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RESEARCH ARTICLE

Comparative metagenomics of two shallow marine microbial communities in western Greenland

Daniel G. Dick
School of Earth, Environment & Society, McMaster University, Hamilton, ON, Canada

Abstract

Metagenomic profiles of marine microbial communities from Greenlandic coastal waters remain scarce, despite the central role played by this region in discussions of global climate change. This study characterizes the taxonomic and functional structure of two near-shore shallow marine fjord mouth microbial communities from sites in western Greenland that differ in sea-surface temperatures, mean annual ice-coverage levels and annual glacial meltwater flux rates. Results indicate limited taxonomic and functional overlap between these two locations, with significant differences in the normalized abundance of 3372 species (25% of observed taxa) and 620 functional genes (49% of functional genes observed). At Sisimiut, a typical open-water "Baffin Bay" site characterized by moderate sea-surface temperatures, minimal annual sea-ice cover and limited glacial input, the metagenome is dominated by diverse chemolithotrophic taxa, including sulphate-reducing, nitrogen-fixing and methanogenic lineages. At the Ilulissat Icefjord, where low sea-surface temperatures, high turbidity, low salinity and strong glacial influences prevail, the community is less diverse and is dominated by psychrophilic (cold-adapted) bacteria such as *Colwellia hornerae* PAMC 20917. Functional profiles further distinguish these sites: the Ilulissat metagenome is enriched in genes common to ice-associated and cold-adapted metabolisms (e.g., exopolysaccharide biosynthesis, dimethyl-sulphide and dimethylsulfoniopropionate cycling), whereas these genes are comparatively rare at Sisimiut. Together, these data sets provide a descriptive baseline for these two sites and a framework for future comparative studies in the region.

Keywords

Psychrophiles; sea ice; Sisimiut; Ilulissat; eDNA; chemolithotrophic taxa; ice-associated bacteria

Correspondence

Daniel G. Dick, School of Earth, Environment & Society, McMaster University, 1280 Main Street West, Hamilton, L8S 4K1 ON, Canada. E-mail: dickd3@mcmaster.ca

Abbreviations

Cq: quantification cycle
DMSP: dimethylsulfoniopropionate
eDNA: environmental DNA
PCR: polymerase chain reaction
PERMANOVA: permutational multivariate analysis of variance
qPCR: quantitative PCR

To access the supplementary material, please visit the article landing page

Introduction

As summer sea-surface temperatures in the polar regions continue to increase (alongside concomitant changes in ice coverage, seawater pH, partial pressure of CO_2 and nutrient availability), marine microbial communities in these regions are expected to undergo an array of taxonomic and functional changes (Tomanek 2008; Lenoir & Svenning 2015; Seabra et al. 2015; Hutchins & Fu 2017; Macias-Fauria & Post 2018; Baker 2021; Freer et al. 2021). Psychrophilic and cold-adapted microbes structure polar ecosystems via several pathways (Boetius et al. 2015; Buongiorno et al. 2019) and are anticipated to be directly impacted by many of the environmental changes that are predicted to accompany ongoing warming, such as increased sea-surface temperatures (Macias-Fauria & Post 2018; Lauritano et al. 2020). Quantifying and understanding the microbiome-level ecological impacts of ongoing warming in the polar regions is hindered by the relative dearth of published metagenomic profiles in these areas, combined with the overall complexity of microbial communities in these areas. For example, Maccario et al. (2019) noted that microbial communities found within snowpack in a Greenlandic fjord were the result of a complex mixture of terrestrial, atmospheric and marine influences. Similarly, Yergeau et al. (2017)

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noted widespread changes in metagenome composition within the Canadian Arctic, driven by an array of shifting environmental parameters.

Here I compare the taxonomic and functional structure of two microbial communities from fjord mouth sites in western Greenland (Fig. 1). One is an ice-associated shallow-water marine microbial community collected near the Ilulissat Icefjord, in Disko Bay. The other, represented by samples collected near the town of Sisimiut, is a more southerly microbial community in the primarily ice-free Amerloq Fjord. Despite their relative geographical proximity, these two sampling locations experience significant differences in sea-ice coverage, mean sea-surface temperature, glacial meltwater flux and primary productivity (Heide-Jørgensen et al. 2007; Gladish et al. 2015; Sha et al. 2017; Møller et al. 2023). Results indicate significant differences in taxonomic and functional composition between these two sites. While necessarily descriptive because of the small sample size and environmental differences between the two sampling localities, the data sets included here provide a baseline for future metagenomic research in the region.

