RESEARCH ARTICLE

Metagenomic insights into diazotrophic communities across Arctic glacier forefields

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One sentence summary: Diverse communities of nitrogen fixing bacteria are identified across Arctic glacier forefields, revealed using community genomic sequencing.

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ABSTRACT

Microbial nitrogen fixation is crucial for building labile nitrogen stocks and facilitating higher plant colonisation in oligotrophic glacier forefield soils. Here, the diazotrophic bacterial community structure across four Arctic glacier forefields was investigated using metagenomic analysis. In total, 70 soil metagenomes were used for taxonomic interpretation based on 185 nitrogenase (nif) sequences, extracted from assembled contigs. The low number of recovered genes highlights the need for deeper sequencing in some diverse samples, to uncover the complete microbial populations. A key group of forefield diazotrophs, found throughout the forefields, was identified using a nifH phylogeny, associated with nifH Cluster I and III. Sequences related most closely to groups including Alphaproteobacteria, Betaproteobacteria, Cyanobacteria and Firmicutes. Using multiple nif genes in a Last Common Ancestor analysis revealed a diverse range of diazotrophs across the forefields. Key organisms identified across the forefields included Nostoc, Geobacter, Polaromonas and Frankia. Nitrogen fixers that are symbiotic with plants were also identified, through the presence of root associated diazotrophs, which fix nitrogen in return for reduced carbon. Additional nitrogen fixers identified in forefield soils were metabolically diverse, including fermentative and sulphur cycling bacteria, halophiles and anaerobes.

Keywords: nitrogen fixation; metagenomics; forefield; Arctic; diversity; diazotrophs

INTRODUCTION

Arctic glaciers are undergoing fast retreat, exposing soils that have been locked under ice for thousands of years (Bradley, Singarayer and Anesio 2014). Microbial communities have been identified as the primary colonisers of these newly exposed soils (Schmidt et al. 2008; Bradley et al. 2015) and are important for...
building up initial carbon and nitrogen pools, enhancing soil stability through the release of exopolymeric substances, and mediating forefield soil pH (Sattin et al. 2009; Schulz et al. 2013; Bradley, Singarayer and Anesio 2014). However, there is a lack of coherent understanding on the diversity and biogeochemical importance of these bacterial communities in relation to nitrogen fixation (Brankatschk et al. 2011). Bacterial nitrogen fixation uses the enzyme nitrogenase to convert atmospheric nitrogen (N₂) into fixed ammonia (NH₃) for biological uptake by non-diazotrophic organisms (Brill 1975). As nitrogen is a key nutrient for microbe and plant growth, nitrogen limited forefield soils may place restrictions on heterotroph colonisation, productivity and succession (Duc et al. 2009a). Subsequently, diazotrophic organisms have been proposed as crucial facilitators of succession in newly exposed forefield soils (Knelman et al. 2012). Nitrogen fixing Cyanobacteria have been identified as key in building these initial nitrogen stocks, and therefore expediting the establishment of heterotrophic organisms (Kaštovská et al. 2005; Schmidt et al. 2008; Duc et al. 2009a).

Whilst the importance of early diazotrophs is evident, similarities and variations in the nitrogen-fixing communities across forefields, in terms of both diversity and phylogeny, have received limited attention. The majority of research to date has focused on understanding changes in nitrogen fixation within individual forefields, along transects or chronosequences of soil development (Duc et al. 2009a; Brankatschk et al. 2011). Thus far, the taxonomic diversity and abundance of the nifH gene has been shown to decrease with soil age and distance from the glacier terminus, in line with increasing fixed nitrogen in soils, and a reduced need for diazotrophy (Duc et al. 2009a; Brankatschk et al. 2011). The dominant diazotrophic community composition in forefields is likely to be influenced by factors such as soil physicochemical status, climate, topography, the establishment of plants and any disturbances, such as water flow pathways, which may elicit both similarities and differences in diazotrophy between sites (Hodkinson, Coulson and Webb 2003; Nicol et al. 2005; Schütte et al. 2010; Liu et al. 2012). Furthermore, the current body of evidence surrounding microbial succession in forefields has a limited geographical range, with most studies conducted in the Damma Glacier forefield in Switzerland (Duc et al. 2009a; Frey et al. 2010; Bernasconi et al. 2011; Brankatschk et al. 2011; Brunner et al. 2011; Zumsteg et al. 2012, 2013; Bradley et al. 2015). Investigation across multiple glacier forefields is needed to fully explore similarities and differences between forefields in terms of diazotrophic community composition and their phylogenetic relations (Schütte et al. 2010). This will help highlight the microbial community diversity involved in nitrogen fixation among glacier forefields.

Bacterial nitrogen fixation is encoded by clustered nitrogenase genes, typically through an enzyme containing an iron (Fe) cofactor and a molybdenum-iron (Mo-Fe) cofactor (Dixon and Kahn 2004). Overall, the abundance of bioavailable nitrogen controls the transcription of nitrogenase genes, whilst the variant of nitrogenase transcribed is regulated by the presence of molybdenum (Oda et al. 2005; Teixeira et al. 2008). In the absence of Mo, nitrogenase is transcribed with vanadium (Fe-V co-factor), or exclusively with iron (Fe-Fe cofactor) in the absence of both Mo and V (Raymond et al. 2004; Teixeira et al. 2008). These nitrogenases are in turn encoded by the nifHDK, vnfH-vnfDGK and anfHDGK operons (Dixon and Kahn 2004; Teixeira et al. 2008). The phylogenetically conserved nifH gene can be used to classify bacterial diazotrophs into Clusters I-IV based on the nitrogenase (Chien and Zinder 1996). Cluster I covers the typical Mo nifH, whilst Cluster II covers the alternative vnfH and Cluster III generally includes a diverse range of anaerobic bacteria (Zehr et al. 2003). Furthermore, Cluster IV contains organisms with ‘nif-like’ sequences, as opposed to conventional nif genes (Zehr et al. 2003).

Previous research conducted on microbial succession in glacial forefields, including those on functional genes, has mostly focused on marker gene data, such as 16s rRNA and amplified nifH (Schmidt et al. 2008; Brankatschk et al. 2011; Rime, Hartmann and Brunner 2015). However, studies are now applying alternative methods, such as metagenomics, to study microbial communities (Wooley, Godzik and Friedberg 2010). This is because metagenomics provides gene sequences for the entire microbial community gene pool, rather than target sequences (Handelsman 2004; Daniel 2005). Thus, both microbial diversity and functional potential can be inferred using one approach (Wooley, Godzik and Friedberg 2010; Thomas, Gilbert and Meyer 2012). In order to maximise the quality of the output metagenome, the short DNA fragments from next generation sequencing should be assembled (Vázquez-Castellanos et al. 2014). This generates longer continuous DNA reads (contigs), which provide more accurate functional and taxonomic annotations (Howe et al. 2014; Vázquez-Castellanos et al. 2014).

