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**Ecological processes associated with the glacial-  
proglacial ecosystem transition**

**Ekosystémové změny spojené s odledňováním**

Doctoral thesis

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## Abstract

Ongoing deglaciation in the Arctic is rapidly exposing and mobilising organic matter (OM) overridden by previous glacial advances, releasing an important biogeochemical legacy into downstream ecosystems. This thesis investigates the critical interface between glacial and proglacial zones, bridging the gap between inferred subglacial dynamics and measurable proglacial processes. Analysis of freshly thawed subglacial sediments from a wide range of retreating Arctic glaciers reveals that subglacial OM is extensively degraded by in situ microbial activity, with the resident microbial community structure correlated with  $^{14}\text{C}$  age and decomposition stage of the organic substrate. These sediments provide sufficient phosphorus but limited nitrogen and labile carbon for early proglacial succession. Analysis of microbial assemblages exported from Arctic glaciers shows how microbial processes in the subglacial ecosystem are linked to subglacial hydrological evolution and dependent on local energy sources and identifies specific taxa as sensitive indicators of hidden subglacial microhabitats often undetectable via bulk chemistry analysis. Finally, experimental simulations of deglaciation and the associated ecosystem transition demonstrate that mixing distinct glacial substrates induces non-additive priming effects: anoxic conditions significantly enhance  $\text{CH}_4$  production, whereas oxic conditions suppress it. Collectively, these findings establish the subglacial environment as a biogeochemical precursor that shapes the trajectory of proglacial ecological succession, with an important role of the increasingly connective supraglacial ecosystem in the process.

## Abstrakt

V souvislosti s aktuálním rapidním ústupem arktických ledovců dochází k mobilizaci organické hmoty, která byla v minulosti překryta během expanze ledovců, čímž dochází k uvolňování biogeochemicky významného materiálu do navazujících ekosystémů. Tato práce zkoumá kritické rozhraní mezi glaciální a proglaciální zónou a překlenuje mezeru mezi nepřímo odvozenou subglaciální dynamikou a přímo měřitelnými proglaciálními procesy. Analýza subglaciálních sedimentů z ledovců napříč Arktidou odhaluje, že vyskytující se organická hmota je značně degradována mikrobiální aktivitou *in situ*, přičemž struktura přítomného mikrobiálního společenstva koreluje s radiouhlíkovým stářím a stupněm rozkladu organického substrátu. Tyto sedimenty obsahují dostatečné množství fosforu, avšak nedostatek dusíku a labilního uhlíku, což může vést k limitaci rané proglaciální sukcese. Analýza mikrobiálních společenstev vyplavovaných z arktických ledovců ukazuje, že mikrobiální procesy v subglaciálním ekosystému jsou provázané s vývojem hydrologie a dostupností lokálních zdrojů energie. Zároveň identifikuje specifické taxony jako citlivé indikátory skrytých mikrobiotopů pod ledovci, které jsou běžnou chemickou analýzou vody často nedetekovatelné. Experimentální simulace odlednění a souvisejícího přechodu mezi ekosystémy dále demonstrují, že mísení odlišných glaciálních substrátů vyvolává neaditivní „priming“ efekty: anoxické podmínky významně stimulují produkci metanu (CH<sub>4</sub>), zatímco oxické podmínky ji potlačují. Tato zjištění souhrnně definují subglaciální prostředí jako biogeochemický prekurzor, který udává trajektorii ekologické sukcese proglaciálního ekosystému, zatímco důležitost propojení se supraglaciálním ekosystémem stoupá.

## Acknowledgement

This thesis has been a long time coming and would have been impossible to complete without the help and support of many individuals to whom I am deeply grateful.

I wish to thank my supervisor, Marek Stibal, for establishing the CryoEco research group; an inviting environment where the curiosity to understand underlying processes and publish unique, relevant research is prioritized above all else. I would like to thank the members of CryoEco: Kristýna Vrbická, Lia Wentzel, Jade Hatton, Anna Stehrer Polášková, Philip Píka, Arthur Fouillé, Jakub Žárský, Tyler Kohler, Lukáš Falteisek, and Jakub Trubač, for keeping me sane and motivated throughout the years. My sincere thanks go to my international collaborators and friends: Jacob Yde, Petra Luláková, Jon Hawkings, Alun Hubbard, Guillaume Lamarche-Gagnon, Stefan Hofer, Marie Bulínová, and the CH<sub>4</sub> Arctic Drill Team. You have taught me a great deal, challenged me when necessary, offered new perspectives, and brought laughter to lengthy days of fieldwork. I also thank the members of the Department of Ecology for creating a supportive space for discussion and growth, while providing new opportunities for students.

Last but not least, I would like to thank my family, and especially my husband, for his unwavering support over the years and for looking after our dog for months straight while I was digging through mud, water, and ice in the Arctic. Oh, and, of course, thanks to curling, CrossFit, and other sports... so my physical and mental resilience in the field was rarely in question, and so I can always tackle the stairs to the 3<sup>rd</sup> floor office no matter what.

## Declaration

I declare that this thesis has not been submitted for the purpose of obtaining the same or any other academic degree earlier or at another institution. My involvement in the research presented in this thesis is expressed through the author order of the included publications/manuscript, and is detailed in the *Author's contribution statements*. All literature and other sources used when writing this thesis have been properly cited.

## Prohlášení

Prohlašuji, že žádná část této práce nebyla použita k získání stejného nebo jiného akademického titulu, dříve nebo na jiné instituci. Mé zapojení ve výzkumu uveřejněném v této práci je vyjádřeno pořadím autorů zahrnutých publikací / manuskriptů, podrobněji pak v rámci *Author's contribution statements*. Veškerá literatura a další použité zdroje jsou řádně odcitovány.



Petra Klímová

In Prague, 14 January 2026

## List of Chapters and Author's Contribution Statements

### CHAPTER I.

**Vinšová P**, Kohler TJ, Simpson MJ, Hajdas I, ... & Stibal M (2022) The Biogeochemical Legacy of Arctic Subglacial Sediments Exposed by Glacier Retreat. *Global Biogeochemical Cycles*.

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*Conceptualization: PV, TJK, JCY, JDŽ, MS, Funding acquisition: PV, TJK, MS, Investigation: PV, TJK, MJS, IH, JCY, LF, JDŽ, TY, VT, FM, EH, MS, Methodology: MJS, IH, JCY, VT, MS, Supervision: MS, Visualization: PV, Writing – original draft: PV, JCY, MS.*

I led this study, participated in sample collection, evaluated results, and wrote the manuscript with help from all co-authors.

\* Recognized as the top 10 most-cited article among work published in GBC between 1st Jan 2022 – 31st Dec 2023.

### CHAPTER II.

Kohler TJ, **Vinšová P**, Falteisek L, ... & Stibal M (2020) Patterns in Microbial Assemblages Exported From the Meltwater of Arctic and Sub-Arctic Glaciers. *Frontiers in Microbiology*.

DOI: 10.3389/fmicb.2020.00669. Citations: **33**.

*TK, JŽ, JY, and MS conceived of the project. TK, PV, JŽ, JY, LF, GL-G, EH, KC, and MS performed the fieldwork and collected samples. TK, PV, GL-G, JŽ, and LF performed molecular laboratory work. LF performed bioinformatics analyses. JRH and JEH performed all geochemical analyses. TK analyzed the data and wrote the manuscript with significant input and editing from all co-authors.*

I participated in the sample collection, laboratory work, result evaluation, and manuscript preparation.

### CHAPTER III.

**Klímová P**, Yde JC, Skoblia S, & Stibal M (*submitted*) Enhanced microbial CH<sub>4</sub> production as a response to simulated deglaciation.

*PK and MS conceived the project. PK and JCY obtained funding and conducted fieldwork. PK and SS did laboratory work. PK analyzed data. MS supervised the project. PK wrote the manuscript with significant help from MS and JCY. All authors contributed on editing and finalization of the manuscript.*

I led this study, obtained funding, collected samples and did laboratory work. I analysed the data and wrote the manuscript with help from all co-authors.

### CHAPTER IV.

Znamínko M, Falteisek L, Vrbická K, **Klímová P**, ... & Stibal M (2023) Methylophilic communities associated with a Greenland Ice Sheet methane release hotspot. *Microbial Ecology*.

DOI: 10.1007/s00248-023-02302-x. Citations: **6**.