Methods and materials

Sample collection

Free-floating microorganisms and eDNA were collected at two localities in western Greenland—Sisimiut (66.9369, –53.6981) and Ilulissat (69.2200, –51.1121)—between 16 and 17 August 2023 (Fig. 1). Five samples were collected with a Waterra eDNA Sampling Pump from shore, with seawater being collected at the surface (<10 cm), at each locality. Sampling at a third locality—Kangerlussuaq (66.9663, –50.9489)—yielded significantly fewer reads than the other two localities, potentially because of low biomass and/or the presence of silt in the water, which clogged the filters (Supplementary Table S1). The samples from Kangerlussuaq were therefore excluded from this analysis but are included in the full data set in Supplementary Folder S1 for reference. For each sample, three litres of seawater was pumped through the sterile 0.22 µm eDNA filter (Supplementary Table S2). Following this, 50 ml of Zymo Research DNA/RNA Shield was injected into the filter capsule. Zymo Research DNA/RNA Shield inactivates the collected microorganisms while ensuring soft tissues and eDNA are preserved during transport (Trivedi et al. 2022). To dislodge the collected microorganisms and eDNA, the filter capsule was agitated for 60 seconds (with the capsule being rotated once after 30 seconds) using a Waterra eDNA Filter Shaker. Once agitation was complete, the DNA/RNA Shield—containing preserved microorganisms and eDNA—was transferred to a sterile 50 ml Falcon test tube. The Falcon tubes containing collected microorganisms and eDNA preserved in DNA/RNA Shield were then frozen at –20°C for the remainder of the voyage. Using 4 DNA/RNA Shield precluded the need to store samples at colder temperatures (see Trivedi et al. (2022) for a review of the use of DNA/RNA Shield with samples from the polar regions). Samples

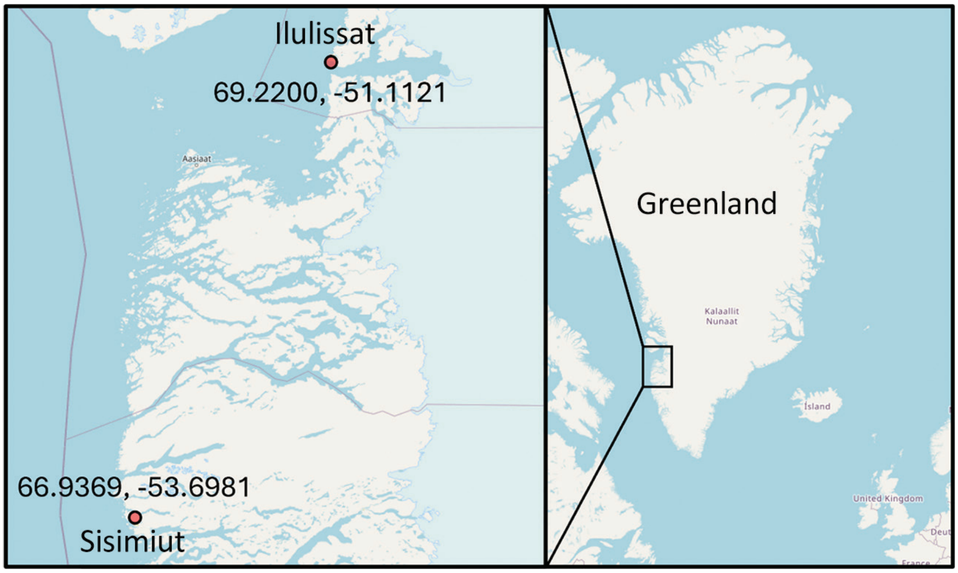

Fig. 1 Sampling sites: the southern sample was collected near the town of Sisimiut, adjacent to the Amerloq Fjord, and the northern sample was collected near the town of Ilulissat, adjacent to the Ilulissat Icefjord. The two locations are separated by approximately 275.9 km (haversine distance), a difference of about 2.28 degrees of latitude.

Table 1 Mean Nonpareil values for each of the three sites discussed here.

Site	κ	C	Library read size	Model R	Target library read size	Diversity
Kangerlussuaq	0.226264	0.256909	5.34E+08	0.999841	5.38E+10	21.10641
Sisimiut	0.400166	0.432892	4.44E+09	0.999765	9.37E+11	22.42186
Ilulissat	0.594248	0.621388	4.27E+09	0.997777	2.46E+11	20.71278

were collected under a non-exclusive licence for non-commercial utilization of Greenland genetic resources (licence no. G23-045), provided by the Government of Greenland (Supplementary material).

