontal moraine is approaching exhaustion. Three drainage mechanisms are proposed: buried ice collapse, sandur channel capture, and permafrost degradation.

Together, these findings characterise the Hørbyebreen forefield as a sediment-flux-dominated, meltwater-driven paraglacial system in an advanced stage of deglacial

transition, with implications for understanding forefield evolution across Svalbard's polythermal landsystems.

Effects of cloud cover and cloud genera variability on shortwave solar radiation at J.G. Mendel station, northern Antarctic Peninsula

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Shortwave solar radiation (SWin) variability is affected by many atmospheric and other factors, namely solar zenith angle, cloud cover, ozone, water vapor, albedo etc. Even though solar zenith angle is a leading factor influencing SWin through the year, daily variability is caused mostly by changes in cloud cover. Variations in SWin intensity are caused by cloud type, height, amount, thickness and other cloud properties same as position of the cloud relative to the Sun. The effects of cloud cover and cloud genera on SWin intensity were investigated at the Czech J.G. Mendel station, located in the northeastern part of the Antarctic Peninsula. This area is characterised by high cloud cover variability associated with its location within the circumpolar trough of mean sea level pressure. Summer experiment was conducted between February and March 2026, using ground-based instrumentation and observation techniques. All-sky images were obtained by Wx Labs camera every 5 minutes in HDR and automatic, long and short exposure to estimate cloud cover properties. The total cloud cover, layer cloud amount and cloud genera were also observed manually every hour from 7:00 to 21:00 local time. SWin intensity was measured using Kipp&Zonen CMP-11 pyranometer at 10-min interval while clear-sky SWin was estimated by Bird and Hulstrom radiative transfer model. To further analyse effects of cloud cover variability and different cloud genera on SWin, cloud modification factor (CMF) and cloud radiative effect (CRE) were calculated. Mean observed cloud cover was 60 %. Cirrus, altocumulus, stratus and stratocumulus were cloud genera occurring the most during the studied period. The attenuation of SWin was the lowest when cirrus and cirrostratus clouds were present and even led to its enhancement on several occasions. Typical CMF values were between 0.8 and 1.1 while CRE values predominantly fell between -200 and 100 W.m-2. In comparison, stratus clouds showed the strongest attenuation of SWin with typical CMF values ranging from 0.1 to 0.5 and CRE values between -500 and -100 W.m-2.

Long-term variability and trends in Antarctic total ozone column based on LOTUS regression

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This study assesses long-term changes in total column ozone (TOC) and the atmospheric factors affecting its variability at three Antarctic stations, Dumont d'Urville, Amundsen–Scott South Pole, and Marambio, over the period 1980–2024. Ground-based TOC measurements were used, with missing observations supplemented by the Multi-Sensor Reanalysis (MSR2). TOC variability and trends were analysed using the LOTUS multiple linear regression model, including dynamical and external predictors such as the El Niño–Southern Oscillation, Quasi-Biennial Oscillation, solar activity, eddy heat flux, stratospheric temperature, aerosol optical depth, and the Indian Ocean Dipole. The model explains 86–92 % of the observed TOC variability at the three stations. The regression analysis shows a change in the long-term TOC evolution around 2000, with decreasing trends during 1980–2000 followed by increasing trends during 2000–2024. The strongest decrease was found at Dumont d'Urville (−13.82 ± 2.89 DU decade^{-1}), while the slightest decrease occurred at Amundsen–Scott South Pole (−5.53 ± 3.56 DU decade^{-1}). After 2000, positive trends were found at all three stations, with the largest increase at Dumont d'Urville (5.98 ± 2.17 DU decade^{-1}). The analysis was further extended to the entire Antarctic region using MSR2 data. The spatial application of the model shows that the explained TOC variability is generally high across Antarctica, while the estimated trends and the effects of individual predictors vary regionally. The spatial analysis further reveals clear regional differences in both the magnitude of the trends and the response of TOC to the individual predictors.