*MS conceived the project; KV, PK, JRC, CJJ, and MS conducted field work; MZ, LF, KV, and PK did laboratory work, bioinformatic processing, and statistical analyses; JRC and CJJ provided CH<sub>4</sub> measurement data; MZ and MS wrote the manuscript. All authors commented on previous versions of the manuscript and all authors read and approved the final manuscript.*

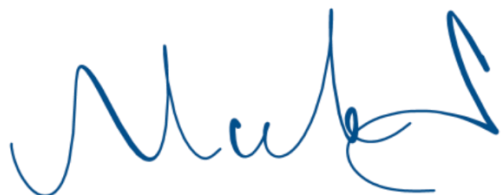
I participated in the study preparation, sample collection, laboratory work, result evaluation, and manuscript preparation.

## Letter of Consent

Dear members of the dissertation committee,

I hereby declare that Petra Klímová has made a significant contribution to the publications which I led as senior author. I concur with the Author's Contribution Statements.

Sincerely,

A handwritten signature in blue ink, appearing to read 'Marek Stibal', with a stylized flourish at the end.

Marek Stibal, Ph.D.

# 1 Introduction

The cryosphere occupies a substantial portion of the Earth's surface, with glaciers and ice sheets collectively covering ~10 % of Earth's terrestrial area (Meredith et al. 2019). Glaciers and ice sheets are no longer viewed as sterile ice masses but are recognized as active ecosystems and biogeochemical factories (Hawkings et al. 2025) that play vital roles in regional and global biogeochemical cycles (Anesio and Laybourn-Perry 2012, Hodson et al. 2008, Stibal et al. 2020).

Within a frozen environment, liquid water is an essence of life. Its presence in glacial ice reflects the heat budget and the structure of the hydraulic system, allowing water to exist as separate channels, pockets, veins or thin films located in interstices or along ice and grain boundaries (Hodson et al. 2008). However, most biological activity within glacial environments occurs not in the ice itself but rather in the supraglacial (surface) and subglacial (bed) zones that, although vastly different in many aspects, serve as the primary hubs for microbial life and support the highest concentrations of biomass and metabolic turnover within the glacial system (Achberger et al. 2017, Edwards & Cameron 2017, Hodson et al. 2008).

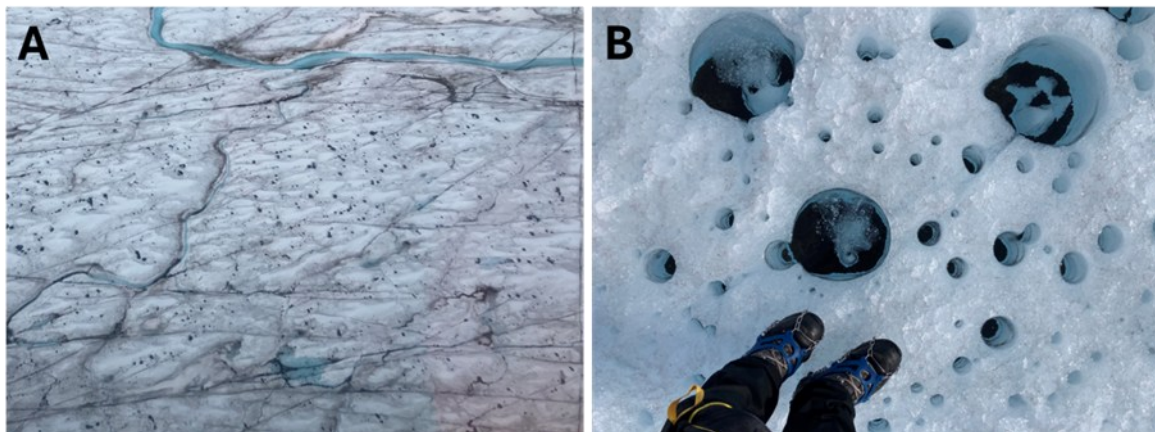
## *Supraglacial ecosystems*

The supraglacial environment in the ablation zones of glacier surfaces acts as a dynamic network of aquatic and semi-aquatic habitats (**Fig. 1**). Particles deposited on glacial surface are usually darker than the surrounding ice and consequently reduce its albedo (surface reflectivity), inducing ice melt and, eventually, creating water-filled depression called cryoconite holes (Cook et al. 2015, Takeuchi 2002). Cryoconite holes are recognized as biodiversity hotspots on glaciers (**Fig. 1B**), supporting a wide range of microorganisms (i.e., bacteria, archaea, algae, fungi, ciliates, and invertebrates) with unique species and community structure (Franzetti et al. 2017, Rozwalak et al. 2022, Stibal et al. 2015a, 2020, Zawierucha et al. 2019). The abundances of microbial cells found in cryoconite vary between  $10^6$  and  $10^9$  cells  $g^{-1}$  (Bagshaw et al. 2012, Stibal et al. 2015a).

Highly active phototrophs (cyanobacteria and algae) produce autochthonous organic matter (OM) by fixing inorganic carbon (IC) from the atmosphere (Stibal et al. 2012a, Yallop et al. 2012). Heterotrophs then mineralize the labile organic carbon (OC) produced but also degrade more recalcitrant wind-blown OC from surrounding (or distant) terrestrial habitats, while scavenging oxygen (Bhatia et al. 2010, Margesin et al. 2002, Ponięcka et al. 2018, Sanyal et al. 2020, Xu et al. 2010). Biological activity within the supraglacial ecosystem during the summer melt season is considerable; the *in situ* primary production and respiration rates may match those measured in soils in much warmer and nutrient richer regions (Anesio et al. 2009). Much less is known about the activity during the Arctic winter season, when air temperatures are below freezing point and there are months of total darkness. It is expected that microbes are in a state of dormancy for prolonged time but can resume activity within 24 hours after thawing (Bradley et al. 2023). With the shifting Arctic climate and thus more melting events observed during winter season, microbial activity would favour respiration and anaerobic processes and could push supraglacial environments into acting predominantly as a carbon

sources. Therefore, cryoconite holes may act as both carbon sources and sinks, depending on the community structure, environmental conditions, and possibly also the distance from the edges that is affecting the availability of allochthonous OC sources, as well as supraglacial hydrological features (Hodson et al. 2008, Stibal et al. 2010, 2012a).

Life in the supraglacial environment is characterized by specific metabolic adaptations to consistently low temperatures around freezing point and fluctuating physical conditions like solar radiation and hydraulic washout. Although the glacier surface appears mostly aerobic, anaerobic microenvironments may develop in the depth of accumulated cryoconite within cryoconite holes, especially within large mature cryoconite granules (Poniecka et al. 2018, Segawa et al. 2020, Uetake et al. 2016, 2019). Anaerobes exploit the redox gradients and establish populations and communities within the anoxic inner core, avoiding the aerobic outer layer supporting phototrophs and oxygen-rich surrounding environment (Pittino et al. 2023, Segawa et al. 2020). The concerted metabolic activities of the supraglacial guilds, spanning from photosynthetic CO<sub>2</sub> fixation to oxidative and reductive decomposition, effectively render the glacier surface a dynamic and biogeochemically diverse ecosystem (Anesio et al. 2009, Stibal et al. 2012a).

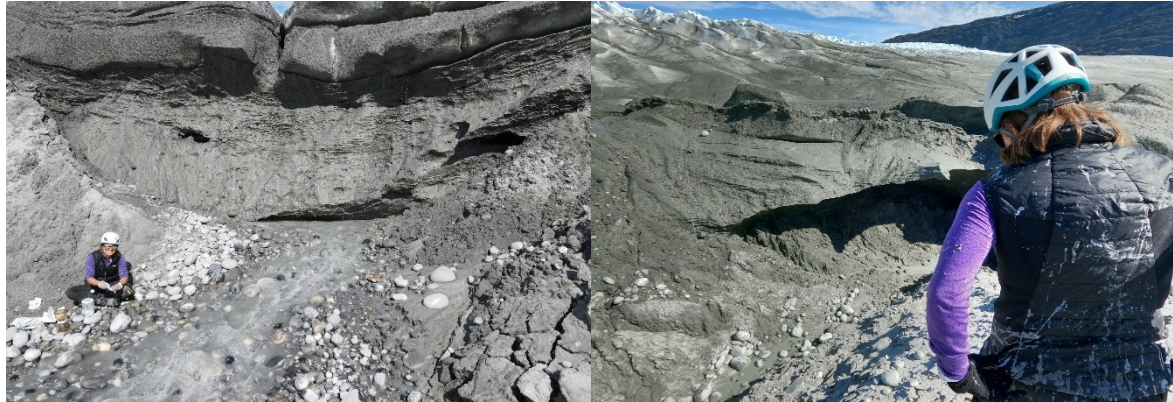


**Figure 1.** Glacier surface (A) with supraglacial streams, cracks, meltwater pools, cryoconite holes, and debris-covered weathered ice. Close-up to cryoconite holes (B) of various width and remains of ice-lids – note the middle one with entrapped bubbles of gas. Photos by the author.