Shotgun metagenomic analysis

Shotgun metagenomic analyses and qPCR and were conducted at Microbiome Insights (Richmond, BC, Canada) using the following protocol. DNA was extracted using the Qiagen MagAttract PowerSoil DNA KF kit and a KingFisher robot. DNA quality was evaluated visually via gel electrophoresis and quantified using a Qubit 3.0 fluorometer. To assess DNA quantity and integrity prior to advancing to full metagenomic sequencing, qPCR was performed using standard protocols (Supplementary Folder S2). Amplification was monitored using SYBR Green chemistry, and Cq values were compared against a standard curve (Supplementary Folder S2). As samples from the Kangerlussuaq locality showed high Cq values, indicating very low DNA concentrations (likely the result of low biomass and/or the exceptionally high amount of silt in the water at this site), they were excluded from the remainder of the analysis.

Libraries were prepared using an Illumina Nextera library preparation kit with an in-house protocol. Paired-end sequencing (150 bp × 2) was done using a NovaSeq 6000 instrument. Shotgun metagenomic sequence reads were processed with the Sunbeam pipeline (Clarke et al. 2019). Initial quality evaluation was done using FastQC version 0.11.5 (Clarke et al. 2019). Processing took part in four steps: adapter removal, read trimming, low-complexity-reads removal and host-sequence removals. Adapter removal was done using cutadapt version 2.6 (Martin 2015). Trimming was done with Trimmomatic version 0.36 using custom parameters (LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36; Bolger et al. 2014). Low-complexity sequences were detected with Komplexity version 0.3.6 (Clarke et al. 2019). High-quality reads were mapped to the human genome (Telomere-to-Telomere assembly, T2T-CHM13v2.0, GCF_009914755.1) and those that mapped to it were removed from the analysis. The remaining reads were taxonomically classified using Kraken2 with the PlusPF database version 2022-09-26 (Wood et al. 2019). For functional profiling, high-quality (filtered) reads were aligned against the SEED database (Overbeek et al. 2013) via translated homology search and annotated to subsystems structured into functional levels 1–3 using the Super-Focus tool (Silva et al. 2016).

Statistical analyses

To assess the coverage, that is, the fraction of the population metagenome represented by the metagenome data sets, of the three sets of samples, Nonpareil (Rodriguez-R & Konstantinidis 2014) was used (Table 1, see Supplementary Folder S3 for full results). Results indicate intermediate average coverage values (C) for Sisimiut ($C = 0.432892$) and Ilulissat ($C = 0.621388$). Low average C values ($C = 0.256909$) alongside low average shape parameter values for the redundancy curve ($\kappa = 0.226264$) in the Kangerlussuaq samples corroborate the qPCR results indicating under-sampling at this site, likely due to filter clogging in the highly turbid water at this location (Table 1). The difference between library read size and target library read size for each site suggests that additional sampling would reveal more taxa and/or gene functions (Table 1). Despite this, the moderate coverage values seen for Sisimiut and Ilulissat (Table 1) suggest that most abundant taxa/gene functions have already been sampled, such that additional sequencing will yield only marginal improvements in coverage. In all cases, the level of sequencing needed to reach 95% coverage was infeasible, requiring between 40 and 500 times as much sequencing as what was performed here, depending on the sample (Supplementary Folder S3).

Functional gene abundance was expressed using pseudocounts (wherein counts of an individual functional gene are divided by the number of hits in the complete database) following the method described by Silva et al. (2016). To account for differences in sampling depth and composition between different samples, DESeq2 normalization, that is, geometric means (Love et al. 2014), was used to normalize taxon read counts and functional gene pseudocounts. Low-abundance taxa were retained, with DESeq2 normalization being used to avoid biasing the comparison towards differences in extremely rare taxa. To quantify differences in the distribution of taxa and functional genes between localities, pairwise dissimilarities were calculated using the Bray-Curtis index (Bray & Curtis 1957), and samples were compared using PERMANOVA (Anderson 2001), using functions from the vegan *R* package (Oksanen et al. 2024). Comparisons of functional genes were made using the Level 3 SEED Subsystem (Overbeek et al. 2013). Alpha diversity of samples was quantified using the Shannon index (Shannon 1948) and compared between locations using the Kruskal–Wallis chi-squared test (Kruskal & Wallis 1952). Finally, to better understand the differences between these two localities, Wald tests (Wald 1943) were used to test for significant differences in the normalized abundance of specific taxa and specific functional genes, using the DESeq2 *R* package (Love et al. 2014).