Freezing-Thawing Cycles of Saturated Sand Sample

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Freezing and thawing of soils play a critical role in the dynamics of permafrost and seasonally frozen ground, affecting water movement, mechanical stability, and heat transfer in cold regions. This study investigates the thermal and hydraulic behaviour of a fully saturated, packed sand sample (10 cm in diameter, 10 cm in height) subjected to freezing-thawing cycles under controlled laboratory conditions.

A newly designed experimental setup was used, in which the sand sample was housed in a cylindrical tube manufactured by 3D printing; the outer wall of the printed tube served as thermal insulation. The column was placed in a precisely controlled freezer chamber. Following equilibration at +10 °C, the chamber temperature was lowered to –10 °C, initiating the freezing process. The internal temperature of the sample was continuously measured inside the sample using thin temperature sensors (PT100, TH&L Systems, CZ) inserted vertically into the sample. The inner temperature was also monitored by fibre optic temperature probes. The external temperature in the freezing unit was monitored by two additional temperature sensors.

Observing temperature trends provides insight into the dynamics of freezing and the thermomechanical changes that occur during freeze-thaw cycles. The measured data will serve as the basis for mathematical modelling. These findings contribute to a better understanding and prediction of frost action in saturated granular media, with relevance to permafrost and periglacial environments studied in polar and alpine regions.

Monitoring and networking activities in High latitude Dust in THE arctic region

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Earth's climate is changing, with some of the most pronounced changes occurring at high latitudes, where High Latitude Dust (HLD) is an important climate driver. HLD deposited on snow and glaciers reduces albedo and accelerates melting, while airborne dust affects atmospheric radiation and cloud microphysics. Frequent dust storms impair air quality, reduce visibility, disrupt transportation, and disturb vulnerable ecosystems.

HLD not only causes severe air pollution locally in the Arctic, but also travels several thousands of km whitin the Arctic and > 3,500 km towards Europe. Studies have confirmed the presence of Icelandic and Greenlandic dust in Svalbard, as well as Icelandic dust in Ireland and Serbia. Contrarily, Saharan and Asian dust frequently arrive in the Arctic and we have obtained observations in Iceland, Lapland and Finland. The newly supported project Dusthila (Dust changing the high latitudes) will extent existing HLD monitoring network in Iceland and Antarctica to Svalbard and Greenland.

Sand and dust storms, including HLD, have been identified as hazards affecting 11 of the 17 Sustainable Development Goals. The World Meteorological Organization's Sand/Dust Storm Warning and Advisory System (WMO SDS WAS) is a member and advisor in the UN Coalition on Combating Sand and Dust Storms, which includes HLD storms. The UArctic Thematic Network on HLD is highly active. The Icelandic Aerosol and Dust Association (IceDust) has > 110 members from 57 institutions in 22 countries (https://ice-dust.com) and has held a seat on the board of the European Aerosol Assembly since 2022. Another key player in HLD and air pollution monitoring in Iceland is the Copernicus Atmosphere Monitoring Service (CAMS)

National Collaboration Programme Iceland. The activities of these networks contribute to university education, research, and climate reports from organizations such as AMAP, GIOS, and SIOS.

Responses of Arctic soil microbial communities to a changing climate

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Climate models predict substantial changes in temperature and precipitation patterns across Arctic regions in the coming decades. Microbes play key roles in determining the stability of soil carbon (C) and its potential release into the atmosphere as carbon dioxide and methane. Carbon-rich Arctic soil ecosystems are particularly vulnerable to C losses due to ongoing warming and subsequent ecosystem disturbances, such as wildfires. On the other hand, increased plant growth could mitigate the release of C from soil to the atmosphere.

I will present our ongoing projects aiming to identify the responses of soil microorganisms to climate warming. Our projects use a unique framework combining *in situ* large-scale climate manipulation experiments with detailed taxonomic and functional characterization of soil microbial communities using metagenomics, metatranscriptomics and stable isotope probing (DNA-SIP). The results provide a comprehensive picture of microbial responses to ongoing climate change, as well as insights into the structure and function of microbial communities involved in carbon cycling in Arctic soils.