### *Subglacial ecosystems*

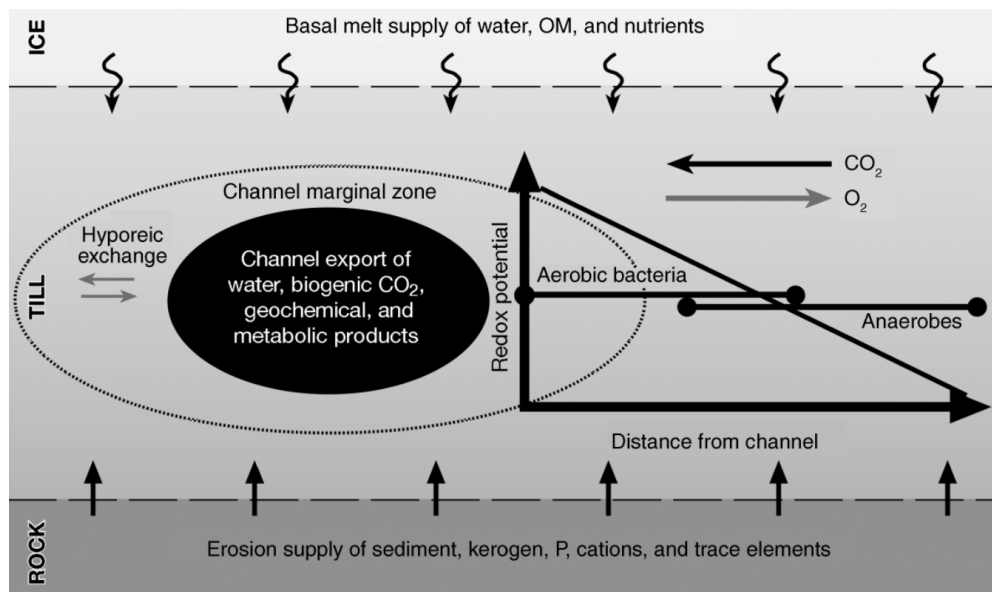
In contrast to the glacier surface, the subglacial environment formed at the ice-bed interface constitutes a realm isolated from the atmosphere (Wadham et al. 2008, 2019). Here, the microbial oxidation of legacy OM (see the *Glacial organic matter* section) and sulfide minerals, combined with geothermal heat flux, can deplete dissolved oxygen to create widespread sub-oxic or anoxic conditions (Bottrell & Tranter 2002, Burns et al. 2018, Tranter et al. 2005, Wadham et al. 2004). Complex thermal and rheological gradients characterize the subglacial environment, creating significant spatiotemporal variability across the ice-bed interface (Menziés & Shilts 2002). This physical heterogeneity supports a diverse array of microbial habitats, including saturated soft sediments (Hofstede et al. 2023), linked cavities (Clarke 2005, Walder 1986), and subglacial lakes (Livingstone et al. 2022, Wilson et al. 2025). These zones function as biogeochemical reactors, maintaining microbial communities within aquifers that remain hydraulically distinct from the high-energy channels dominating meltwater export.

The isolation, low temperature and darkness make subglacial environment uninviting yet still, the sediments underneath glaciers and ice sheets (**Fig. 2**) are host to unique and diverse communities of microorganisms, although at low cell densities ( $10^5$ – $10^6$  cells  $g^{-1}$ ; Stibal et al. 2012b). Despite the logistical challenges to properly describing and characterizing subglacial ecosystems, insights can be gained via ice drilling and sediment coring (Christ et al. 2021, Christner et al. 2014) and subglacial outflows exporting products of subglacial processes (Lawson et al. 2014, Hawkings et al. 2014, Skidmore et al. 2005, Wadham et al. 2010).



**Figure 2.** Sampling of minor subglacial outflow (left) showing glacier front and the sediment-rich basal ice. An overview on the exposed ice-bed interface (right), and thawing basal-ice sediments, with glacier surface peaking at the back. Photos by CryoEco's Jakub Žárský and Anna Stehrer Polášková.

Subglacial chemolithoautotrophic microbial communities oxidize reduced iron, sulfur, and nitrogen compounds to fuel primary production at the glacier bed (Achberger et al. 2017, Boyd et al. 2014, Christner et al. 2014, Hamilton et al. 2013, Skidmore et al. 2000). This metabolic activity is sustained by the interaction of basal water and glacier sliding, which comminute bedrock into fine-grained ‘glacial flour’ characterized by highly reactive surfaces (Tranter et al. 2002, Wadham et al. 2010). Consequently, glacial erosion continually supplies the labile minerals and elements (such as Fe,  $SO_4^{2-}$ , and  $H_2$ ) required by chemolithotrophs (Hawkings et al. 2014, Telling et al. 2015, Tranter et al. 2002, Wadham et al. 2010). The availability of reactive surfaces fosters strong mineral-microbial associations, making the sediment surface the primary habitat rather than the water column (Skidmore et al. 2005). Furthermore, legacy OM buried beneath ice during glacier advance, supplemented by labile OC produced *in situ* via chemolithoautotrophy and, potentially, exported from the surface via meltwater (Irvine-Fynn et al. 2021, Stibal et al. 2012a), provide an important substrate for heterotrophic metabolism and nutrient cycling within waterlogged subglacial habitats away from the main subglacial channels (Wadham et al. 2019). According to Tranter et al. (2005), the proximity to active subglacial drainage channels determines the availability of electron acceptors. Well-oxygenated sediments near channels support aerobic respiration, while the transition to distributed drainage systems creates anoxic environments that favour denitrification, metal reduction, and methanogenesis (**Fig. 3**). Isotopic data further imply that these distinct metabolic zones may overlap due to the presence of anoxic microenvironments, allowing syntrophic associations and cyclic oxidation-reduction to occur even in broadly aerated sediments (Grasby et al. 2003, Wadham et al. 2004).



**Figure 3.** Conceptual model of how microbial community functioning is likely to change from largely aerobic processes in the sediments that are within active drainage channels to sub-oxic/anaerobic processes such as denitrification,  $Fe^{3+}/Mn^{4+}/SO_4^{2-}$  reduction, and eventually methanogenesis at increasing distances away from oxygenated channels. In the channel marginal zone, regular (diurnally fluctuating) exchanges take place between pore waters in the till and channel waters otherwise in transit. From Hodson et al. (2008).

Under anoxic conditions typical for subglacial environments, the final step of OM degradation is methanogenesis, the biological production of methane ( $CH_4$ ) by methanogenic Archaea. This process proceeds via three pathways: hydrogenotrophic methanogenesis, which reduces carbon dioxide using  $H_2$ ; acetoclastic methanogenesis, which disproportionates acetate into  $CH_4$  and  $CO_2$ ; and methylotrophic methanogenesis, which utilizes methylated compounds such as methanol and methylamines (Thauer et al. 2008, Liu & Whitman 2008). Produced  $CH_4$  may be stored under the ice (Weitemeyer & Buffett 2006) and/or released into basal meltwater and subsequently exported through drainage channels to escape the subglacial lockdown (Dieser et al. 2014, Lamarche-Gagnon et al. 2019, Pain et al. 2021). However, the net release of  $CH_4$  is modulated by biological filters, particularly at the anoxic-oxic interface, such as the top layer of subglacial sediment (Pika et al. *in review*) where  $CH_4$  encounters oxygen-rich meltwater. Oxygen is introduced into the system either via basal ice melting or directly through supraglacial meltwater supply. This supports the activity of methanotrophic bacteria, which oxidize  $CH_4$  to  $CO_2$ , acting as a crucial biological sink that potentially mitigates atmospheric emissions (Adnew et al. 2025, Burns et al. 2018, Conrad 2009, Michaud et al. 2017). Furthermore, non-methanotrophic methylotrophs may outcompete methanogens for methylated substrates under (sub-)oxic conditions, diverting methanol or methylamines toward aerobic respiration (Chistoserdova et al. 2009). Both functional groups have been detected in elevated abundance within  $CH_4$ -supersaturated glacial outflows (Dieser et al. 2014, Vrbická et al. 2022), suggesting a potential metabolic shift from methanogenic to methanotrophic states following changes in redox conditions.