In this study, we investigated 70 soil metagenomes spanning transects and chronosequences across four Arctic forefields in N-Sweden, Greenland and Svalbard. The datasets have been assembled separately and subsequently annotated for use in a comparative metagenomics analysis. Here, we present an investigation into the taxonomy and phylogenetic relationships of the functional genes recovered relating to bacterial nitrogen fixation in the four forefields. This analysis aims to contribute to the existing knowledge on pioneer microbial communities, helping to identify key genera of diazotrophic bacteria, which may have a key role building labile nitrogen stocks and soil development in oligotrophic forefield soils.

### MATERIALS AND METHODS

#### Field sampling

Four Arctic glacier forefields were selected for sampling and analysis, in front of Rabots glacier (Rb), N-Sweden (67° 54′ 25.6284″ N, 18° 26′ 51.0792″ E); Storglaciaren (St), N-Sweden (67° 52′ 21.1116″ N, 18° 34′ 2.676″ E); Midtre Lovenbreen (Ml), Svalbard (79° 6′ 1.8″ N, 12° 9′ 21.996″ E) and Russell Glacier (Rl), Greenland (67° 9′ 23.4324″ N, 50° 3′ 50.342″ W). Samples were obtained in July 2013 (Midtre Lovenbreen) and July 2014 (Russell, Rabots and Storglaciaren). Surface soil from each site was sampled using a chronosequence/transect-based approach, constructing three parallel transects along the forefield moving away from the terminus (Bradley, Singarayer and Anesio 2014). Chronosequence-based sampling was used to capture the diversity in nutrient concentration and microbial taxonomy of each forefield, to make more holistic comparisons between glacial forefields. Bulk surface samples were collected into sterile Whirlpak bags, and frozen at −20°C. Observationally, the sites comprised soils at very different development stages. A ‘typical’ smooth successional chronosequence from bare ground, to more developed, plant colonised soil was observed in the Ml forefield. However, the other sites sampled had a more heterogeneous chronosequence, with earlier and often more patchy plant colonisation.
Soil organic carbon and total nitrogen content

Soil total nitrogen (TN) and total organic carbon (TOC) were determined using mass spectrometry on a FastEA 1112 nitrogen and carbon elemental analyser. The protocol described in Hedges and Stern (1984) was used for sample preparation. In brief, for TN analysis soil samples were weighed and dried at 50°C overnight, before subsamples were transferred into tin capsules. For TOC analysis, 2 ml of 1 M HCl was incrementally added to 0.1 g of sample (Wo) until effervescence stopped. Subsequently, samples were again dried overnight at 50°C, left to equilibrate with hydroscopic salts, and re-weighed (Wf). Finally, subsamples were transferred into tin vials for analysis. The percentage of TOC in each sample was calculated using a correction for acidification induced weight change (Equation 1, Supporting Information). Where possible, three environmental replicates were analysed for each TN and TOC per sampling site.

DNA extraction, library preparation and sequencing

As this study was focused on the microbial diversity in bulk surface soil, DNA was extracted using a Mo-Bio DNAEasy PowerSoil DNA extraction kit (QIAGEN, UK), with DNA yield quantified using a Qubit 2.0 fluorometer. Samples that yielded less than 50 ng of DNA during extractions were pooled with their field replicates prior to sequencing. This method has been previously shown to obtain high DNA yields from soils and has been used for soil microbial diversity analysis in a number of studies, including root microbiomes (Fierer et al. 2007; Allison et al. 2008; Inceolu et al. 2010; Carvalhais et al. 2013; Vishnivetskaya et al. 2014). However, as this approach is not directly targeting the soil rhizosphere communities, there may be limitations to DNA extraction from this subset of the microbial community. Metagenomes were sequenced using an Illumina Next-Seq 500 (Rb, St and Rl) and an Illumina-Mi Seq (Ml), with a TrueSeq library prep kit at the University of Bristol Genomics facility. A total of 70 metagenomes were sequenced across the four sites using 2x 150bp (Rb, St, Rl) and 2x 100bp (Ml) paired-end reads (Table S1, Supporting Information). Sequencing read output for each site can be identified in Table S2 (Supporting Information), ranging between 3 817 852 and 10 510 0186 reads per metagenome.

Metagenome assembly and annotation

The 70 sequenced datasets were quality trimmed and subsequently assembled individually using the SPAdes 3.10.0-dev assembler (Bankevich et al. 2012). These assemblies were carried out in collaboration with the DOE Joint Genome Institute (Walnut Creek, CA), using the BFC algorithm for read error correction (Li 2015), and the –meta and –only-assembler flags. Furthermore, incremental Kmer lengths were used (22, 33, 55 and 77) to identify the most appropriate value for assembly. Assembly size for each metagenome ranged between 241660 and 429543524 bases (Table S2, Supporting Information). Functional annotation of the 70 metagenomes was subsequently carried out using the Integrated Microbial Genomes with Microbiome Samples (IMG/M) system (Chen et al. 2017). Rarefaction curves were created in MG-RAST 4.0.3 for each metagenome (Figs S1–S4, Supporting Information). The taxonomic distribution of all nif sequences (HDKNE) was carried out using the Basic Local Alignment Search Tool for Proteins (BLAST-p) with an e-value of 1e−5 and extracted. As nif genes are generally found in a phylogenetically conserved nitrogenase cluster (with nif D, K, N and E), these genes were also searched for and extracted (Howard and Rees 1996). Nif genes were dereplicated, removing duplicate copies, using vsearch 2.6.0, leaving a total of 185 assembled nif genes for subsequent analysis (Rognes et al. 2016). The nif genes used for the analysis have been deposited in GenBank, under accession numbers MH551286 - MH551470. Gene abundance was calculated as a combined value of nifHDKNE, normalised in relation to the abundance of the bacterial single copy housekeeping gene, rpoB, for each site (Vos et al. 2012; Ishii et al. 2015). As this method relies on sequencing unamplified genes, the nif gene counts are limited and may not be exhaustive for individual samples. This is particularly the case for unamplified sequencing of complex microbiome datasets, such as soil samples (Rodriguez and Konstantinidis 2014). Additionally, diazotrophs can contain multiple different nif genes, and several copies of a single variant, so should not be used as a measure to enumerate the explicit number of diazotrophs in each sample (Zehr et al. 2003). Finally, the raw sequencing reads were mapped to the extracted nif contigs for each metagenome using the BWA-MEM algorithm (Li and Durbin 2009). The alignment score (AS) of each read/contig is reported, which numerically indicates the quality of the alignments.