Environmental properties

Samples were collected at the Sisimiut site at 15:00 on 16 August 2023. Samples were collected at the Ilulissat site at 11:30 on 17 August 2023. Whereas in situ measurements of sea-surface temperature (8.3 °C) and salinity (27.8 ppt) were made at the Ilulissat site, they were not done at the Sisimiut site. Copernicus Marine Service remote sensing data supplemented the missing environmental measurements from the Sisimiut site, and expanded on those collected at Ilulissat (Fig. 2; Supplementary Folder S4). The remote sensing-based estimates of monthly mean sea-surface temperature and salinity for August 2023 are consistent with the measurements collected during fieldwork at Ilulissat on 17 August 2023, suggesting that the Copernicus Marine Service data can be used as an estimate of surface-level environmental parameters when in situ measurements are not available (Supplementary Folder S4). Mass concentration of chlorophyll-*a* in sea water (a measure of primary productivity), the volume attenuation coefficient of downwelling radiative flux in sea water (KD490, a measure of turbidity) and mass concentration of suspended particulate matter in seawater (a more direct measure of turbidity, expressed as a monthly average) were measured using Copernicus Global Ocean Colour (CMEMS no date a), Bio-Geo-Chemical, L4 (monthly and interpolated) from Satellite Observations (1997-ongoing; Fig. 2; Supplementary Folder S4). Seawater salinity and sea-surface temperature were obtained from Copernicus Global Ocean Physics Analysis and Forecast data (CMEMS no date b; Fig. 2; Supplementary Folder S4). Finally, daily sea-ice fraction was obtained from the Copernicus Global Ocean OSTIA Sea Surface Temperature and Sea Ice Analysis (Good et al. 2020; Fig. 2; Supplementary Folder S4). Remote sensing data (Fig. 2) corroborate published descriptions of the environmental properties at these two sites. Ilulissat is characterized by a stable, low-salinity meltwater layer at the surface, caused by runoff from the nearby Jakobshavn Isbræ glacier (Gladish et al. 2015). In addition, the waters around Ilulissat are characterized by elevated turbidity, with large-scale plumes of particulate matter visible in the remote sensing data, largely driven by glacial melt from

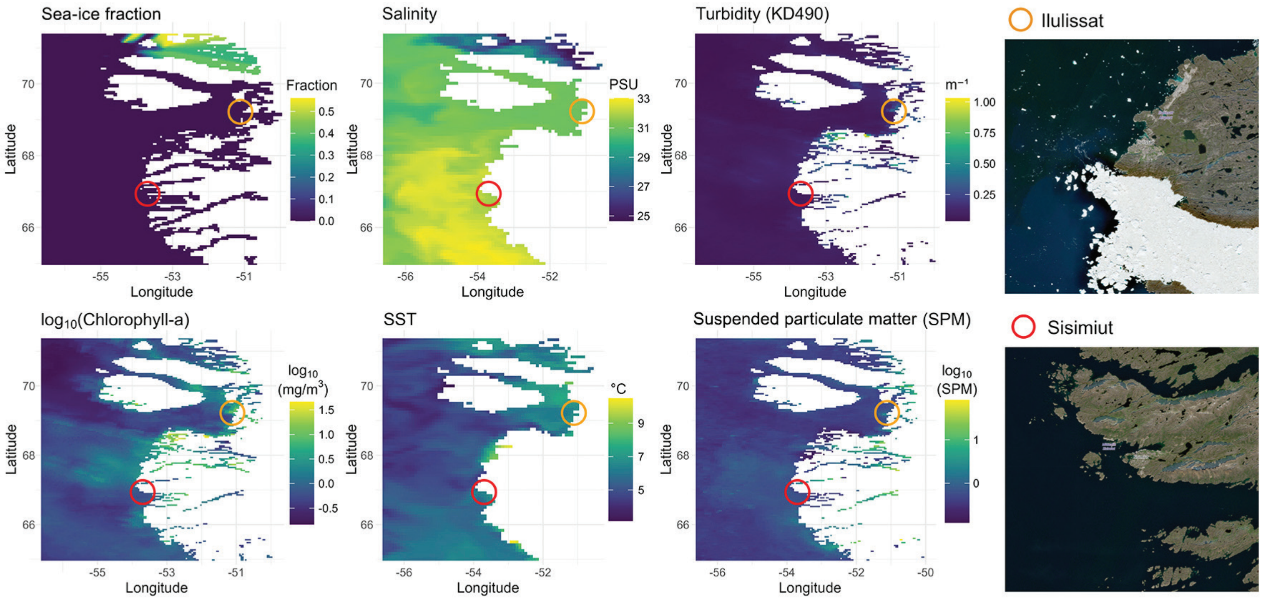

Fig. 2 Copernicus Marine Service maps showing six environmental parameters at Ilulissat and Sisimiut on 16 August 2023: sea-ice fraction, salinity, turbidity, chlorophyll-*a*, sea-surface temperature and suspended particulate matter. Satellite imagery shows the two locations on the same day (Sentinel-2 L2A True Color Optimized imagery; 2023 Modified Copernicus Sentinel data processed in Sentinel Hub).

the Jakobshavn Isbræ. Finally, the area is characterized by high primary productivity. Conversely, the waters around Sisimiut are more typical of Baffin Bay open-water regimes: salinity consistent with marine averages, minimal turbidity, low primary productivity and virtually no ongoing freshwater runoff from glacial or sea-ice melt.