### *The Arctic amplification*

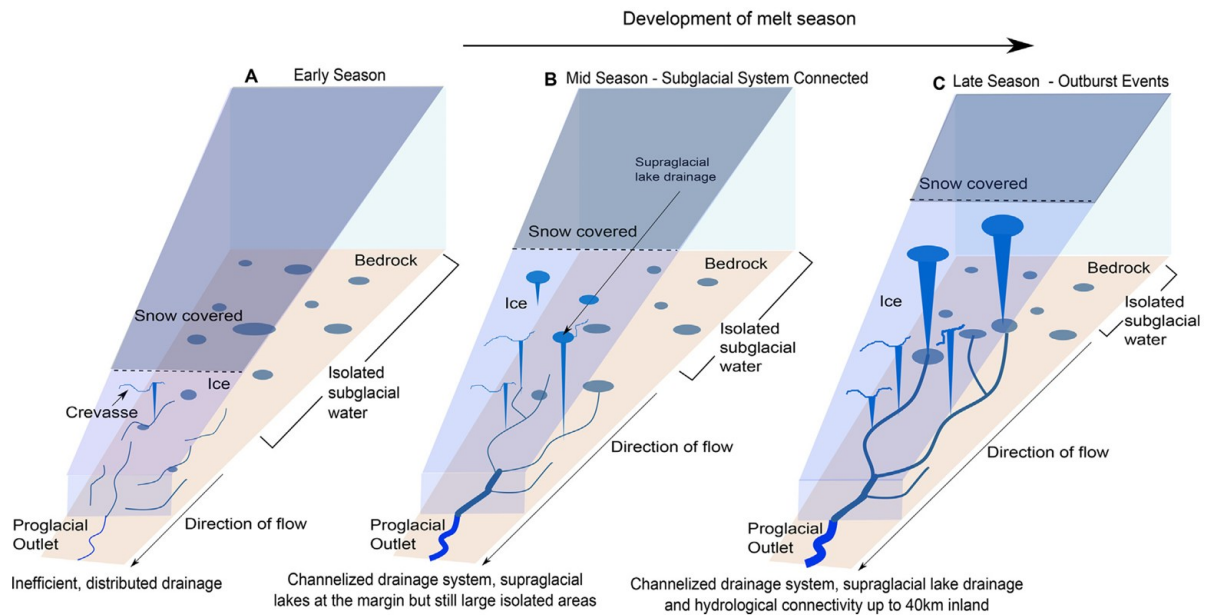
The stability of glacial habitats and ecosystems is being disrupted by the accelerated warming of the Arctic, which is significantly outpacing the global average. Since 1979, the Arctic region has warmed nearly four times faster than the rest of the planet (Rantanen et al. 2022). Snowfall

is more frequently being replaced by rainfall events during wintertime (Adakudlu et al. 2019), triggering widespread snowmelt and water pooling and refreezing, shifting the Arctic ecosystems' functioning (Bradley et al. 2025). This Arctic amplification is exacerbated by powerful feedback loops, including the loss of sea ice and the darkening of glacier surfaces, both of which lower the Earth's albedo and increase heat retention in the ocean (Serreze & Barry 2011, Stroeve & Notz 2018, Tedesco et al. 2016). As a result of increasing air temperature, glaciers worldwide have been losing  $273 \pm 16$  Gt in mass annually since 2000, with a 36% decadal-increasing rate (The GlaMBIE Team 2025).

In addition to ice loss and sea level rise, the increased melt rates and retreat of glaciers cause a significant shift in ecological functioning, affecting both the glacial and downstream ecosystems (Fox-Kemper et al. 2021, Hawkings et al. 2025, Hotaling et al. 2017, Milner et al. 2017). For example, the Greenland ice sheet (GrIS) has been experiencing intensified and prolonged melt seasons (Hanna et al. 2021), a higher proportion of precipitation as rainfall (Doyle et al. 2015), and an expansion of the ablation area in the last decades (Noel et al. 2019, Ryan et al. 2019, Stibal et al. 2012a), resulting in the spatial and temporal expansion of the supraglacial ecosystem and its increasing connectivity with the subglacial and other downstream ecosystems.

### *Seasonal melt and glacier hydrology*

The seasonal melt begins with the transition from a highly reflective snow-covered ice surface to a darkened bare ice surface (Box et al. 2012). During this period, the bare-ice area is marked by the presence of a porous ice weathering crust (Irvine-Fynn et al. 2021). This porous surface delays the runoff of supraglacial meltwater (Smith et al. 2017) and provides a habitat for microbes within its photic zone (Christner et al. 2018). As the season advances, the ablation zone moves up glacier, expanding the total biologically favourable area and further decreasing glacier-wide albedo, while increasing surface melt (Box et al. 2012, Ryan et al. 2019). Supraglacial inorganic and organic debris, including microbes and nutrients, are carried downslope by the supraglacial meltwater drainage network that develops during the melt season (Smith et al. 2015). Supraglacial streams often end in moulins, which provide an access to the subglacial environment (Chudley et al. 2019, Yang & Smith 2016). For example, Irvine-Fynn et al. (2021) emphasized the contribution of cellular carbon flushed from the GrIS weathering crust each summer, estimating a flux of up to  $37 \text{ kg km}^{-2}$  down to the ice-bed interface. Moreover, unusual weather patterns increasing air temperature over GrIS may trigger high surface melt events, thawing tens of centimetres of surface ice within a few days (*personal observation, July 2021*) and flushing out cryoconite from destroyed holes and pools, which can substantially increase the flux of labile OM into the subglacial environment.



**Figure 4.** Diagram illustrating the concept of subglacial hydrology development as the melt season progresses. Subglacial drainage is getting less isolated (distributed, **B**) and more connected (channelized, **C**) as higher volume of meltwater is introduced from the surface with season progress. ‘Isolated subglacial water’ aka subglacial wetlands with waterlogged soft sediments. ‘Bedrock’/soft sediments. Note that the volume of water is size-indicated. From Hatton et al. (2019).

Concurrently, the dynamics of subglacial hydrology is undergoing rapid changes driven by increased supraglacial meltwater input (**Fig. 4**). While basal melting and subglacial water flow persist year-round, primarily sustained by frictional heating (Karlsson et al. 2021), the seasonal influx of meltwater is accelerating the expansion and efficiency of subglacial drainage networks. High meltwater input increases basal water pressure and facilitates the transition from an inefficient distributed drainage system to a more efficient, channelized hydrological network (Chandler et al. 2013), which can be spatially different from year to year (Rada & Schoof 2018). This shift enhances water flow rates and connectivity beneath the ice, influencing ice dynamics, sediment transport, and may tap into subglacial microbial habitats.

Large areas of waterlogged soft sediments, isolated cavities, and subglacial lakes, the presumed sites of high microbial activity and organic carbon transformation (Achberger et al. 2016, Lamarche-Gagnon et al. 2019, Livingstone et al. 2022), may get interconnected as a result of evolving subglacial drainage (Nienow et al. 2017). These lacustrine or wetland-like areas may be rapidly flushed out during so-called ‘subglacial outburst’ events, when previously isolated regions at the bed become evacuated downstream (Andrews et al. 2014, Driedger & Fountain 1989, Gray et al. 2024, Hoffman et al. 2016). Later in the season, as surface meltwater input declines, subglacial water pressure drops significantly and the efficiency of the drainage system diminishes (Rada & Schoof 2018). Subsequently, late-season meltwater entering the subglacial drainage may be retained under the ice in isolated cavities and pools for over-wintering. Supraglacial microbes may establish in such pools and deplete nutrients and dissolved organic carbon (DOC) over the course of several (undisturbed) months (Dubnick et al. 2023). The variability of subglacial hydrology thus regulates both the connectivity of subglacial habitats and the residence time of water, determining the physical constraints on biogeochemical processing at the glacier bed.

### *Glacial organic matter*

OM in glacial ecosystems has various sources with distinct characteristics. It can be autochthonous, produced *in situ* via microbial autotrophy on or beneath the glacier, or allochthonous, from aeolian deposits (i.e., anthropogenic and biomass combustion, wind-blown terrestrial OM) and also as ‘legacy carbon’ (Wadham et al. 2019).

As ice sheets and glaciers expanded in the past during cold climate periods, they overrode and incorporated soils, vegetation, and lacustrine and marine sediments (Wadham et al. 2019). For example, the amount of particulate organic carbon (POC) under the GrIS is estimated to be 0.5–27 Pg C, mainly of ancient paleosol origin (Wadham et al. 2019). As the most recent example of OM burial, major deglaciation occurred along the W margin of the GrIS during the so-called Holocene Climate Optimum (HCO; ca 9-5 ka BP) (Box et al. 2022, Hatton et al. *in revision*), when ice retreated beyond the current margin, enabling vegetation growth and accumulation of fresh OM in proglacial areas. These areas were then overridden by (re-)advancing ice during the late Holocene. Today, we can observe the result of the mineralization of overridden OM in the form of CH<sub>4</sub> released along the GrIS margin (Christiansen & Jørgensen 2018, Dieser et al. 2014, Hatton et al. *in revision*, Lamarche-Gagnon et al. 2019, Pain et al. 2021). In contrast, further inland from the current margin, overridden tundra and/or boreal forest from warmer Pleistocene Interglacial periods may be well preserved and incorporated within basal ice (Bierman et al. 2024, Christ et al. 2021, Souchez et al. 1997). While the bed of the ice sheet offers (quasi)stable environment that enhances the preservation of terrestrial remains and unaltered character of OM (Christ et al. 2021), dynamic marginal glacier-specific processes such as glacier comminution, freeze-thaw cycles, and entrainment of oxygen-rich meltwaters may support OM transformation and biological degradation.