Nif taxonomy

The taxonomic distribution of all nif sequences (HDKNE) was carried out using a Last Common Ancestor (LCA) analysis in MEGAN 6.9.0 (Huson et al. 2016). For each forefield, nifHDKNE sequences were nucleotide BLAST (BLASTn) searched against an NCBI GenBank database of complete bacterial genomes. The sequences were subsequently binned based on the NCBI taxonomy, using an LCA algorithm, and visualised at the genus level for each forefield (Huson et al. 2016).

Gene phylogeny

A phylogeny for nifH, based on clusters identified in Zehr et al. (2003), was carried out, as this gene is supported by the largest body of research. Sample nifH sequences were aligned to sequences of cultured isolates, largely derived from the phylogeny by Deslippe and Egger (2006). GenBank and UniProtKB accession numbers for cultured isolates are available in Table S3 (Supporting Information). DNA sequence alignments were generated in SATé 2.2.7, using MAFT, MUSCLE and FASTTREE (Liu et al. 2011). The GTR+CAT model was implemented, with the decomposition set to longest (to minimise long branch attraction) and a maximum number of iterations set to 8. Alignments were manually edited in Mesquite, alongside generating Nexus and Phylip format files (Maddison and Maddison 2017). Maximum likelihood phylogenies were carried out using the CIPRES implementation of RAXML-HPC2 8.2.10 on XSEDE1, with 1000 bootstrap iterations (Stamatakis 2014). The GTR+G

1https://www.phylo.org/
model of nucleotide substitutions was implemented, as identified with j model test (Guindon and Gascuel 2003; Darriba et al. 2012). Trees were evaluated using Figtree 1.4.3, before annotation with EvolView v2 (He et al. 2016). Graphical enhancements were made using Inkscape 0.92.23. Comparisons between nifH sample sequences and cultured isolates were made using NCBI BLASTn, to identify nearest cultured relatives.

RESULTS AND DISCUSSION

Soil carbon and nitrogen

The range of values obtained within and between forefields for TOC and TN for samples from each forefield is listed in Table 1. These values include TOC and TN from both microbial and plant sources. Looking at average nutrient contents, comparing across the forefields, TN content ranges from averages below detection to 1.95 mg g\(^{-1}\), between St and Rb, respectively (Table 1). TOC content follows the same trend, increasing from the two Swedish glaciers (St and Rb), to Ml and Rl. Results from a one-way ANOVA with EvolView v2 (He et al. 2016). However, whilst differences in soil nutrient content do occur between sites, the values fall into the general range observed from other forefields (1–2 mg g\(^{-1}\) nitrogen, and 0.1–40 mg g\(^{-1}\) carbon) (Bradley, Singarayer and Anesio 2014) and are indicative of a generally oligotrophic environment.

| Table 1. Summary statistics for TN and TOC across the four forefields (Midtre Lovenbreen Ml, Russell Rl, Storglaciren St and Rabots Rb). The average, minimum, maximum and standard deviation (SD) across each forefield is given. The detection limit for both TN and TOC was 0.1 mg g\(^{-1}\). Sites recording values below detection (b.d) are shown. |
|---|
| **TN** (mg g\(^{-1}\)) | Average | Minimum | Maximum | SD |
| Ml | b.d. | b.d. | 4.90 | 1.56 |
| Rl | 1.95 | b.d. | 6.94 | 2.15 |
| St | b.d. | b.d. | 4.19 | 0.93 |
| Rb | 1.04 | b.d. | 3.35 | 1.33 |
| **TOC** (mg g\(^{-1}\)) | Average | Minimum | Maximum | SD |
| Ml | 10.56 | b.d. | 72.36 | 21.14 |
| Rl | 26.36 | b.d. | 82.70 | 26.35 |
| St | 2.78 | b.d. | 27.89 | 6.25 |
| Rb | 6.81 | b.d. | 22.90 | 9.66 |

Nif genes recovered

The total abundance of dereplicated *rpoB* normalised contigs containing nif genes (nifHDKNE), in relation to the variation of TN and TOC, spanning all sampling sites is shown in Fig. 1. A total of 185 nif genes contained on assembled contigs were recovered from the datasets. In 75% of samples where nif genes were detected, the TN and TOC concentrations fell below 1 and 5 mg g\(^{-1}\), respectively (Fig. 1). Conversely, in samples where nif genes were not detected, 61% and 49% measured below 1 and 5 mg g\(^{-1}\), of TN and TOC, respectively (Fig. 1). As sequencing output varied substantially between metagenomes, further sequencing may reveal additional genes due to the complex nature of soil microbiome samples (Table S2, Supporting Information; Rodriguez and Konstantinos 2014). This may indicate that samples with limited TN/TOC could have a larger relative abundance of genes for diazotrophy, as these were recovered through the sequencing effort undertaken. Interestingly, a similar trend between nitrogen fixation and TN has been reflected by the assays carried out by Telling et al. (2011), whereby fixation rates on Arctic glaciers were negatively correlated with total inorganic nitrogen content. Additionally, a link between nif gene abundance and activity is supported theoretically, as fixation becomes less metabolically beneficial when labile nitrogen stocks increase (Gutschick et al. 1978). When applied to forefield soils, both TN and TOC have been shown to increase over successional chronosequences, indicating nitrogen fixation may
Normalized nif abundance

0 0.05 0.10 0.15 0.20 0.25

TOC (mg g⁻¹)

0 1 2 3 4 5 6 7

Normalized nif abundance

0 0.05 0.10 0.15 0.20 0.25

TN (mg g⁻¹)

0 1 2 3 4 5 6 7

Figure 1. Relationship between normalised nif gene abundance (nifHDKNE) and concentration of TOC and TN per gram of soil, across all sampling sites. Nif gene abundance values are normalised against the bacterial single copy housekeeping gene, rpoB, for each metagenome. Values across the different forefields are noted, including: Midtre Lovenbreen (Ml), Russel (Rl), Rabots (Rb) and Storglaciren (St).

become less profitable with soil development (Duc et al. 2009a; Brankatschk et al. 2011; Bradley, Singarayer and Anesio 2014). Furthermore, research by Brankatschk et al. (2011) identified a link between nif gene abundance and enzyme activity, indicating sites with high numbers of nif genes, such as Storglaciren, would have enhanced nitrogen fixation activities. However, the relationship between gene abundance and nitrogen fixation activity is not always fully defined, as areas with low nitrogenase activity have previously been linked to high gene abundance in the Damma Glacier (Swiss Alps) (Duc et al. 2009a).