Stochasticity dominates microbial community assembly in Deception Island, Antarctica

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Mechanisms of microbial community assembly in cryospheric ecosystems remain largely unexplored, although they are critical to understanding how associated habitats will respond to future change. Specifically, microbial communities in Antarctica are predicted to shift with general warming and terrestrial “greening”, though studies investigating these responses are limited. To gain insights into these processes, we characterized microbial communities (bacteria and microeukaryotes) from soil and moss habitats over three geothermal transects in the volcanically active Deception Island, South Shetland Islands, Antarctica. We hypothesized that both habitat type and soil temperature will be influential for microbial diversity and community structure, which were characterized through 16S and 18S amplicon sequencing. We also tested whether warmer underlying soils harbored greater microbial diversity than their colder counterparts. Using both univariate and multivariate statistical approaches, we found that bacterial and microeukaryotic communities were primarily shaped by habitat type. Meanwhile, the accompanying environmental parameters (notably soil temperature, nutrient concentrations, and soil CO_2 flux) explained less variability, and we found no evidence suggesting that warmer soils harbored more microbial diversity. Instead, phylogenetic overdispersion analyses (iCAMP) indicated that stochastic mechanisms, such as dispersal limitation and drift, appear to be the main drivers of community assembly in these barren terrestrial habitats. Collectively, we suggest that while Antarctic warming and “greening” may indeed come with shifts in terrestrial microbial community structure, variability therein may not be entirely predictable, having a stochastic element such as that observed in other nascent ecosystems located in cryosphere-adjacent ecosystems such as glacial lakes and streams.

Microbial Life Across Arctic Landscapes: Carbon Stability, Nutrient Limitation and Succession

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Arctic ecosystems harbour diverse and active microbial communities that control carbon and nutrient cycling despite low temperatures, nutrient limitation and repeated freezing. Our studies across Siberia, the western Canadian Arctic, Greenland and Svalbard between 2015 and 2025 demonstrate that microbial responses to warming are governed not by temperature alone, but also by soil horizon, mineralogy, hydrology, vegetation and organic-matter quality. Mineral associations stabilize much permafrost carbon and reduce its temperature sensitivity, whereas fresh plant-derived carbon and nitrogen can stimulate the decomposition of older organic matter. Cryoturbated horizons contain specialized oligotrophic decomposers, wet polygon tundra represents a potential methanogenic hotspot, and extracellular-enzyme patterns reveal site-specific carbon, nitrogen and phosphorus limitations. In Svalbard glacier forefields, carbonate-rich substrates accelerated early microbial development, while silicate soils followed more gradual succession. Arctic willow root exudates further promoted nutrient release, rhizosphere microbial biomass and initial soil formation. Pan-Arctic analyses revealed a surprisingly low-diversity methane filter dominated by Methylobacter-like methanotrophs, whereas drying after permafrost degradation favoured atmospheric methane oxidizers. Together, these findings demonstrate that microbial feedbacks to Arctic climate change are strongly ecosystem- and context-dependent.

Permafrost degradation and SOC vulnerability: interplay of microbes, hydrology, and soil structure

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Permafrost soils represent a globally significant reservoir of sequestered soil organic carbon (SOC) and host ancient and uniquely adapted microbial communities that persist under freezing conditions. With the ongoing rise in global temperatures, permafrost areas in the Arctic are rapidly thawing, as the depth and extent of the seasonally thawed active layer are progressively expanding. This increase in the thickness of the active layer leads to permafrost degradation and exposes large amounts of previously frozen organic matter pools to microbial decomposition, creating a potential positive feedback to climate change. After permafrost degradation, contrasting hydrological conditions develop, yet it remains unclear how these regimes differentially affect SOC vulnerability, microbial community composition, and microbially mediated soil aggregation via extracellular polymeric substances (EPS). In this study we investigated the active layer of a non-degraded and two degraded permafrost soils with different hydrological landscapes near Fairbanks, Alaska, USA. We quantified SOC stocks and the distribution of carbon between particulate and mineral-associated fractions within macro- and microaggregates. Microbial community composition was characterized at bulk and aggregate scales using 16S rRNA gene amplicon