Glacial OM is (if not directly mineralised) released into subglacial runoff in both the particulate and dissolved form (POM/DOM), from which we can infer its sources, degradation, and/or age of origin (Kohler et al. 2017). Recently, Holt et al (2024) focused on glacier DOM worldwide, and found a highly heterogenous pool of OC compounds assigned mostly to microbial origin. Collected glacier DOM exhibited high contents of aliphatic and heteroatom-containing formulae (peptide-like), while the content of polyphenolic and condensed aromatic compounds was relatively low (Holt et al. 2024). The high heteroatom formulae contents correspond to energy-rich, highly bioavailable OM (Behnke et al. 2021, Lawson et al. 2014b), while the aliphatic-rich composition and low aromaticity suggests a microbial origin and limited input from unprocessed soils and vegetation (Bhatia et al. 2010, Kellerman et al. 2021). However, the sources and character of glacial OM can have temporal variability over the melt season, linked to the seasonal evolution of the drainage system (see previous section), mobilization of ancient subglacial OM, and shifts in the magnitude and sources of autochthonous production and atmospheric deposition (Dubnick et al. 2017, Kellerman et al. 2020, Lawson et al. 2014a, Musilova et al. 2017, Spencer et al. 2014). Kellerman et al. (2020) found that the composition of DOM exported from Leverett Glacier (SW GrIS) shifts from subglacial sources with a dominant terrestrial signal in the early melt season towards microbially sourced OM during peak melt season, after efficient subglacial drainage has been established. Such OM may be produced also under the ice, in isolated areas of long water residence time, only to be accessed by the expanding subglacial drainage, and subsequently evacuated into the main drainage following a water pressure drop (Kellerman et al. 2020, Kohler et al. 2017). While most studies focus on DOM (and DOC) in glacial runoff, only a handful of studies have analysed the

particulates (POM and POC) that are more likely to be derived from glacier bed via the erosion of the bedrock and overridden OM (Lawson et al. 2014a, Stibal et al. 2012b). Due to the high amount of sediment load, the particulate fraction may represent the majority (70–93 %) of glacially exported C (Bhatia et al. 2013, Lawson et al. 2014a). Moreover, terrestrial plant lipid character and total extractable lipid concentration decrease as particle size diminishes (Meyers & Ishwitari 1993), making the particulate fraction of OM better in characterizing subglacial OM archive. However, POC might not be directly biologically available in comparison with DOC in meltwater, as it may contain less reactive mineral-associated and recalcitrant OM. Highly recalcitrant OM may also be photodegraded on the glacier surface, which increases its aliphatic content and bioavailability downstream (Doting et al. 2025, Holt et al. 2021). Despite the dominance of POC in glacial export budgets, its ultimate fate remains poorly constrained. While the glacially-derived dissolved fractions appear highly bioavailable even when aged (Hood et al. 2009), the role of organic particulates as either a refractory sink or a delayed source of C likely depends on its *in situ* processing, such as recycling to more bioavailable composites.

### *Microbial assemblages as bioindicators of glacial processes*

Microbial assemblages exported by glacial runoff provide robust biological proxies for subglacial physicochemical conditions and drainage evolution (Cameron et al. 2017a, Tranter et al. 2005), retaining information frequently obscured in bulk hydrochemical datasets. Unlike solute concentrations which represent integrated signals subject to dilution, microbial assemblage composition data contain the distinct signatures of discrete subglacial microhabitats. This enables the identification of metabolic hotspots where resident populations proliferate prior to export. For example, the detection of methanogens and methanotrophs in oxygenated outflows (Dieser et al. 2014, Lamarche-Gagnon et al. 2019), or sulfur and iron-oxidizing chemolithotrophs, indicates the drainage of upstream anoxic sediments and syntrophic communities adapted to local redox potentials (Bottrell & Tranter 2002, Cameron et al. 2017b, Wadham et al. 2004, 2010). Conversely, phototrophic cyanobacteria serve as a tracer for supraglacial inflow, delineating hydraulic connectivity between the photosynthetically active surface and the aphotic bed (Cameron et al. 2017a, Dieser et al. 2014).

### *The glacial-proglacial transition zone*

Glaciers are retreating at unprecedented rates, transitioning from marine- to land-terminating, exposing thousands of kilometres of new coastal areas (Kavan et al. 2025), enlarging proglacial areas and opening them for ecological succession and pedogenesis (Heckmann et al. 2016). The termini of retreating glaciers have often been considered an ecological point zero, which implies a new pristine environment. It has, however, become evident that it is not an initial stage but rather a continuation of the glacial ecosystem legacy left behind by the retreating glaciers (Bardgett et al. 2007, Bradley et al. 2016, Edwards et al. 2013, Kaštovská et al. 2007, Rime et al. 2016). Glacial recession exposes subglacial sediments and deposits supraglacial debris, providing both a physical substrate and a microbial inoculum for the emerging ecosystem. Consequently, the proglacial habitat is supplied with legacy carbon, nutrients, minerals, and microbial biomass, and thus effectively primed for ecological succession. Pioneering microbial communities originate mostly from endogenous subglacial and

supraglacial habitats rather than from exogenic atmospheric deposition (Rime et al. 2016; **Fig. 5**), with the chemolithoautotrophs dominating over the heterotrophs in early stages after deglaciation (Bradley et al. 2016). A large portion of microbes in glacial environments may be inactive (Bradley et al. 2023, Stibal et al. 2015b), awaiting their time in a strategic dormancy stage (Bradley et al. 2025), to establish populations and communities upon deglaciation in proglacial habitats.



**Figure 5.** An example of the glacial-proglacial ecological transition. Left: moss growing on the glacier surface as a ‘glacier mouse’, and right: establishing in the glacier foreland on fine glacial till following glacier retreat (photos by CryoEco; Bøverbreen, Norway, 2016).

Glacially deposited substrates fuel pioneering microbes, which initially consume old legacy carbon (Bardgett et al. 2007). This reliance is mirrored in the functional microbiome: early communities possess genes for degrading recalcitrant organic matter, while later stages shift toward utilizing labile, plant-derived inputs (Feng et al. 2023). Nitrogen dynamics follow a similar necessity; as finite legacy pools are exhausted (Göransson et al. 2011), diazotrophs establish in the earliest soils (Bradley et al. 2016, Kaštovská et al. 2005, Nemergut et al. 2007), enabling a transition from the mineralization of legacy N to active N<sub>2</sub>-fixation (Brankatschk et al. 2011, Ollivier et al. 2011). Concurrently, phosphorus pools shift from mineral sources (Hawkings et al. 2016) to organic forms (Bernasconi et al. 2011, Turner et al. 2007), eventually driving the ecosystem from N/C co-limitation to P-limitation (Göransson et al. 2011, Jiang et al. 2019, Yoshitake et al. 2007).

Moreover, the geomorphic instability of glacial foreland acts as a primary filter for biological colonization, as physical factors may postpone or entirely reset successional processes (Wojcik et al. 2021). Consequently, ecological succession occurs in a patchy manner, restricted to (semi-)stable proglacial habitats that offer protection from geomorphic activity, such as hydrological wash-out or wind erosion, and instead increase water retention and temperature stability (Wojcik et al. 2021). Additionally, the heterogeneity of the foreland creates distinct aquatic and semi-aquatic habitats, such as proglacial lakes with potential subglacial history (Livingstone et al. 2015), and meltwater streams, which provide an alternative aquatic environment for exported microbial communities (Cameron et al. 2017b, Mindl et al. 2007).