The results of mapping sequencing reads to the nif genes is provided in Table S7 (Supporting Information). This highlights the Alignment Score (AS), which indicates the alignment quality between reads and contigs (Table S7, Supporting Information). The number of nif genes for each score threshold is provided, alongside the percentage of reads with AS over 60. The Alignment Score ranges between 0 and the maximum length of the reads (0–100 for Ml dataset and 0–150 for Rb, St and Rl datasets). For each forefield, the percentage of alignments with an AS greater than 60 was 1.06x10⁻³ (Ml), 4.23x10⁻⁵ (Rl), 2.38x10⁻⁴ (Rb) and 9.56x10⁻⁴ (St). Plots of the normalised nif genes recovered and the number of reads aligning to genes with an AS over 60, for each metagenome, are available in Figs S5–S8 (Supporting Information).

Nitrogenase clusters

Our newly sampled bacteria were analysed and grouped with previously published relatives, as shown in Zehr et al. (2003). Forefield sequences were distributed across Cluster I (23 sample sequences) and III (3 sample sequences), with no representatives in Cluster II or IV (Fig. 2). Thus, 88.5% of sample sequences were attributed to Cluster I, which contains the typical Mo nifH,
Environmental samples in Cluster I included the groups Alphaproteobacteria, Betaproteobacteria, Cyanobacteria and Firmicutes (Fig. 2). The first group, associated with Alphaproteobacteria and Betaproteobacteria, incorporated five environmental samples that clustered most closely with *Azorhizobium caulinodans* and *Azoarcus tolulyticus*. These are plant-associated diazotrophs, important for establishing stocks of fixed nitrogen for legume uptake, supporting plant growth (Hurek and Hurek 1995; Dreyfus, Garcia and Gillis 1988). The second group was comprised of six sample sequences, clustering with the Cyanobacteria, *Nostoc* and *Anabaena*, which are free living nitrogen fixers (Zehr et al. 2003). Cyanobacteria have been proposed as crucial for building labile nitrogen pools in newly exposed soils, important for facilitating heterotroph colonisation, and have been identified in other forefields using SSU rRNA amplicon sequencing (Schmidt et al. 2008; Duc et al. 2009a; Frey et al. 2013). Group 3 contained 11 highly related sample nifH sequences, grouping closely to *Frankia*. This genus is composed of nitrogen fixing bacteria that are symbionts of actinorhizal plant roots, and again provides evidence for bacterial support of plant growth and establishment, through supplies of fixed nitrogen (Benson and Silvester 1993). Whilst the forefields may have a low diversity of root symbiotic diazotrophs, they may also relate to sub-optimal cell lysis and separation of root-associated cells during the DNA extraction process, or that these organisms were at low abundance and thus not captured through sequencing.

Environmental samples were also present in Cluster III, which is attributed to a group of anaerobic bacteria (Zehr et al. 2003). The three sample sequences clustered most closely to *Geobacter uraniireducens*, an anaerobe common in sediments under metal reducing conditions, capable of dissimilatory Fe(III) reduction (Shelobolina et al. 2008). However, no sample sequences were linked to Cluster II, which is associated with organisms containing the alternative anfH, containing an Fe–Fe cofactor, used in the absence of molybdenum and Vanadium (Zehr et al. 2003).

These results reflect those of Duc et al. (2009a), who used clone libraries to evaluate the phylogeny of diazotrophs across the Damma Glacier, Switzerland. Interestingly, nifH sequences from their analysis also grouped with nitrogenase Clusters I and III (Duc et al. 2009a). Additionally, genera identified by Duc et al. (2009a) included the key genera identified in this analysis, such as Geobacter, Nostoc and *Anabaena*, suggesting that these organisms are common across forefields (Duc et al. 2009a). The prevalence of these organisms may be due to adaptations or attributes to cold environments, such as cold or UV tolerance, and the release of protective exudates (Tamaru et al. 2005; Chattopadhyay 2006; Pattanaik, Schumann and Karsten 2007). Cyanobacteria such as *Nostoc* have been shown to produce extracellular polysaccharides (EPS) which are important for desiccation and freeze-thaw tolerance in Arctic environments (Tamaru et al. 2005). Geobacter are commonly found in anaerobic environments, and therefore may tolerate any anoxia in forefield soils created by frequent meltwater flooding and the formation of melt pools (Duc et al. 2009a). The consistent identification of *Geobacter*, *Nostoc* and *Frankia* in forefield soils using nifH analysis indicates that a core group of diazotrophs may be present across...
Arctic forefields. These diazotrophs may be important for facilitating plant colonisation and establishment, either by building labile pools in newly exposed soils (Cyanobacteria) or through symbiosis (Frankia, Azorhizobium).

Results from BLASTn searching each nifH sequence against cultured isolates revealed forefield sample sequences were divergent, with sequence identity ranging between 80%–95% (Table S8, Supporting Information). This indicates that the diazotrophs present in the samples are novel compared to those which have been previously identified and may be unique or contain adaptations to cold oligotrophic forefield conditions. However, as less abundant organisms will contribute to a minor proportion of the unamplified sequenced DNA and nifH gene pool, using additional nif genes may help highlight the presence of rare organisms in samples (Cowan et al. 2005). This may be especially helpful for metagenomes where sequencing coverage was not sufficient to profile the complete community structure, and thereby some low abundance organisms may not have been represented in the final dataset (Figs S1–S4, Supporting Information).

**Diazotroph community structure**

LCA analysis with multiple nif genes (HDKNL) identified the key organisms consistent between two or more forefields, including Geobacter, Frankia and Nostoc, which were also highlighted in the nifH analysis. Additional genera, for example Polaromonas, Pelobacter and Microcoleus were also identified here through the inclusion of additional nif genes (nifDKNE) (Fig. 3). This suggests including multiple nitrogenase genes provides a more holistic view of the diazotroph community structure in each forefield, due to the low copy number of these genes in unamplified samples. This is a particular issue of highly diverse metagenome samples, such as those from soils, as sequencing depth may not profile the complete community structure (Rodriguez and Konstantinidis 2014).