sequencing, and EPS content and composition were quantified to assess potential microbial controls on SOC stabilization. Our results revealed that both degraded permafrost sites developed structurally complex mineral topsoils enriched in fresh organic matter inputs and mineral-associated organic matter, resulting in higher SOC stocks than non-degraded topsoil. In contrast, mineral subsoils of degraded sites showed pronounced SOC depletion despite elevated EPS contents and diverse microbial communities. However, contrasting hydrological conditions did not result in a clear divergence in SOC losses, with dry and wet degraded soils showing comparable SOC depletion. Microbial communities varied strongly with soil depth and aggregate fraction. Topsoil communities in both bulk soil and aggregate fractions were enriched in taxa associated with the utilization of relatively labile organic substrates, whereas subsoil communities shifted toward taxa adapted to resource limitation. Our findings indicate that permafrost degradation transforms soils from cryogenically protected SOC reservoirs into biologically active systems in which microbial processes increasingly regulate carbon fate. Although hydrological regimes shape soil structure, community composition, and functional traits, overall SOC vulnerability remains high and comparable across degraded landscapes. Continued Arctic warming is therefore likely to increase the vulnerability of previously protected SOC to microbial decomposition.

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Using SIP-metagenomics to characterise the microbial taxa responsible for transforming carbon compounds in Arctic soil

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The Arctic is particularly vulnerable to warming due to climate change. Warming increases the rates of microbial activity and the decomposition of stored carbon. Arctic microbes release stored carbon as carbon dioxide and methane, potentially resulting in a positive feedback loop. These processes can not be accurately modelled without a solid understanding of the microbes involved and how they are affected by temperature.

We characterised the microbial sub-populations involved in the transformation of carbon compounds (glucose, cellulose and acetate) in an incubation experiment using Greenland tundra soils collected from control (ambient) and warmed (open top chambers and snow fences-treated) plots. We have generated a dataset of metagenome assembled genomes labelled with ^{12}C and ^{13}C-carbon from the three carbon compounds after 28 days of incubation. We show the composition of the abundant microbial community which can be assembled into medium- and high-quality MAGs as well as how their abundance and incorporation of different substrates differs based on warming. We further use whole-genome data to investigate the metabolic capabilities of different taxa to compare their measured substrate use with their potential substrate use. Finally, we compare the functional potential of substrate-specific communities.

Although microbes play a crucial role in the impacts of climate change, they are seldom considered in policy development. Our results provide details about the metabolic potential and activity of Arctic microbial communities and how it is affected by warming. This information can be integrated in global models of climate change to improve the quality of their predictions.

Light intensity downregulates photosynthetic performace of Antarctic lichens from James Ross Island during their thalli desiccation

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Mosses stand out for their ability to sustain photosynthetic activity even when exposed to severe desiccation, i.e at thallus relative water content (RWC) ranging from 70 to 20%. During evolution, mosses have developed several protective strategies that safeguard photosynthesis from dehydration. At RWCs below 20%, however, inhibition of primary photosynthetic processes happens even in such highly adapted poikilohydric autotrophs. Several studies focused the exlusive effect of dehydration and high light (photoinhibition) on inhibition of photosystem II (PSII) functioning. Combined effect of desiccation and high light on PSII functioning, however has been investigated scarcely, more frequently in mosses (e.g. Giordano et al. 2026). Therefore, our recent study was aimed to evaluation of negative co-action of high light and thallus desiccation on photosyntehtic processes in three contrasting Antarcic lichen species.

Thalli of *Xanthoria elegans*, *Leptogium puberulum*, and *Umbilicaria decussata* were collected in the neigbourhood of Mendel station, James Ross Island, Antarctica. In a laboratory of the station, they were exposed to gradual dessication from fully wet to fully dry state under low and high light (LL = 60 mmol(photons) m^{-2} s^{-1} fo photosynthetically active radiation (PAR), HL = 1500 mmol(photons) m^{-2} s^{-1} PAR). During desiccation, relative water content of thalli was measured gravmetrically and several chlorophyll fluorescence (ChlF) parameters, were evaluated. They were maximum quantum yield of photochemical photosynthetic processes in PSII (FV/FM), effective quantum yield of PSII (ΦPSII), vitality index expressed as relative ChlF decrease (RFd), and non-photochemical quenching (NPQ). Additionally, two components related to fast-, and slow-activated photoprotective mechanisms were evaluated: (1)energy-dependent quenching (qE), and (2)photoinhibitory quenching (qI) related to structural changes in PSII supercomplex.