### *Downstream ecosystems*

Glacial runoff serves as a critical vector for biogeochemical export, conveying bioavailable dissolved organic matter and reactive glacial flour that stimulate downstream heterotrophy (Hawkings et al. 2014, Hood et al. 2009). Beyond solutes, these hydrological pathways disseminate subglacial microbial assemblages and dissolved greenhouse gases, effectively transplanting subglacial biogeochemical potential to proglacial environments (Cameron et al. 2017a, Lamarche-Gagnon et al. 2019, Hotaling et al. 2017). Where suspended sediments settle, particularly in stream banks, proglacial fluvial ponds and lakes (Grider et al. 2025, Liu et al. 2024), they create distinct microenvironment that support anaerobic metabolisms, including methanogenesis (Brosius et al. 2024, Cameron et al. 2017b). However, accelerated glacier shrinkage is rapidly destabilizing these inputs. The associated shifts in meltwater flux (Milner et al. 2017, Zemp et al. 2016), lake expansion (Shugar et al. 2020), sediment and OM transport regimes (Holt et al. 2023, Hood et al. 2008, Pryer et al. 2020, Zhang et al. 2022) fundamentally alter resource delivery, threatening the resilience and biodiversity of these specialized cryospheric communities (Anesio et al. 2009, Boetius et al. 2015, Edwards et al. 2014, Stibal et al. 2020).

## 2 Aims and Objectives

This thesis aims to investigate the fragile interface between the glacial and proglacial zones, bridging the observational gap between inferred subglacial dynamics and the directly measurable proglacial processes. The research focuses on three central objectives:

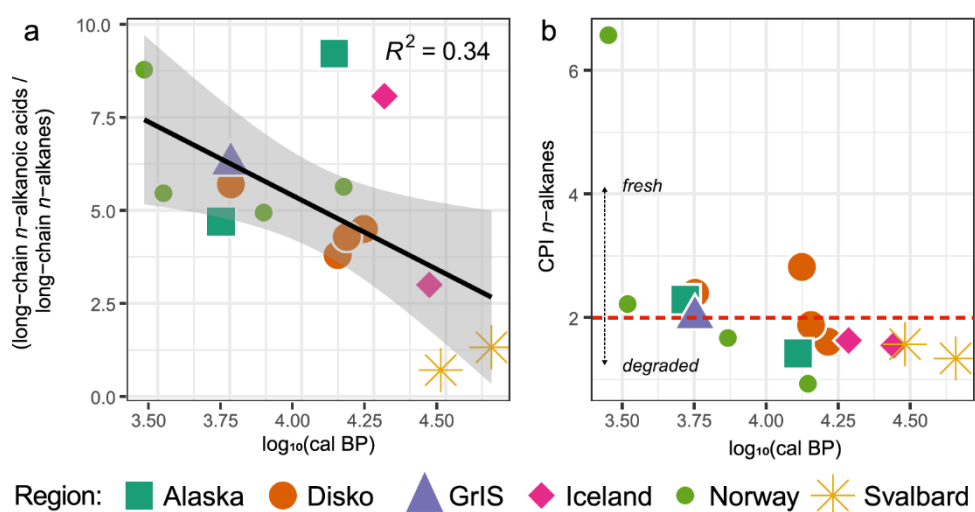
- Characterizing the subglacial biogeochemical legacy: To define the properties and provenance of subglacial POM in freshly exposed sediments, establishing how this legacy material determines the trajectory of early proglacial ecosystem development (**Chapter I**).
- Evaluating exported assemblages as bioindicators: To analyse exported microbial assemblages and determine the extent to which they reflect specific subglacial processes, thereby elucidating the unique insights these biological tracers provide into the subglacial environment (**Chapters II and IV**).
- Simulating deglaciation dynamics: To experimentally simulate the physical mixing of glacial substrates during deglaciation (and retreat), quantifying the response of CH<sub>4</sub> production and consumption pathways under different redox regimes (**Chapter III**).

This thesis explores the complex links between climate-driven deglaciation and the associated ecological changes, driven by microbial communities adapted to the cryospheric environment. **Chapter I** (Vinšová et al. 2022) characterizes the biogeochemistry of subglacial sediments to define the ‘legacy package’ of OM, nutrients, and microbial cells transferred to the onset of the proglacial trajectory. **Chapter II** (Kohler et al. 2020) then examines microbial assemblages in glacial runoff of a similar set of glaciers as that studied in Chapter I, to assess the regional diversity patterns and their utility as bioindicators of the subglacial conditions. **Chapter III** (Klímová et al. *submitted*) employs laboratory incubation experiments to simulate deglaciation, tracking C mineralization and CH<sub>4</sub> dynamics across a simulated gradient of anoxic and oxic zones present under and in front of retreating ice. Finally, **Chapter IV** (Znamínko et al. 2023) zooms in on a CH<sub>4</sub>-supersaturated glacier outflow and exported microbial assemblages associated with the GHG turnover.

Collectively, this thesis synthesizes the complex interactions between the subglacial legacy substrates, the microbial mediators of their transformation, and their metabolic products, to assess how these glacial inputs shape the ecological trajectory of the emerging proglacial landscape.

### 3 Extended Summary

Research in **Chapter I** (Vinšová et al. 2022) demonstrates that subglacial sediments Arctic-wide constitute substantial reservoirs of OM, predominantly derived from ancient terrestrial vegetation overridden during past glacial advances. This subglacial recalcitrant C pool was found to be majorly degraded (**Fig. 6**), indicating significant in situ processing, which is in contrast to better preserved OM released from thawing permafrost. This quality directly shapes the resident microbiome; the dominant taxa such as *Delftia*, *Rhodoferrax*, and *Polaromonas* are likely selected for their metabolic versatility, possessing the capacity to degrade complex organic substrates and switch between oxic and anoxic life strategies.

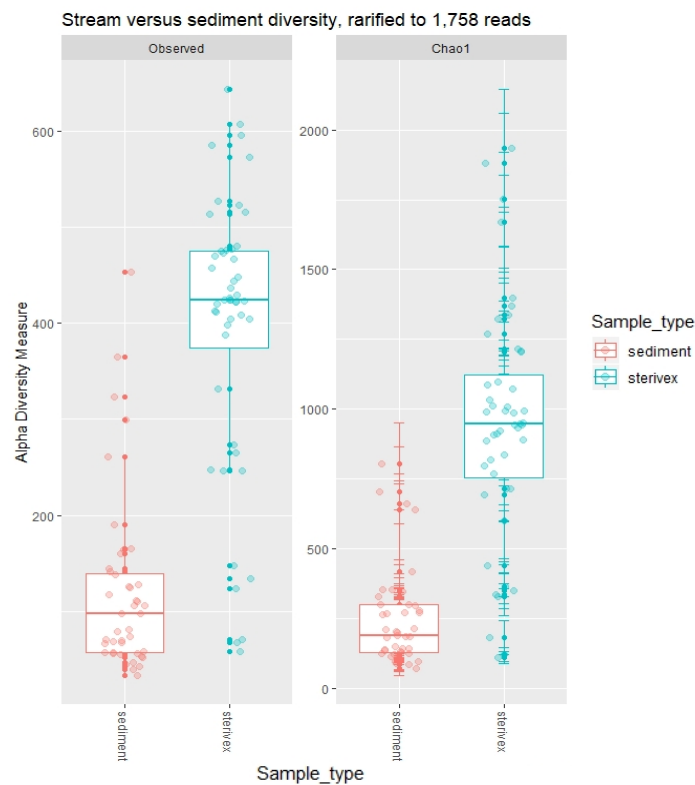


**Figure 6.** Degradation of OM based on the ratio of long-chain *n*-alkanoic acids to long-chain *n*-alkanes (**a**) and the CPI of *n*-alkanes over the cal.  $^{14}\text{C}$  age (**b**) of subglacial sediments. From Vinšová et al. 2022.

While these core taxa are primed to utilize legacy resources immediately upon exposure, the sediment matrix likely harbours a diverse ‘seed bank’ of less abundant, dormant taxa that resume metabolic activity only after environmental conditions shift (Bradley et al. 2025, Lloyd et al. 2021). The transition to the proglacial environment therefore acts as an environmental trigger for groups such as *Actinobacteria*, which are less abundant in the subglacial microbiome but successfully colonize proglacial soils (Bradley et al. 2016, Kaštovská et al. 2007). Furthermore, OM provenance appears to be a deterministic driver of community assembly; while species richness decreased with increasing  $^{14}\text{C}$  age and degradation state, the community structure was significantly controlled by  $^{14}\text{C}$  age, OM/mineral P fraction, and organic carbon (OC) content. OC content was also identified as a driver for structuring the exported microbial assemblages in **Chapter II** (Kohler et al. 2020), which focused on suspended sediment in outflows of a similar glacier set as that in Chapter I. Collectively, the findings from Chapters I & II confirm that OC acts as a critical environmental filter for (sub-)glacial microbial communities, where both quantity and biological reactivity dictate which taxonomic subsets successfully proliferate.