The assignment of nif genes in the Rl forefield covers two key genera, Geobacter and Frankia. Limited research has been conducted into the presence of Frankia in Greenland; however, these organisms are typically associated with common actinorhizal plants (Benson and Silvester 1993; Chaia, Wall and Huss-Danell 2010). This group forms nitrogen fixing root nodules with Frankia in exchange for reduced carbon and therefore are commonly found as early colonisers of undeveloped, oligotrophic soils (Wall 2000; Schwinter 2012). This is in agreement with the limited nitrogen content detected in this forefield, at 2.04 TN g⁻¹ (Fig. 1 and Table 1). Additionally, the presence of plants has been identified as a key control on microbial community structure over the Damma Glacier forefield, Switzerland (Miniaci et al. 2007). Furthermore, the identification of the anaerobic Geobacter indicates the presence of periodically saturated and anoxic conditions along the forefield, possibly attributed to meltwater flooding (Duc et al. 2009a). Geobacter are dissimilatory metal and sulphur reducing bacteria and have been proposed as key players in sediment nutrient cycles, oxidation of organic matter, bioremediation and soil gleying (Lovley 1993; Childers et al. 2002; Methe et al. 2003). Geobacter have been consistently identified across glacier forefield soils, which may relate to their metabolic diversity, thereby making these organisms well suited to fluctuating environmental conditions in forefield soils (Duc et al. 2009a,b; Edwards and Cook 2015; Rime, Hartmann and Brunner 2015). This group has been shown to use chemotaxis to access Fe(III) oxides as an electron acceptor, which may explain their prevalence over other non-motile Fe(III) reducers (Rime, Hartmann and Brunner 2015). Whilst deeper sequencing in some metagenomes may highlight additional rare diazotrophic bacteria in Rl samples, it is likely that Geobacter and Frankia were the most dominant nitrogen fixers present, as these were identified through direct sequencing of unamplified DNA (Cowan et al. 2005; Fig. S2, Supporting Information).

Similarly to Rl, the taxonomic diversity detected in the N-Swedish Rb forefield was largely comprised of root associated diazotrophs, including the genera Bradyrhizobium, Frankia, Methylobacterium and Rhodopseudomonas (Fig. 3). This may relate to the lack of bare soil observed at this forefield, and therefore limited requirement for free living diazotrophs (Miniaci et al. 2007). This site also had a low average soil nitrogen content, at 1.04 mg g⁻¹ (Fig. 1 and Table 1), which, alongside the detection of Rhizobia, Fabaceae root-nodule symbionts, indicates that nitrogen limitation for plant growth may have been occurring in soils (Myiuna, Pawlowski and Bisseling 1995). Actinorhizal and legume plants, which directly benefit from biological nitrogen fixation through symbiosis, such as Clover, are likely to prevail in developing forefield soils (Fagerli and Svenning 2005; Chaia, Wall and Huss-Danell 2010). This is because they maintain a competitive advantage over other plants in nitrogen limited conditions, typical of newly exposed soils (Menge and Hedin 2009; Bradley, Singarayer and Anesio 2014). Additionally, Rb had a lower average soil TOC content than other forefields, at 6.8 mg g⁻¹ (Fig. 1 and Table 1). Thus, Rhizobia are likely to benefit from symbiosis with plants through the supply of reduced carbon (Denison and Kiers 2004). Plants may therefore be acting as a control on the forefield microbial community structure, endorsing the presence of root-associated diazotrophs (Miniaci et al. 2007). Rarefaction curves for Rb sites were shown to be nearing saturation, indicating much of the microbial community structure was profiled (Fig. S4, Supporting Information). Additional sequencing for these samples may reveal further low abundance taxa; however, it is likely that the most dominant fraction of diazotrophs have been identified adequately through our analysis.

The nif genes recovered from the Ml forefield showed a wider taxonomic diversity of diazotrophs and contained sequences linked to the genera Nostoc, Polaromonas, Bradyrhizobium, Pelobacter, Azorarcus and Anaeromyxobacter. The presence of the Cyanobacteria, Nostoc, was expected due to the greater extent of bare soil observed in this forefield, enhancing the need for early colonisers (Frey et al. 2013). Additionally, EPS production enables this group to resist harsh freeze-thaw cycles, common in Arctic environments (Tamaru et al. 2005). Given the high latitude of this forefield, it is also not surprising to find Polaromonas, which are known psychrophiles (Irgens, Gosink and Staley 1996). The presence of Bradyrhizobium and Frankia indicate plants may require additional fixed nitrogen through symbiosis, corresponding with low nitrogen stocks detected (Benson and Silvester 1993; Mylona, Pawlowski and Bisseling 1995; Chaia, Wall and Huss-Danell 2010; Fig. 1 and Table 1). Additionally, the presence of legume symbiotic diazotrophs is interesting, as Fabaceae are non-native to Svalbard, having been introduced over the 20th Century (Fagerli and Svenning 2005). The absence of early plant colonisation in the forefield may also have been a control on overall microbial community structure, endorsing a range of non-symbiotic diazotrophs (Knelman et al. 2012). Alongside Geobacter, the identification of Pelobacter, Thiocystis and Anaeromyxobacter, again indicates permanent or periodic anaerobic conditions in the glacier forefield, similarly to Rl (Schink and Stieb 1983; Sanford et al. 2002). Pelobacter are anaerobic organisms containing diverse fermentative
metabolisms, which may make this group well suited to the rapidly changing conditions in forefield soils (Schink 2006). For example, Pelobacter have been shown to ferment acetylene using acetylene hydratase to acetate for cell growth or using nitrogenase to ethylene through nitrogen fixation (Akob et al. 2017). The genomic results for the Ml forefield falls in line with 16s amplicon data presented by Bradley et al. (2016). This study also found Frankia, Rhizobium, Nostoc and Geobacter in the Ml forefield (Bradley et al. 2016). The identification of additional organisms such as Devosia, Sphingomonas and Rhodoplanes may relate to the use of amplification in their methodology, thereby aiding the discovery of low abundance organisms (Bradley et al. 2016). Additionally, some metagenomes from this forefield would have benefited from greater sequencing depth in order to completely profile the microbial community composition (Fig. S1, Supporting Information). Therefore, deep sequencing of these samples may reveal additional low abundance diazotrophs, unidentified in this analysis.