Results

The taxonomic diversity of the sampled communities at Ilulissat and Sisimiut is significantly different (Kruskal-Wallis chi-squared = 6.8182, $df = 1$, $p = 0.009023$; Fig. 3). This difference in diversity resulted in a significant difference between these two communities in terms of taxonomic composition (PERMANOVA, $df = 1$, sum of squares = 0.815, $R^2 = 0.845$, $F = 43.492$, $p = 0.014$) and functional composition (PERMANOVA, $df = 1$, sum of squares = 0.035, $R^2 = 0.738$, $F = 22.586$, $p = 0.014$). Of the 13629 taxa (8887 bacteria, 4144 viruses, 455 archaea and 143 eukaryotes) identified from these two localities, the normalized abundance of 3372 differed significantly between the two sites (see Supplementary Folder S5 for the full list). When compared to Ilulissat, the Sisimiut community contained far fewer psychrophilic bacteria, with significant differences in the normalized abundance of those belonging to the genera *Colwellia*, *Paraglaciecola*, *Octadecabacter*, *Polaribacter* and *Psychrobacter* (Supplementary Folder S5; Fig. 4a). At the species level, the largest difference was a significantly lower normalized abundance of the ubiquitous Arctic bacterium *Colwellia hornerae* PAMC 20917 (Wald test: $W = -18.1697$, $\log_2$, fold change = −8.32955, $p_{adj} = 7.90E-05$), closely followed by a significantly lower normalized abundance of the psychrophile *Cognaticolwellia beringensis* (Wald test: $W = -20.3154$, $\log_2$ fold change = −8.23488, $p_{adj} = 5.79E-05$; Fig. 4a). Conversely, the Sisimiut community contained a significantly greater normalized abundance of the sulphate-reducing bacterium *Desulfosarcina widdelii* (Wald test: $W = -17.41028$, $\log_2$ fold change = 6.917221, $p_{adj} = 7.90E-05$), a difference which has broader functional implications (Fig. 4b). While eukaryotic metagenome databases are relatively sparse compared to those available for bacteria, available results indicate a significantly lower normalized abundance of the diatom *Thalassiosira pseudonana* at Sisimiut (Wald test: $W = -12.992$, $\log_2$ fold change = −2.92474, $p_{adj} = 0.000141$; see Supplementary Folder S5), potentially corroborating the decrease in primary productivity described in the literature (Møller et al. 2023) and in the remote sensing data (Fig. 2). Likely correlated with the decrease in normalized abundance of *T. pseudonana* at Sisimiut is a significantly lower normalized abundance of the opportunistic bacterium *Reinekea forsetii* (Wald test: $W = -29.7779$, $\log_2$ fold change = −7.42238, $p_{adj} = 1.69E-05$), which tracks the abundance of phytoplankton including *Thalassiosira* (Avcı et al. 2016; Fig. 4a). A significantly lower normalized abundance of bacteria in the genus *Shewanella* can be seen at Sisimiut (Supplementary Folder S5), particularly *Shewanella psychromarinicola* (Fig. 4a). High levels of terrestrial runoff at Ilulissat are likely responsible for the relatively higher normalized abundance of terrestrial/lacustrine viruses (e.g., *Gallivirus* A, *Winklervirus xtwenty*, *Ictalurivirus* Ictalurid herpesvirus 2, *Alphabaculovirus Helicoverpa armigera* nucleopolyhedrovirus and *Alphabaculovirus* sp.) and elevated levels of the bacterium *Streptococcus parasuis* (Fig. 4a).