However, a distinct contrast between bulk and suspended sediments (Chapter I, and II, respectively) emerged regarding latitudinal influence. While the diversity of exported assemblages was negatively correlated with increasing latitude, this gradient was absent in bulk sediments. This discrepancy likely reflects the connectivity of meltwater to surface

environments; higher temperatures and productivity at lower latitudes enhance supraglacial inputs, factors that are effectively decoupled from the dark, isolated subglacial beds. Moreover, these differences highlight the integration scale of the sampling methods. While bulk sediment samples represent localized point sources, glacial runoff integrates inputs from the wider catchment, evacuating sediments from evolving drainage networks and capturing a broader cross-section of the subglacial diversity (Kohler et al. 2017, Lamarche-Gagnon et al. 2024). Consequently, exported assemblages consistently yielded higher diversity than their bulk sediment counterparts (**Fig. 7**).

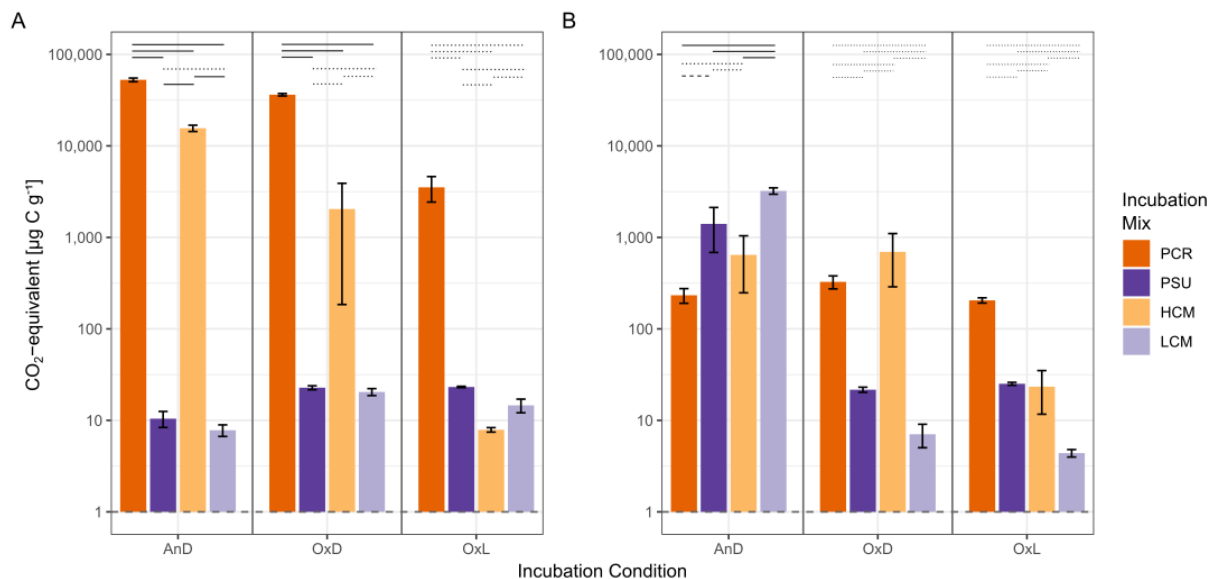


**Figure 7.** Comparison of richness (Observed) and diversity (Chao1) of bulk subglacial sediments (sediment) and suspended sediment (sterivex) in glacial outflows. Compilation of microbial data from Chapter I & II.

Exported microbial assemblages can serve as indicators of subglacial processes not necessarily reflected in bulk water chemistry (Chapter II). Proxies for subglacial weathering, including total suspended sediments (TSS) and pH, help identify the subglacial origin of exported taxa. *Thiobacillus* sp and *Rhodofera* sp appear to be sourced from these habitats, with the latter also dominating bulk subglacial sediments (Chapter I, Žárský et al. 2018). In contrast, other taxa show no correlation with functionally associated chemical signatures, which suggests the existence of ‘microhabitats’ within the glacial system, such as localized areas accessed by evolving subglacial drainage (Kohler et al. 2017). While the specific chemical signature of such zones is diluted in the bulk meltwater, the specialized taxa exported from them persist as biological tracers.

Subglacial sediments located away from active meltwater channels are frequently anoxic and primed for anaerobic metabolism. Where organic matter or H<sub>2</sub>/CO<sub>2</sub> substrates are available, methanogenesis can drive elevated methane concentrations at subglacial portals (Christiansen & Jørgensen 2018, Lamarche-Gagnon et al. 2019). Furthermore, exported anaerobes in suspended sediments may establish and produce CH<sub>4</sub> in downstream ecosystems, such as

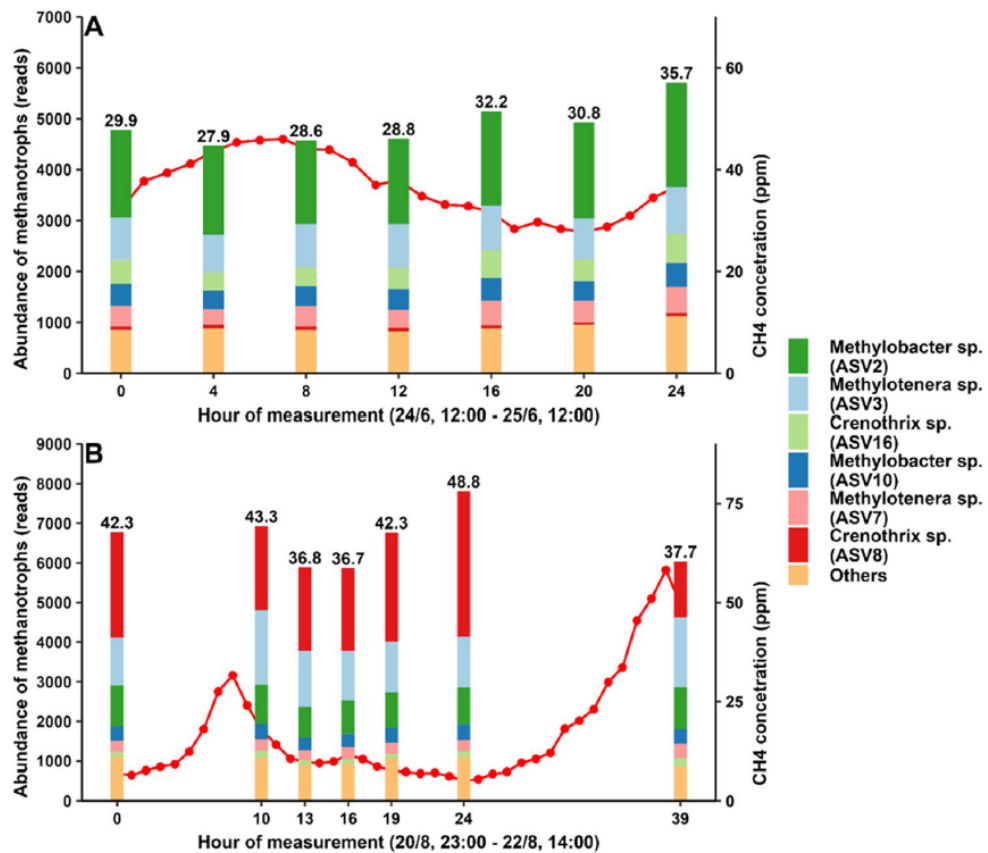
proglacial lake sediments (Brosius et al. 2024) and stream banks (Cameron et al. 2017b). These habitats, however, receive mixed glacial inputs, where the addition of labile organic matter likely stimulates production. **Chapter III** (Klímová et al. *submitted*) investigates this interaction by mixing subglacial sediments with cryoconite to simulate sediment coalescence during deglaciation. While baseline activity varied by substrate type and site, the mixing of these distinct carbon pools consistently enhanced anaerobic methane production (**Fig. 8**). This study utilized substrates from Svalbard, where currently, to the best of my knowledge, only geologic methane export is reported from a glacier outflow (Kleber et al. 2024). Our results demonstrate that the metabolic potential for methanogenesis is present within these glacial substrates.



**Figure 8.** The CO<sub>2</sub>-equivalent [µg C g<sup>-1</sup>] showing radiative forcing of released CO<sub>2</sub> and CH<sub>4</sub> from incubation microcosms utilizing substrates from Nansenbreen (A) and Sefströmbreen (B) experimental sites. Mean value ± SE; note the log<sub>10</sub> scale of the y-axis. Significant difference between incubations within similar conditions is indicated by solid line (p < 0.001), dashed line (p < 0.05), and dotted line (n.s.). From Klímová et al. *submitted*.