Finally, the St forefield contained sequences relating to Nostoc, Geobacter, Rhizobium, Polaromonas and Frankia, in line with the other forefields sampled (Fig. 3). This supports the identification of a core group of diazotrophs present across Arctic glacier forefields. However, several diazotrophs detected at this site may also have importance in sulphur cycling, alongside nitrogen fixation (Fig. 3). The detection of the anaerobic diazotrophs Geobacter and Desulfovibrio indicates the potential for sulphur reduction, whereby energy is gained through reducing sulphur (S) or sulphate (SO_{4}^{2-}) to hydrogen sulphide (H_{2}S), with the oxidation of organic carbon (Boopathy and Kulpa 1993; Caccavo et al. 1994). However, inorganic S and SO_{4} have been found to be limiting for both plants and microbes in newly exposed glacier forefield soils (Allison et al. 2007; Prietzel et al. 2013). Nevertheless, desulphonating bacteria, whom metabolise organically bound sulphur to labile sulphates, have been found in forefield soils, and may therefore help overcome S limitation (Schmalenberger and Noll 2009; Prietzel et al. 2013). Additionally, suitable anaerobic growth conditions for sulphur reducing bacteria may occur frequently in stagnated proglacial meltwater pools and during periods of meltwater flushing (Duc et al. 2009a). Furthermore, the detection of organisms such as Chlorobaculum, Thioflavicoccus, Halorhodospira and Thiocystis indicates the potential for St forefield bacteria to carry out both nitrogen fixation and sulphur oxidation (Fig. 3). These organisms have the potential to oxidise H_{2}S to S and SO_{4}, alongside gaining fixed nitrogen through diazotrophy (Imhoff and Pfenning 2001; Chan, Morgan-Kiss and Hanson 2008; Peduzzi et al. 2011; Challacombe et al. 2013). The ability of these organisms to overcome nitrogren limitation through fixation, and to respire anaerobically in anoxic soils, may make this group well suited to harsh forefield environments. Additionally, as Halorhodospira is also halophilic, this may indicate resistance to high salinity environments, such as ice brine channels, or evaporation ponds in the St forefield (DasSarma and DasSarma 2006).
The diazotroph community composition observed using LCA nifHDKNE analysis was again largely consistent with those found at the Damma Glacier, Switzerland (Duc et al. 2009a,b; Frey et al. 2013). This includes genera such as *Methylobacterium*, *Bradyrhizobium*, *Azotobacter*, *Anaabaena*, *Nostoc* and *Geobacter* (Duc et al. 2009a). This supports the results from the nifH phylogeny, indicating the presence of consistent genera across forefields, which may be well adapted to the cold, oligotrophic and high UV conditions. Plant colonisation has also been identified as an influence on the diazotrophic community composition, in agreement with studies on the Damma Glacier, Switzerland (Miniaci et al. 2007; Duc et al. 2009a; Zumsteg et al. 2012). However, it is important to acknowledge that additional factors, such as latitude, bedrock mineralogy, organic matter and aeolian nitrogen deposition, may also have an influence on diazotroph community structure and abundance (Duc et al. 2009a; Zumsteg et al. 2012). Some genera found by Duc et al. (2009a), such as *Oscillatoria*, *Ideonella* and *Paenibacillus* were not identified in this study (Fig. 3). This may relate to the absence of these organisms in the four forefields in this analysis, but also may relate to the alternate approach used. As this analysis uses unamplified nifH sequences, some low abundance organisms may not be sequenced due to incomplete sequencing depth in highly complex samples (Rodriguez and Konstantinos 2014; Figs S1–S4, Supporting Information). Thus, it cannot be ruled out that these organisms were also not present in the forefields, but at a lower abundance than those captured by the sequencing effort (Prakash and Taylor 2012). In order to profile the complete community of some metagenomes, including low abundance organisms, deeper sequencing would be required, due to the diverse nature of soil samples (Rodriguez and Konstantinos 2014). Despite this, this analysis has been able to capture a diverse group of diazotrophs that appear to be common across glacier forefields and are likely the most abundant fraction of the nitrogen fixing community, as these were captured by unamplified DNA sequencing (Rodriguez and Konstantinos 2014).

Overall, this study has used a nifH phylogeny to identify a key group of diazotrophs across four Arctic forefields, associated with both Cluster I and II nitrogenase, linked to aerobic and anaerobic organisms containing the typical Mo nifH (Zehr et al. 2003). Incorporating multiple nif genes (HDKNE) revealed additional organisms from unamplified metagenome samples, compared to using the nifH gene exclusively. This may relate to the complex nature of soil metagenome samples, whereby sequencing depth is not always adequate to profile the complete microbial community diversity. Thus, to reveal all low abundance diazotrophs, some metagenomes would require additional deep sequencing. Key diazotrophs were found to be metabolically diverse, including genera such as *Geobacter*, *Frankia*, *Nostoc*, *Polaromonas* and *Bradyrhizobium*. A range of diazotrophic organisms outside the key group were also highlighted, including halophiles, psychrophiles and bacteria associated with fermentative metabolisms and sulphur cycling. Therefore, this analysis has shown a diverse group of diazotrophic bacteria present in Arctic forefield soils, including a consistent core subset. These diazotrophs have the potential to build labile nitrogen stocks in forefield soils, which may support further colonisation and soil development.

**SUPPLEMENTARY DATA**

Supplementary data are available at FEMSEC online. The nifH sequences used for analysis have been deposited in GenBank under accession numbers MH551286 - MH551470.

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**REFERENCES**

Akob, DM, Baesman SM, Sutton JM et al. Detection of diazotrophy in the acetylene-fermenting anaerobe Pelobacter sp. strain SFB93. *Appl Environ Microb* 2017;83:e01198–17.

Allison SD, Treseder KK. Warming and drying suppress microbial activity and carbon cycling in boreal forest soils. *Global Change Biol* 2008;14:2898–909.

Allison VJ, Condron LM, Peltzer DA et al. Changes in enzyme activities and soil microbial community composition along carbon and nutrient gradients at the Franz Josef chronosequence, New Zealand. *Soil Biol Biochem* 2007;39:1770–81.

Bankevich A, Nurk S, Antipov D et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 2012;19:455–77.

Benson DR, Silvester WB. Biology of Frankia strains, actinomycete symbionts of actinorhizal plants. *Microbiol Rev* 1993;57:293–319.

Bernasconi SM, Bauder A, Bourdon B et al. Chemical and biological gradients along the Damma glacier soil chronosequence, Switzerland. *Vadose Zone J* 2011;10:867–83.

Boopathy R, Kulpa CF. Nitroaromatic compounds serve as nitrogen source for Desulfovibrio sp. (B strain). *Can J Microbiol* 1993;39:430–3.

Bradley J, Singarayer JS, Anesio A. Microbial community dynamics in the forefield of glaciers. *Proc Royal Soc B* 2014;281:1–9.