The above-specified ChlF parameters showed species-specific responses to the combined stress. Species specifity was apparent from different shapes of desiccation-response curves (S-curves) of particular ChlF parameters. In all lichen species, strong inhibition of the ChlF parameters was found at the RWC below 20%. Such finding is consistent with earlier

studies (Barták et al. 2021) and supported by the decline of the parameters derived form fast ChlF transient (OJIP). In conclusion, our study highlights interspecific differences among Antarctic lichen species (chlorolichens/cyanolichens) in their sensitivity to photoinhibition during thallus desiccation. Therefore, light intensity during desiccation is an important factor to be considered in future ecophysiological studies, carried out both in a laboratory, and in the field.

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Chasing elements: interdisciplinary approaches for supraglacial microinvertebrates and why we need crazy ideas in polar ecology

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Microinvertebrates that inhabit glacier surfaces (the supraglacial) occupy top positions in food webs, influencing the turnover of essential macroelements such as carbon (C), nitrogen (N) and phosphorus (P). Understanding the elemental composition of supraglacial invertebrates can therefore substantially improve our understanding of supraglacial ecology and the processes that affect the composition of supraglacial organic matter (OM), which can also provide dietary energy for downstream habitats. But how can you get such information from such small creatures?

This talk will present some classic and some innovative (i.e., crazy, at least for ecologist) interdisciplinary methodological approaches chasing stable isotopes of C and N, and P content in supraglacial microinvertebrates, as well as offering insights into the implications of these findings for supraglacial ecology.

Stable isotopes of carbon and nitrogen revealed that different groups of supraglacial consumers have different food preferences and/or macronutrient requirements. Results on phosphorus (P) have revealed that some supraglacial tardigrades exhibit a high P content comparable to that of phosphorus-rich and fast-growing invertebrates, but also a low mass-specific P-content in cryoconite that has a high available P and the opposite at some glaciers.

The aim of the talk is to provide ideas on using various methodological approaches to facilitate further opportunities for elemental analyses in microinvertebrates and deepen our knowledge of the ecological role of important limno-terrestrial consumers in the rapidly disappearing and changing cryosphere.

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Change is the only constant: comparison of cryoconite communities across a dynamic Alpine glacier

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The iconic feature of glaciers worldwide are cryoconite holes – water-filled depressions filled with dark granules of mineral and organic material. Cryoconite biota metabolises both locally produced, and deposited material which can be then transported out of the glacier surface, potentially impacting downstream and adjacent ecosystems. Given the dynamic nature of the glacier surface, cryoconite holes can collapse and reopen multiple times throughout the melt season, and cryoconite sediment can be found in various forms. While the communities of cryoconite holes are relatively well understood, the knowledge of the biota at various stages of cryoconite sediment degradation is lacking.

This contribution presents research comparing biotic communities, primarily photoautotrophs and their top consumers, in three stages of cryoconite sediment degradation across the ablation zone of a dynamic alpine glacier, Forni. Using an integrative approach linking traditional microscopy with molecular methods and stable isotope analysis, this research aims to advance knowledge on community structure, activity, spatial patterns and trophic dynamics of these understudied, but rapidly changing supraglacial habitats.

Shedding light on the processes following the formation and transitions of cryoconite sediment, and exploring the differences in their characteristics is crucial for further understanding and contextualising their role in the light of glacier retreat. Investigating these systems through the lense of trophic ecology provides a valuable insight into the role of biotic interactions within the supraglacial processes.

Besides presenting the preliminary results, the aim of this contribution is to inspire discussion about multifocal approaches that can be taken in studying microscopic communities in dynamic glacier habitats and the possible role of biotic controls in primarily abiotically driven ecosystems.