In natural environment, however, ideal conditions for methanogenesis may swiftly change into ideal conditions for methanotrophy, as oxygen is supplied by meltwater that is often evacuating CH<sub>4</sub> from places of origin (Dieser et al. 2014). Similar conditions, where O<sub>2</sub> and CH<sub>4</sub> meet, can be also found on water-sediment interface in proglacial waterlogged habitats. **Chapter III** further focuses on such environments by incubating mixed sediments in oxic conditions. These conditions limited CH<sub>4</sub> production and yielded higher abundance of methylotrophs and methanotrophs. This shows that glacial substrates may be primed for both processes and that the environment selects, as observed in glacier forelands shifting from methanogeny to methanotrophy (Bárcena et al. 2010). We found methanogens similar to those previously reported from subglacial sources, such as representatives of *Methanosarcinales* and *Methanomicrobiales* (Chapter IV, Boyd et al. 2010, Dieser et al. 2014, Lamarche-Gagnon et al. 2019, Stibal et al. 2012b); these methanogens may thus represent cryospheric specialists, also able to establish within river banks downstream (Cameron et al. 2017b). Methylotrophs were represented by e.g., *Methylophilus* sp and *Methylotenera* sp, which are highly abundant in glacial outflows (Kohler et al. 2020, Vrbická et al. 2022) and can dominate the exported microbial assemblage of CH<sub>4</sub>-supersaturated runoff (Chapter IV). The abundance of

methanogens was extremely low in the incubations (<1 %), even in the highly productive ones, which is surprising and should be acknowledged in further research.



**Figure 9.** Changes in the abundance of top 6 methylotrophs from subglacial portal samples within sampling days in June (A) and August (B). Red lines correspond to CH<sub>4</sub> concentration measured in the air. The average concentration of CH<sub>4</sub> in June was 38.7 ppm (28–53 ppm). The average concentration of CH<sub>4</sub> in August was 19.2 ppm (5–58 ppm). The number above the column shows the RA of methylotrophs in %. From Znamínko et al. 2023.

Methylotrophic communities may be highly abundant in glacial outflows, especially when there is continuous CH<sub>4</sub> export from under the ice. In **Chapter IV** (Znamínko et al. 2023), we zoom in on the microbial assemblage exported by one of the GrIS CH<sub>4</sub> release hotspot (Christiansen & Jørgensen 2018). Here, methylotrophs constituted approximately 30 % of the microbial communities exported, dominated by type I methanotrophs from the Gammaproteobacteria class. While the relative abundance of methylotrophs increased over the melt season, likely reflecting the evolution of subglacial drainage system, so as the abundance of specific taxa (**Fig. 9**). While early melt season was characterized by methanotrophs (such as *Methylobacter* sp), high melt season included an increased abundance of methylotrophs (such as *Methylophilus* sp). *Methylophilus* sp is likely not able to directly utilize CH<sub>4</sub>; instead, it can benefit from syntrophic interactions with methanogens (van Grinsven et al. 2021) or utilize methylated substrates produced by OM degradation, which may be in indirect competition to methylotrophic methanogens. This taxon is omnipresent in glacial outflows (Chapter II, Dieser et al. 2014, Vrbická et al. 2022) and was found also in bulk subglacial sediments (Chapter I) and the mixing incubation (Chapter III) further confirming its ecological importance in the (sub-)glacial ecosystem. The findings in Chapter IV indicate that subglacial CH<sub>4</sub> release hotspots host microorganisms capable of mitigating the CH<sub>4</sub> emissions.

## 4 Conclusions and Future Perspectives

The central message of this work is that **the subglacial environment is an essential biogeochemical precursor for proglacial ecological succession.**

The main conclusions of this thesis are as follows:

- Arctic subglacial OM is primarily derived from terrestrial vegetation overridden by glacial advance and is extensively degraded due to *in situ* microbial processing.
- The degradation state of this legacy C determines microbial community structure, selecting for taxa specialized in metabolizing recalcitrant substrates.
- The specific stoichiometry of subglacial sediments, characterized by advanced C degradation and relatively high P content, imposes a C and N co-limitation regime at the onset of proglacial succession.
- Exported microbial assemblages...
  - can be used as indicators of glacial hydrological routing, and subglacial processes not reflected in bulk chemistry;
  - from subglacial methane hotspots are dominated by methylotrophs, indicating the potential to mitigate emissions at the glacier margin;
  - exhibit distinct spatiotemporal variability, driven by the seasonal evolution of subglacial drainage networks.
- Supraglacial cryoconite, despite its natural oxic environment, has potential to produce significant levels of CH<sub>4</sub> under anoxic conditions.
- Priming of the subglacial sediments with labile cryoconite substrate may both enhance and suppress CH<sub>4</sub> production, depending on redox conditions.

Future advancements in this field hinge critically on successful drilling operations into subglacial ecosystems such as the one beneath the Greenland Ice Sheet interior. Current knowledge relies on the analysis of marginal sediment and glacial runoff, which likely reflect advanced degradation states induced by transport. Accessing the bed upstream of the margin is therefore essential to capture unaltered organic matter signatures and microbial community structures. These pristine samples are requisite for determining precise reaction kinetics in the laboratory. Specifically, the lack of empirical rates for methanogenesis, methanotrophy, and anaerobic oxidation of methane (AOM) remains a significant barrier to accurate modelling of cryospheric CH<sub>4</sub> release. Furthermore, while the provenance of exported DOM is relatively well understood, the particulate fraction remains understudied, despite of it being a dominant C vector. Comparative studies are scarce, and the connectivity of POC age and bioavailability is also highly speculative. Finally, this work focused on prokaryotes, yet the subglacial fungal contribution remains undefined. Given their prominence in supraglacial habitats (Nikitin et al. 2024) and enzymatic capacity for degrading recalcitrant organic substrates, fungi may play an important, yet unacknowledged, role in mobilizing subglacial carbon reserves.

*One never notices what has been done; one can only see what remains to be done. ~Marie Curie-Skłodowska*

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## Appendices



## CHAPTER I.

### *The Biogeochemical Legacy of Arctic Subglacial Sediments Exposed by Glacier Retreat*

Global Biogeochemical Cycles

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Jacob C. Yde, Lukáš Falteisek, Jakub D. Žárský, Tiange Yuan,  
Václav Tejnecký, Filip Mercl, Eran Hood, Marek Stibal

*In this study, we collected and analysed sediments recently exposed by glacier retreat at multiple (sub)Arctic sites to understand their biogeochemical role in early proglacial ecosystems. We show that the character of subglacial sediment is determined by local glaciation history and bedrock lithology and argue the organic substrates originate mainly from overridden terrestrial vegetation and are degraded in situ by the resident microbial communities.*



## CHAPTER II.

### *Patterns in Microbial Assemblages Exported from the Meltwater of Arctic and Sub-Arctic Glaciers*

Frontiers in Microbiology

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<https://doi.org/10.3389/fmicb.2020.00669>

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Eran Hood, Karen A. Cameron, Marek Stibal

*This study shows that glaciers export both widespread, cosmopolitan microbial taxa and microbes unique to specific regions, revealing the heterogeneous nature of glacial environments and their associated microbiota. Microbial diversity was greater at lower latitudes, likely attributable to the variety of available niches and greater productivity rather than geographical isolation or dispersal limitation. We argue that microbial assemblages in glacial meltwaters can act as biological tracers for glacial biogeochemical and hydrological processes, offering insights not achievable through meltwater chemistry alone.*



## CHAPTER III.

*Enhanced microbial CH<sub>4</sub> production as a response to simulated deglaciation*

*submitted*

**Petra Klímová, Jacob C. Yde, Siarhei Skoblia, Marek Stibal**

*This study investigates the transformation of glacial organic carbon driven by deglaciation and the resulting interaction between supraglacial and subglacial sediment. We simulated this process in long-term and show that it has a significant effect on microbial OC mineralisation and CH<sub>4</sub> production that is beyond purely additive. In anoxic conditions, CH<sub>4</sub> production was enhanced significantly, probably due to fresh organic substrate from cryoconite supplied to subglacial methanogens; by contrast, oxic conditions resulted in a significant suppression of CH<sub>4</sub> production, especially when combined with light. We argue that the impact of deglaciation and the associated ecosystem transition on carbon cycling will depend on the redox state, and thus hydrological regime of the resultant environments.*



## CHAPTER IV.

### *Methylotrophic communities associated with a Greenland Ice Sheet methane release hotspot*

Microbial Ecology

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*In this study we investigated the microbial communities at a CH<sub>4</sub> release hotspot at the SW margin of the GrIS, finding that methylotrophs made up ~30 % of the exported microbial assemblages, primarily dominated by Methylococcaceae and Crenotrichaceae. Our findings suggest that subglacial CH<sub>4</sub> release sites can be colonized by microbes that consume CH<sub>4</sub> as a carbon source and thus reduce CH<sub>4</sub> emissions.*