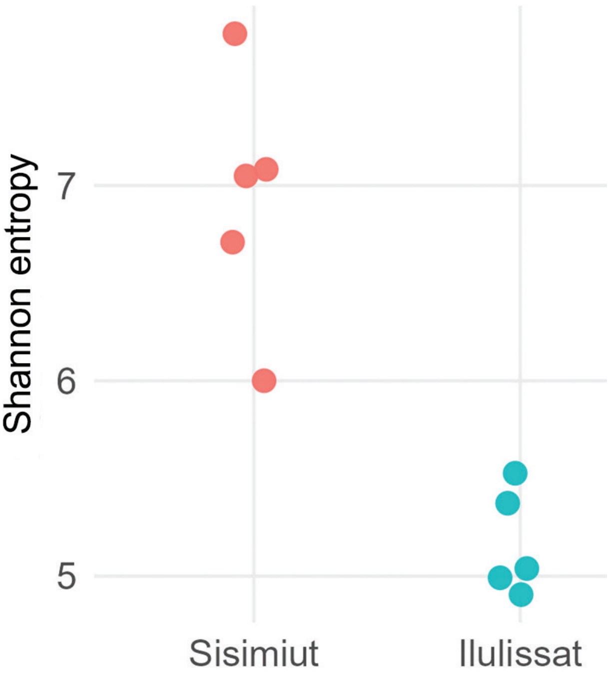

Fig. 3 Microbial taxonomic diversity (Shannon entropy) at Sisimiut and Ilulissat.

Of the 1270 functions (Level 3 SEED subsystems) identified from these two localities, the normalized abundance of 620 differed significantly between the two sites (see Supplementary Folder S6 for the full list). Among the most ecologically relevant differences was a significantly higher normalized abundance of genes associated with sulfate reduction, methanogenesis and nitrogen fixation at the Sisimiut location (Fig. 4d). This is evidenced by an increase in the normalized abundance of a number of related level 3 SEED subsystems, including “Pyrrolysine” (Wald test: $W = 11.16227$, $\log_2$ fold change = 7.060684, $p_{adj} = 3.86E-05$), “Methanogenesis from methylated compounds” (Wald test: $W = 10.50489$, $\log_2$ fold change = 6.032853, $p_{adj} = 5.43E-05$), “Methanogenesis”