Small organisms, large ranges? Molecular diversity and biogeographic structure of bdelloid rotifers in cryoconite holes

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Cryoconite holes harbour diverse microscopic metazoans whose distributions provide an opportunity to investigate dispersal and population differentiation across spatially fragmented glacier habitats. Previous analyses of cryoconite rotifers have revealed substantial mitochondrial diversity and several molecular lineages occurring across geographically distant Arctic regions. However, broad geographic occurrence does not necessarily imply genetic homogeneity, and the spatial structure hidden within widespread lineages remains largely unexplored. Here, we first reassessed molecular lineage delimitation in a dataset of approximately 1000 cytochrome c oxidase subunit I (COI) sequences of cryoconite rotifers using complementary distance-, tree- and coalescent-based approaches, including ASAP, ABGD, PTP and GMYC. Rather than treating any single partition as definitive, we compared the degree of agreement among methods and used the resulting operational hypotheses to identify well-supported and geographically informative lineages. We then focused on one well-represented MOTU occurring across multiple Arctic regions and analysed its fine-scale geographic structure using haplotype relationships and spatial population analyses. The haplotype network revealed a combination of geographically restricted and geographically shared variants. Some haplotypes were associated predominantly with particular regions, whereas others occurred across distant localities, producing a spatial pattern inconsistent with either complete geographic isolation or unrestricted homogenisation. Spatial Analysis of Molecular Variance (SAMOVA) was used to evaluate whether sampling localities could be grouped into geographically coherent

genetic units and to quantify differentiation among these groups. These results reveal a hierarchical biogeographic pattern in cryoconite rotifers: molecular delimitation identifies distinct evolutionary lineages at a broad scale, while variation within a widespread lineage reveals additional geographic structure that would remain invisible from occurrence data alone. Our findings suggest that long-distance dispersal and regional differentiation can operate simultaneously in microscopic glacier inhabitants, challenging simple interpretations of widespread Arctic distributions as evidence of unrestricted connectivity.

Strong spatial structuring of diatom communities across Antarctic cryoconite holes.

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Cryoconite holes are water-filled depressions on glacier surfaces that harbor diverse microbial communities, including diatoms. Because of their environmental simplicity and similarity across space, cryoconite holes make excellent model systems for investigating microbial community assembly. Yet, cryoconite diatom communities remain poorly studied, especially in Antarctica.Here, we use cryoconite holes to investigate spatial variation in diatom communities across the Antarctic Peninsula and Continent. Using a combination of microscopy and rbcL metabarcoding, we assessed patterns in their diversity and community composition across space.

We found well-developed communities present in the Antarctic Peninsula and parts of West and East Antarctica, while they were absent from the subregions in Queen Maud Land. Communities were dominated by a small number of taxa, with six genera accounting for ~95% of diatom valves. Genera Psammothidium and Humidophila were the most abundant and widespread, while Muelleria and species of Luticola showed more restricted distributions. Counterintuitively, genus richness was significantly higher in Continental Antarctica, and strong differences in community composition were present across subregions and even among nearby glaciers. While 44% of genera were shared between regions, nearly 90% of species were region-specific, indicating high taxonomic turnover. Molecular data broadly supported morphological patterns at the genus level, identified 66 diatom ASVs across 13 genera. Dominant genera such as Psammothidium showed low ASV diversity, whereas less abundant taxa such as Nitzschia exhibited higher ASV diversity.

These results highlight pronounced spatial structuring of cryoconite diatom communities across Antarctica, with differentiation occurring not only between regions but also at fine spatial scales. This suggests that local processes and microhabitat variability may play an important role in shaping these communities, alongside broader biogeographic patterns.

Coastal Evolution and Benthic Palaeoecology of Central Svalbard During the Early to Mid-Holocene

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When examining the post-glacial development of High Arctic coastlines, the scientific focus often falls heavily on broad, regional climate shifts. However, in highly dynamic coastal environments, intense local geomorphology can completely override that regional climate signal. This research reconstructs the environmental and ecological evolution of central Svalbard's Billefjorden during the Pleistocene-Holocene transition, integrating relative sea level modelling, coastal sedimentology, and bivalve sclerochronology to tease apart the physiological benefits of regional warming from the severe constraints of local environmental stress.