Bradley JA, Anesio AM, Singarayer JS et al. SHIMMER (1.0): a novel mathematical model for microbial and biogeochemical dynamics in glacier forefield ecosystems. *Geosci Model Dev Discussions* 2015;8:6143–216.

Bradley JA, Arntd S, Sabacká M et al. Microbial dynamics in a High Arctic glacier forefield: a combined field, laboratory, and modelling approach. *Biogosciences* 2016;13:5677.
Dreyfus B, Garcia JL, Gillis M. Characterization of Azorhizobium caulinodans gen. nov., sp. nov., a stem-nodulating nitrogen-fixing bacterium isolated from Sesbania rostrata. Int J Syst Evol Microb 1988;38:89–98.

Duc L, NeuenSchwander S, Rehrauer H et al. Development and experimental validation of a nifH oligonucleotide microarray to study diazotrophic communities in a glacier forefield. Environ Microb, 2009b;11:2179–89.

Duc L, Noll M, Meier, B. E et al. High diversity of diazotrophs in the forefield of a receding alpine glacier. Microb Ecol 2009a;57:179–90.

Edwards A, Cook S. Microbial dynamics in glacier forefield soils show succession is not just skin deep. Mol Ecol 2015;24:963–6.

Fageri IL, Svending MM. Arctic and subarctic soil populations of Rhizobium leguminosarum biovar trifolii nodulating three different clover species: characterisation by diversity at chromosomal and symbiosis loci. Plant Soil 2005;275:371–81.

Fierer N, Breitbart M, Nulton J et al. Metagenomic and small-subunit rRNA analyses reveal the genetic diversity of bacteria, archaea, fungi, and viruses in soil. Appl Environ Microb 2007;73:7059–66.

Frey B, Bühler L, Schmutz S et al. Molecular characterization of phototrophic microorganisms in the forefield of a receding glacier in the Swiss Alps. Environ Res Lett 2013;8:015033.

Frey B, Rieder S.R., Brunner I et al. Weathering-associated bacteria from the Damma glacier forefield: physiological capabilities and impact on granite dissolution. Applied and environmental Microbiology 2010;76(14):4788–96.

Guindon S, Gascuel O. A simple, fast and accurate method to estimate large phylogenies by maximum-likelihood. Syst Biol 2003;52:696–704.

Gutnick PV. Energy and nitrogen fixation, BioScience, 1978;28:571–5.

Handelsman J. Metagenomics: application of genomics to uncultured microorganisms. Microbiol Mol Biol R 2004;68:669–85.

Hedges JI, Stern JH. Carbon and nitrogen determinations of carbonate-containing solids. Limno Oceanogr 1984;29:657–63.

He Z, Zhang H, Gao S et al. Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. Nucleic Acids Res 2016;44:W236–41.

Hodkinson ID, Coulson SJ, Webb NR. Community assembly along proglacial chronosequences in the high Arctic: vegetation and soil development in north-west Svalbard. J Ecol 2003;91:651–63.

Howard JB, Rees DC. Structural basis of biological nitrogen fixation. Chem Rev 1996;96:2965–82.

Howe AC, Jansson JK, Malfatti SA et al. Tackling soil diversity with the assembly of large, complex metagenomes. Proc Natl Acad Sci 2014;111:4904–9.

Hurek T, Reinhold-Hurek B. Identification of grass-associated and toluene-degrading diazotrophs, Azoarcus spp., by analysed 16S rDNA sequences. FEMS Microb Ecol 2008;65:7–16.

Ishii SI, Suzuki S, Tenney A et al. Microbial metabolic networks in a complex ecosystem biofilm recovered from a stimulus-induced metatranscriptomics approach. Sci Rep 2015;5:14840.

Inceolu O, Hoogwout EF, Hill P et al. Effect of DNA extraction method on the apparent microbial diversity of soil. Appl Environ Microb 2010;76:3378–82.
Kaštovská K, Elster J, Stibal M et al. Microbial assemblages in soil microbial succession after glacial retreat in Svalbard (High Arctic). Microbiol Ecol 2005;50:396–407.

Knelman JE, Legg TM, O’Nei1l SP et al. Bacterial community structure and function change in association with colonizer plants during early primary succession in a glacier forefield. Soil Biol Biochem 2012;46:172–80.

Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler Transform. Bioinformatics, 2009;25:1754–60.

Li H. BFC: correcting Illumina sequencing errors. Bioinformatics 2015;31:2885–87.

Liu GX, Hu P, Zhang W et al. Variations in soil culturable bacteria communities and biochemical characteristics in the Dongkemadi glacier forefield along a chronosequence. Folia Microbiol 2012;57:485–94.

Liu K, Warnow TJ, Holder MT et al. SATe-II: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. Syst Biol 2011;61:90–106.

Lovley DR, Giovannoni SJ, White DC et al. Geobacter metal-reducers gen. nov. sp. nov., a microorganism capable of coupling the complete oxidation of organic compounds to the reduction of iron and other metals. Arch Microbiol 1993;159:336–44.

Maddison WP, Maddison DR. Mesquite: a modular system for evolutionary analysis. Version 3.2 2017. http://mesquiteproject.org [Accessed 08-10-17].

Menge DN, Hedin LO. Nitrogen fixation in different biogeochemical niches along a 120 000-year chronosequence in New Zealand. Ecology 2009;90:2190–201.

Methe BA, Nelson KE, Eisen JA et al. Genome of Geobacter sulfurreducens: metal reduction in subsurface environments. Science 2003;302:1697–9.

Meyer F, Faarmann D, D’Souza M et al. The metagenomics RAST server—a public resource for the automatic phylogenetic and functional analysis of metagenomes. BMC Bioinformatics 2008;9:386.

Miniaci C, Bunge M, Duc L et al. Effects of pioneering plants on microbial structures and functions in a glacier forefield. Biol Fertility Soils 2007;44:289–97.

Mylona P, Pawlowski K, Bisseling T. Symbiotic nitrogen fixation. Plant Cell 1995;7:869.

Nicola GW, Tcherko D, Embley TM et al. Primary succession of soil Crenarchaeota across a receding glacier foreland. Environ Microbiol 2005;7:337–47.

Oda Y, Samanta SK, Rey FE et al. Functional genomic analysis of three nitrogenase isozymes in the photosynthetic bacterium Rhodopseudomonas palustris. J Bacteriol 2005;187:7784–94.

Pattanaik B, Schumann R, Karsten U. Effects of ultraviolet radiation on cyanobacteria and their protective mechanisms. Algae Cyanobacteria Extreme Environ 2007;11:29–45.