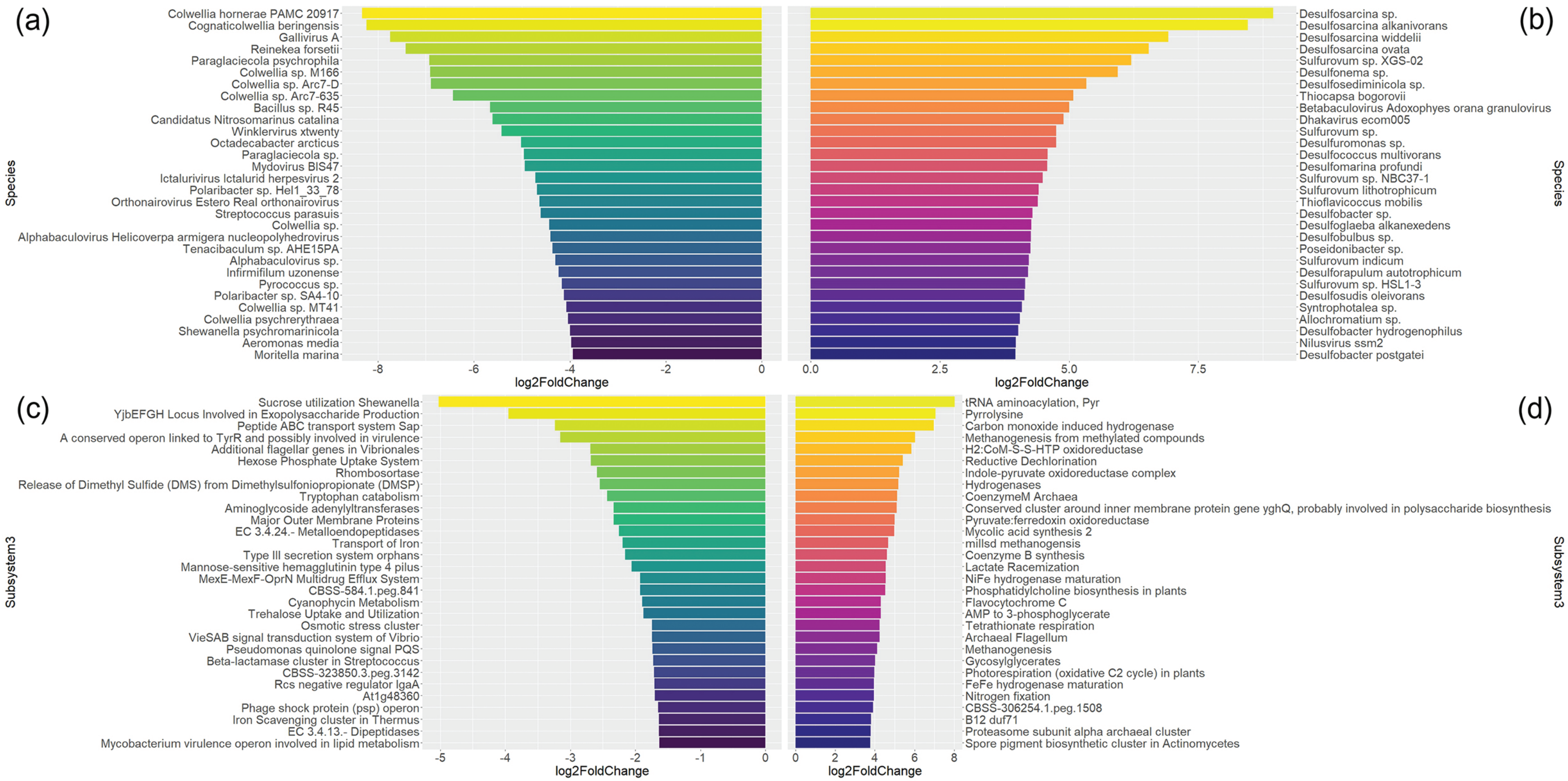

Fig. 4 The 30 most differentially abundant species (based on $\log_2$ fold change) at (a) Ilulissat and (b) Sisimiut. Log_2 fold changes compare Sisimiut to Ilulissat: negative values indicate species that are significantly more abundant in the Ilulissat community, while positive values indicate species that are significantly more abundant in the Sisimiut community. All differences are significant at the $p = 0.01$ level. Log_2 fold change values for Ilulissat are all negative values, indicating a $\log_2$ fold lower normalized abundance at Sisimiut compared to what is observed at Ilulissat. Log_2 fold change values for Sisimiut are all positive values indicating a $\log_2$ fold higher normalized abundance at Sisimiut compared to what is seen at Ilulissat. The 30 most differentially abundant functions (based on $\log_2$ fold change) at (c) Ilulissat and (d) Sisimiut. Log_2 fold changes compare Sisimiut to Ilulissat: negative values indicate genes that are significantly more abundant in the Ilulissat community, while positive values indicate genes that are significantly more abundant in the Sisimiut community. All differences are significant at the $p = 0.01$ level. Log_2 fold change values for Ilulissat are all negative values, indicating a $\log_2$ fold lower normalized abundance at Sisimiut compared to what is observed at Ilulissat. Log_2 fold change values for Sisimiut are all positive values indicating a $\log_2$ fold higher normalized abundance at Sisimiut compared to what is seen at Ilulissat.

(Wald test: W = 12.71732, $\log_2$ fold change = 4.12345, p_{adj} = 2.11E − 05), "Sulfate reduction-associated complexes" (Wald test: W = 7.828108, $\log_2$ fold change = 3.343664, p_{adj} = 0.000337) and "Nitrogen fixation" (Wald test: W = 15.05792, $\log_2$ fold change = 3.945652, p_{adj} = 8.99E − 06; Fig. 4d). This difference between the two sites is likely driven by a higher normalized abundance of sulfate-reducing bacteria such as *Desulfosarcina* and *Sulfurovum* (Fig. 4b), methanogenic archaea including the genera *Methanoculleus*, *Methanosarcina* and *Methanobrevibacter*, and nitrogen-fixing bacteria such as *Azospira oryzae* and members of the genus *Geobacter* (see Supplementary Folder S5). A subset of samples from the Sisimiut community contained relatively large amounts of the methanogen *Methanobrevibacter smithii*, although the difference between the two sites was not statistically significant (Supplementary Folder S5). A significant increase in the normalized abundance of genes in the Archaeal Flagellum level 3 SEED subsystem suggests a large difference in the abundance of motile archaea at Sisimiut (Wald test: W = 5.795147, $\log_2$ fold change = 4.230741, p_{adj} = 0.001232).

Among the functional genes with a significantly increased normalized abundance at the Ilulissat site, a high normalized abundance of genes associated with exopolysaccharide production ("YjbEFGH Locus Involved in Exopolysaccharide Production"; Wald test: W = −13.1329, $\log_2$ fold change = −3.95192, p_{adj} = 1.85E − 05; Fig. 4c) is likely correlated with the increased abundance of psychrophilic bacteria including *Colwellia hornerae* PAMC 20917 (Kim et al. 2018; Fig. 4a). Correlated with the increased normalized abundance of bacteria in the genus *Shewanella* described above, a higher normalized abundance of functional genes associated with this genus can be seen at Ilulissat (e.g., "Sucrose utilization *Shewanella*"; Wald test: W = −23.1659, $\log_2$ fold change = −5.02218, p_{adj} = 1.84E − 06).