By radiocarbon-dating subfossil whale bones and utilizing high-resolution GIS, we quantified an exceptionally rapid Early Holocene glacio-isostatic land emergence of approximately 3 cm per year in Petuniabukta. This extreme uplift forced a continuous shoreline regression that shrank the local marine area by 33%. As the basin rapidly reshaped, dynamic Gilbert- and Hjulström-type deltas prograded into the restricted Mimerdalen embayment, establishing a highly unstable nearshore environment.

The fossil record within these raised marine terraces reveals a distinct four-stage ecological succession. Crucially, the discovery of thermophilous taxa like *Arctica islandica* and *Zirfaea*

crispata advances their known regional arrival to roughly 10.4 cal. ka BP, highlighting the rapid Early Holocene advection of warm Atlantic Water via the West Spitsbergen Current.

Yet, this regional warmth did not guarantee local benthic survival. Independent morphometric and sclerochronological analyses of over 1,600 *Mya truncata* shells demonstrated this contrast vividly. In stable, open-fjord settings like Kapp Ekholm, these bivalves thrived with robust lifespans of up to 35 years. Conversely, populations trapped in the restricted, unstable deltaic environments exhibited heavily stunted growth, altered phenotypic plasticity, and severely reduced lifespans.

This multi-proxy synthesis ultimately challenges linear, climate-driven palaeoecological paradigms. While the Holocene Thermal Maximum provided the potential for high biodiversity, massive influxes of glacial meltwater and extreme seabed instability acted as absolute ecological bottlenecks. Local geomorphology is the ultimate determinant of High Arctic benthic survival, providing a vital historical analogue for understanding the modern warming and freshening of Svalbard fjords today.

Development of the Ferdinandbreen foreland

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Climate warming drives rapid glacial retreat and landscape transformation across Svalbard. Ferdinandbreen, a valley glacier in Petuniabukta, located near the Czech Arctic Research Station, has lost over 90 % of its Little Ice Age climax volume. This poster presents two complementary studies investigating surface and subsurface dynamics in the newly exposed foreland.

The first study focuses on the geomorphological evolution of the deglaciated foreland. By combining in situ sediment sampling, ground-penetrating radar (GPR) profiling, and UAV photogrammetry with the analysis of archival imagery, it aims to reconstruct terrain elevation changes since the Little Ice Age and evaluate slope instabilities.

The second study investigates subsurface processes, focusing on the expected development of the permafrost active layer in the newly exposed area. In Petuniabukta, this layer thaws to a depth of 0.5 to 1.2 m during the summer, reacting rapidly to air temperature fluctuations. This work aims to evaluate the temperature evolution within this active layer and assess the impact of permanent deglaciation on its thermal regime.

Together, these studies deepen the understanding of contemporary paraglacial landscape changes in central Svalbard, provide a baseline for future research, and demonstrate the rapid transitions expected across small Arctic glacier forelands facing imminent ice loss.

Novel lasso peptide from Antarctic microbial mat, produced by heterologous expression

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Lasso peptides are bacterial ribosomally synthesized and post-translationally modified peptides (RiPPs) with a lasso-like structure. While their N-terminus is engaged in a macrolactam bond, their C-terminal part is threaded through the macrolactam ring. This makes them recalcitrant to degradation and, hopefully, feasible as orally-administered peptide pharmaceuticals. Their biosynthesis in bacteria involves a cluster of three genes coding a precursor peptide (usually labeled A), a leader peptidase (B) and a lasso cyclase (C).

Here, we report on a journey that started by sampling of environmental DNA on James Ross Island and led to the discovery of a new lasso peptide. Metagenomic DNA extracted from different samples of microbial mats was sequenced using both long-read and short-read sequencing technologies. After sequencing data processing and sample prioritization, the biosynthetic gene clusters (BGCs) were detected using antiSMASH, resulting in the identification of a putative lasso peptide BGC. Lasso peptide BGC was directly cloned from environmental DNA and assembled into an expression plasmid pET28a(+). Consequent transformation of the plasmid into *E. coli* BAP1 host enabled heterologous expression of the biosynthetic pathway, leading to an accumulation of the expected peptide within the cells. Follow-up extraction and analyses using MALDI-TOF-MS and LC-ESI-QTOF-MS confirmed the presence of a cyclic peptide, consistent with the expectation for the mature lasso peptide.