Peduzzi S, Welsh A, Demarta A et al. Thioctysis chemoclinalis sp. nov. and Thioctysis cadagenonis sp. nov., motile purple sulfur bacteria isolated from the chemocline of a meromictic lake. Intl J Syst Evol Microbiol 2011;61:1682–7.

Prakash T, Taylor TD. Functional assignment of metagenomic data: challenges and applications. Briefings Bioinform 2012;13:711–27.

Prietzel J, Wu Y, Düümig A et al. Soil sulphur speciation in two glacier forefield soil chronosequences assessed by SK-edge XANES spectroscopy. Eur J Soil Sci 2013;64:260–72.

Raymond J, Sievert JL, Staples CR et al. The natural history of nitrogen fixation. Mol Biol Evol 2004;21:541–54.

Rime T, Hartmann M, Brunner I. Vertical distribution of the soil microbiota along a successional gradient in a glacier forefield. Mol Ecol, 2015;24:1091–108.

Rodriguez-r LM, Konstantinidis KT. Estimating coverage in metagenomic data sets and why it matters. ISME J 2014;8:2349.

Rognes T, Flouri T, Nichols B et al. VSEARCH: a versatile open source tool for metagenomics. Peer J 2016;4:e2584.

Sanford RA, Cole JR, Tiedje JM. Characterization and description of Anaeromicrobacter dehalogenans gen. nov., sp. nov., an aryl-halorespiring facultative anaerobic myxobacterium. Appl Environ Microb 2002;68:893–900.

Sattin SR, Cleveland CC, Hood E et al. Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. J Microbiol 2009;47:673–81.

Schink B, Stieb M. Fermentative degradation of polyethylene glycol by a strictly anaerobic, gram-negative, nonsporeforming bacterium, Pelobacter venetiannus sp. nov. Appl Environ Microb 1983;45:1905–13.

Schink B. The genus Pelobacter. In: Dworkin M, Falkow S, Rosenberg E et al. (eds). The Prokaryotes: Volume 7: Proteobacteria: Delta, Epsilon Subclass. New York: Springer, 2006;5–11.

Schmalenberger A, Noll M. Shifts in desulfonating bacterial communities along a soil chronosequence in the forefield of a receding glacier. FEMS Microbiol Ecol 2009;71:208–17.

Schmidt SK, Reed SC, Nemergut DR et al. The earliest stages of ecosystem succession in high-elevation (5000 metres above sea level), recently deglaciated soils. Proc Royal Soc Lond B: Biol Sci 2008;275:2793–802.

Schulz S, Brankatschk R, Düümig A et al. The role of microorganisms at different stages of ecosystem development for soil formation. Biogeosciences 2013;10:3983–96.

Schwantzer CR. The Biology of Frankia and Actinorhizal Plants. Netherlands: Elsevier, 2012.

Schütte UM, Abdo Z, Foster J et al. Bacterial diversity in a glacier foreland of the high Arctic. Mol Ecol 2010;19:54–66.

Shelobolina ES, Vrionis HA, Findlay RH et al. The Biology of Frankia and Actinorhizal Plants. New York: Springer, 2006;5–11.

Shelobolina ES, Vrionis HA, Findlay RH et al. The Prokaryotes: Volume 7: Proteobacteria: Delta, Epsilon Subclass. New York: Springer, 2006;5–11.

Shelobolina ES, Vrionis HA, Findlay RH et al. The Prokaryotes: Volume 7: Proteobacteria: Delta, Epsilon Subclass. New York: Springer, 2006;5–11.

Shelobolina ES, Vrionis HA, Findlay RH et al. The Prokaryotes: Volume 7: Proteobacteria: Delta, Epsilon Subclass. New York: Springer, 2006;5–11.

Souza M et al. Variations in soil culturable bacteria and function and function change in association with colonizer plants during early primary succession in a glacier forefield. Soil Biol Biochem 2011;43:302–10.

Souza M et al. Variations in soil culturable bacteria and function and function change in association with colonizer plants during early primary succession in a glacier forefield. Soil Biol Biochem 2011;43:302–10.

Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 2014;30:1312–13.

Tamaru Y, Takani Y, Yoshida T et al. Crucial role of extracellular polysaccharides in desiccation and freezing tolerance in the terrestrial cyanobacterium Nostoc commune. Appl Environ Microb 2005;71:7327–33.

Teixeira RLF, Von Der Weid I, Seldin L et al. Differential expression of nifH and anfH genes in Paenibacillus durus analyzed by reverse transcriptase-PCR and denaturing gradient gel electrophoresis. Lett Appl Microbiol 2008;46:344–9.

Telling J, Anesio AM, Tranter M et al. Nitrogen fixation on Arctic glaciers, Svalbard. J Geophys Res: Biogeosci 2011;116:1–8.

Thomas T, Gilbert J, Meyer F. Metagenomics—a guide from sampling to data analysis. Microbiol Inform Exp 2012;2:1–12.

Torsvik V, Øvreås L, Thingstad TF. Prokaryotic diversity–a source tool for metagenomics. Appl Environ Microb 2014;80:2349–50.

Tranter M, Skidmore M, Wadhams J. Hydrological controls on microbial communities in subglacial environments. Hydrological Processes 2005;19(4):995–8. 
Vishnivetskaya TA, Layton AC, Lau MC et al. Commercial DNA extraction kits impact observed microbial community composition in permafrost samples. FEMS Microbiol Ecol 2014;87:217–30.

Vos M, Quince C, Pijl AS et al. A comparison of rpoB and 16S rRNA as markers in pyrosequencing studies of bacterial diversity. PLoS One 2012;7:e30600.

Vázquez-Castellanos JF, García-López R, Pérez-Brocal V et al. Comparison of different assembly and annotation tools on analysis of simulated viral metagenomic communities in the gut. BMC Genomics 2014;15:37.

Wall LG. The actinorhizal symbiosis. J Plant Growth Regulat 2000;19:167–82.

Wooley JC, Godzik A, Friedberg I. A primer on metagenomics. PLoS Comput Biol 2010;6:e1000667.

Zehr JP, Jenkins BD, Short SM et al. Nitrogenase gene diversity and microbial community structure: a cross-system comparison. Environ Microbiol 2003;5:539–54.

Zumsteg A, Bååth E, Stierli B et al. Bacterial and fungal community responses to reciprocal soil transfer along a temperature and soil moisture gradient in a glacier forefield. Soil Biol Biochem 2013;61:121–32.

Zumsteg A, Luster J, Göransson H et al. Bacterial, archaeal and fungal succession in the forefield of a receding glacier. Microb Ecol 2012;63:552–64.