Discussion

Ilulissat

The community at Ilulissat is a typical sea ice-associated microbial community (see, e.g., Eronen-Rasimus et al. 2017), with a significantly higher normalized abundance of psychrophilic heterotrophic bacteria such as *Colwellia hornerae* PAMC 20917, *Polaribacter* sp. SA4-10, *Octadecabacter arcticus* and *Paraglaciecola psychrophila* (Fig. 4a). Other taxa showing a significant difference in normalized abundance include cold water-associated heterotrophic bacteria such as *Reinekea forsetti*, *Shewanella psychromarinicola* and *Moritella marina*, alongside marine nitrogen and sulphur cycling taxa (e.g., *Candidatus Nitrosomarinus catalina*, *Tenacibaculum* sp. AHE15PA; Boetius et al. 2015; Lauritano et al. 2020; Fig. 4a). A significantly higher normalized abundance of genes associated with releasing dimethyl sulphide from DMSP strongly suggests a microbial community structured by the timing of phytoplankton blooms, given the large amount of DMSP produced by polar diatoms and associated taxa such as *Phaeocystis* (Teng et al. 2021; Fig. 4c). A significantly higher normalized abundance of genes associated with trehalose uptake and utilization, cyanophycin metabolism, hexose phosphate uptake and sucrose utilization all further corroborate the notion of a community shaped by intermittent pulses of freshwater and the relative abundance of phytoplankton in the area (Welsh 2000; Boetius et al. 2015; Bowman 2015; Fig. 4c). Similarly, a significantly higher normalized abundance of genes associated with osmotic stress likely reflects the need to adapt to irregular pulses of freshwater input, which cause salinity to fluctuate (Welsh 2000; Boetius et al. 2015; Bowman 2015; Fig. 4c). Finally, the significantly higher normalized abundance of flagellar genes, pilus genes, exopolysaccharide production genes and genes linked to the type III secretion system (all associated with motility and surface attachment)—alongside genes associated with iron transport and scavenging—further point to a community largely shaped by a dynamic water column and consequent complex phytoplankton community dynamics (Boetius et al. 2015; Eronen-Rasimus et al. 2017; Fig. 4c).

Sisimiut

Compared to the community at Ilulissat, the community at Sisimiut is composed of taxa commonly found in cold, sulfidic, marine sediments along the Arctic/sub-Arctic margin (Kleindienst et al. 2014). A higher normalized abundance of sulfate-reducing bacteria, such as *Desulfosarcina*, *Desulfonema*, *Desulfosediminicola* and *Desulfomarina*, all point to a more saline and stratified water column, with anoxic bottom waters/sediments allowing for the dominance of sulfate-reducing bacteria (Kleindienst et al. 2014; Fig. 4b). The higher normalized abundance of hydrocarbon degrading taxa, for example, *Desulfosarcina alkanivorans*, *Desulfosudis oleivorans* and *Desulfosarcina widdelii* (Fig. 4b), further suggests increased stratification in this area, with low oxygen bottom waters/sediments allowing for accumulation of organic matter and a consequent high normalized abundance of taxa specialized in anaerobic hydrocarbon degradation, both of which are typical of fjord communities (Glombitza et al. 2015; Watanabe et al. 2017). The functional profile at this community reflects this, with a significantly higher normalized abundance of genes associated with methanogenesis and anaerobic respiration (e.g., NiFe hydrogenase maturation, FeFe hydrogenase maturation, CoenzymeM Archaea and Coenzyme B synthesis) and genes linked to chemolithotrophy (e.g., carbon monoxide-induced hydrogenase; Maltby et al. 2018; Fig. 4d).

Conclusion

This study characterized the taxonomic and functional composition of shallow marine (near-shore) microbial communities found at two fjord mouth locations in western Greenland. The two locations differ in annual ice coverage, mean summer sea-surface temperatures, glacial meltwater flux rates and primary productivity (Fig. 2). They also show significant differences in the normalized abundance of 3372 taxa (25% of observed taxa) and 620 functional genes (49% of functional genes observed; Fig. 4). The microbial community observed near the mouth of the Amerloq Fjord (adjacent to the town of Sisimiut) is characterized by a diverse array of chemolithotrophic taxa, with a consequently high abundance of genes associated with methanogenesis and anaerobic respiration. Further north, the microbial community observed near the outlet of the Ilulissat Icefjord is dominated by psychrophilic and ice-associated bacteria, with a correspondingly high abundance of genes involved in DMSP degradation and exopolysaccharide biosynthesis.

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Disclosure statement

The authors report no conflict of interest.

Data availability

The raw sequence data for this project are available through the NCBI Sequence Read Archive under BioProject accession PRJNA1308514 at http://www.ncbi.nlm.nih.gov/bioproject/1308514.

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