Because this is the first lasso peptide from terrestrial Antarctic ecosystem, we named it antanodin. As far as we know, this is the first heterologously expressed RiPP from Antarctic land. Given the remoteness of Antarctic environment and possible divergent evolution of natural product repertoires, there is a potential for many more interesting discoveries in different fields of study, including microbial ecology and biotechnologies.

Evaluation of electromagnetic induction for estimating active layer thickness on James Ross Island, Antarctica

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Monitoring active layer thickness (ALT) and soil moisture on the Antarctic Peninsula provides an important indicator of climate change in one of the fastest-warming regions. In addition to conventional manual active layer probing, ALT can be estimated using non-destructive geophysical instruments. Electromagnetic induction (EMI) techniques can cover large areas in a relatively short time. The CMD-MiniExplorer 6L device was used in three lithologically different study sites in ice-free areas on James Ross Island in combination with ground-truth measurements of ALT and volumetric water content (VWC). The correlation between geophysical data and VWC ranged from moderate (r = 0.58) to weak (r = 0.24 and r = 0.31). ALT estimates from most of the inverted 2D profiles were lower than those obtained by manual probing. However, the geophysical data showed a clear response to a geological boundary at one of the study sites. These results indicate that EMI can detect subsurface geological variability, but its ability to reliably estimate ALT from 2D inverted profiles was limited at the investigated sites.

The CINCA project - Climate change Impacts on Nutrient and Carbon Allocation in soils of maritime Antarctica

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The CINCA project is intended to shed light on the impact of climate change on nutrient and carbon allocation in soils of maritime Antarctica. Antarctica is a unique ecosystem. While being one of the "simplest" global environments, shaped by only a few factors and minimal anthropogenic influence, Antarctica is home to highly specialized species that have adapted over millions of years to the local harsh conditions, cold temperatures, and limited availability of nutrients and water. Where the ice sheet is interrupted, Antarctic land surfaces are covered by sparse vegetation systems of cryptogams (mosses, lichens, cyanobacteria) and by biological soil crusts (symbiotic communities of photoautotrophic and heterotrophic microorganisms). Together, they are the main contributors to organic matter accumulation in Antarctic soils and are therefore also closely linked to the local carbon and nutrient cycling. However, the distribution of C, N, and P is influenced not only by biotic but also by abiotic factors. Landscape geomorphology, underlying bedrock minerals, and soil physical structure, through processes such as mineral weathering and soil aggregate formation, also contribute to these dynamics. Soil organic matter (SOM), as a source or sink of carbon and nutrients in Antarctic soils, is present in different forms: either as mineral-associated OM (MAOM) or as particulate OM (POM). While MAOM is closely bound to minerals and therefore less bioavailable, POM consists of light organic particles, mostly derived from plant residues, that are more constantly subject to decomposition. The highly specialized ecosystems of Antarctica are considered particularly vulnerable to climatic changes. Temperatures in the Antarctic Peninsula are rising faster than the global average, which is expected to alter biological activity, water dynamics, and the extent of ice cover. These factors influence the local vegetation, the presence and activity of biocrusts, and the overall soil biogeochemistry, which will, in turn, influence the carbon and nutrient allocation. However, so far, only a few studies have focused on the complex interactions between soils, vegetation, and microorganisms in regulating C, N, and P allocation in terrestrial Antarctic ecosystems under climate change. We aim to address these knowledge gaps in the current and future biogeochemical functioning of Antarctic soils. This will provide novel insights into vegetation-soil interactions and nutrient cycling in Antarctic environments under the influence of climate change, and may also improve our knowledge of comparable ecosystems in the Arctic and high-mountain areas, which are likewise undergoing substantial changes through ongoing glacier retreat.

Abstract book

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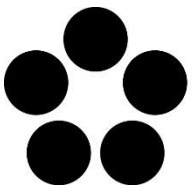

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