Discovery of Eremiobacterota with *nifH* homologs in tundra soil

Igor S. Pessi[1,2,3], Tom Delmont[4], Jonathan P. Zehr[5], and Jenni Hultman[1,2,6,*]

[1]University of Helsinki, Helsinki, Finland
[2]Helsinki Institute of Sustainability Science (HELSUS), Helsinki, Finland
[3]Finnish Environment Institute (SYKE), Helsinki, Finland
[4]Genoscope, Evry, France
[5]University of California Santa Cruz, Santa Cruz, CA, USA
[6]Natural Resources Institute Finland (LUKE), Helsinki, Finland
[*]Corresponding author: jenni.hultman@helsinki.fi

Running title: An Eremiobacterota population with *nifH* homologs

Abstract

We describe a population genome of Eremiobacterota (KWL-0264) recovered from tundra soil metagenomes that contains the minimal set of *nif* genes needed to fix atmospheric N_2. Such putative diazotroph population would link for the first time Eremiobacterota and N_2 fixation. The integrity of the genome and its *nif* genes are well supported by both environmental and taxonomic signals. KWL-0264 contains three *nifH* homologs and the complementary set of *nifDKENB* genes that are thought needed to assemble a functional nitrogenase. The putative role in N_2 fixation of this Eremiobacterota population is also evidenced by the presence of other genes involved with the regulation of the N_2 fixation activity as well as ammonia assimilation and amino acid metabolism. Like other Eremiobacterota, KWL-0264 also encodes the potential for atmospheric chemosynthesis. Interestingly, the presence of a N_2O reductase indicates that this population could also play a role as a N_2O sink in tundra soils. Due to the lack of activity data, it remains uncertain if this Eremiobacterota population is able to assemble a functional nitrogenase and participate in N_2 fixation. Confirmation of this activity would be a testament to the great metabolic versatility of Eremiobacterota, which appears to underlie their ecological success in cold and oligotrophic environments.

Main

The conversion of atmospheric N_2 to ammonia by microbial diazotrophs represents the largest external source of nitrogen in tundra soils [1–3]. Tundra N_2 fixation rates are generally low but are predicted to increase with the rise in atmospheric temperatures and precipitation levels associated with anthropogenic climate change [2, 4]. Greater inputs from N_2 fixation coupled with faster rates of organic matter mineralization will increase the pool of bioavailable nitrogen in tundra soils and potentially lead to higher greenhouse gas emissions, particularly N_2O [4–6]. More knowledge on the microbial drivers of N_2 fixation is thus essential for a better understanding of the dynamics of greenhouse gas production in tundra soils.

Here, we investigated the diversity of microbial diazotrophs in the tundra by leveraging a catalogue of 796 manually curated metagenome-assembled genomes (MAGs) from soils in Kilpisjärvi, northern Finland [7] (see methods in **Supplementary information**). The Kilpisjärvi MAGs represent populations from different types of soil ecosystems (from bare soil to water-logged fens) and encompass a high diversity of Archaea and Bacteria [7, 8]. We searched the MAGs using a hidden Markov model of the *nifH* gene, which encodes the dinitrogenase reductase subunit of the nitrogenase enzyme and is the most widely used marker for N_2 fixation [9–11]. We found *nifH* homologs in 26 of the 796 Kilpisjärvi MAGs, most of which belong to groups that are known to include diazotrophs such as Alpha- and Gammaproteobacteria and methanogenic Archaea (**Supplementary information**).

Surprisingly, we identified *nifH* homologs in the MAG KWL-0264 assigned to Eremiobacterota, a phylum for which no diazotrophic activity and/or nitrogenase sequences have been previously reported. The validity of the MAG as a whole and the inclusion of *nifH* homologs are supported by several features such as homogeneous GC content, coverage in multiple metagenomes, and taxonomical signal for Eremiobacterota across contigs, including those containing the *nifH* homologs (**Fig. 1a**; see also **Supplementary information**). Phylogenomic analysis with other publicly available genomes confirmed the affiliation of KWL-0264 with Eremiobacterota, placing it alongside other MAGs from polar environments in the family Baltobacteraceae (**Fig. 1b**). The phylogenetic placement and low average nucleotide identity (ANI) with other genomes indicates that KWL-0264 represents a distinct genus in this family.

The presence of *nifH* homologs and other related genes suggests a role in N_2 fixation for this Eremiobacterota population (**Fig. 2**; see also **Supplementary information**). KWL-0264 contains three *nifH* homologs, which is not uncommon among known diazotrophs [9], and also includes the additional *nifDKENB* genes that are deemed necessary for the assembly of a functional nitrogenase [10, 11]. Importantly, one of the *nifH* homologs ($nifH_1$) encodes a

nitrogenase affiliated with Cluster III, which is a diverse group of canonical nitrogenases mostly from anaerobic Bacteria and Archaea with demonstrated diazotrophic activities [9–11]. Further hints towards a role in N_2 fixation is given by the occurrence of *nifI₁* and *nifI₂* downstream of *nifH₁*. These genes are usually found in diazotrophs containing Cluster III nitrogenases and encode a type of GlnB/PII protein that inactivates N_2 fixation when ammonia is available [9, 12]. It is important to note that the *nifH₁* homolog is not co-located with *nifDK*, but this is likely due to low genome contiguity rather than gene loss (**Supplementary information**). The other two *nifH* homologs of KWL-0264 (*nifH₂* and *nifH₃*) encode Cluster IV nitrogenases, which have been largely thought as paralogs that do not participate in N_2 fixation [9–11]. However, this view has been challenged by the reported diazotrophic growth of *Endomicrobium proavitum* with a Cluster IV nitrogenase [13]. Importantly, the contig with the *nifH₂* homolog contains the complete set of *nifDKENB* genes, suggesting the capacity to assemble a functional nitrogenase. Further support for a role in N_2 fixation is given by the occurrence, near all three *nifH* homologs, of several genes that are involved in nitrogen and amino acid transport and metabolism. These include genes for the GS-GOGAT pathway of ammonia assimilation (*glnA* and *gltD*), ABC-type branched-chain amino acid (*livFGHKM*) and nitrate (*tauABC*) transporters, and amino acid biosynthesis (*dapD*, *aspB*, *cysE*, *argA*, and *metC*).

Read-recruitment analysis revealed that KWL-0264 is preferentially found in mineratrophic fens compared to upland soils (**Supplementary information**). Interestingly, the genomic composition of KWL-0264 suggests multiple adaptations to the oligotrophic conditions found in these environments. Firstly, the potential to fix N_2 represents an ecological advantage in northern fens and peatlands in general, where most of the nitrogen is bound to the organic matter and thus not available for growth [3, 5]. Secondly, KWL-0264 encodes the potential to fix CO_2 using energy obtained from the oxidation of H_2 and CO. This metabolic strategy, known as atmospheric chemosynthesis, has been reported for other Eremiobacterota genomes, and appears to underlie their ecological success in cold and acidic ecosystems such as tundra soils, polar deserts, and peatlands [14–17]. Thirdly, the potential to oxidize H_2 can help alleviate the high energetic cost of N_2 fixation, as it allows the recovery of part of the spent energy by recycling the H_2 that is produced during the process [18]. Finally, KWL-0264 encodes a clade II N_2O reductase and thus the potential for anaerobic respiration via the reduction of N_2O to N_2, which is favoured in the typically anoxic environment of water-logged fens [7]. Moreover, it can be speculated that the capacity to reduce N_2O to N_2 might also be used as a strategy to fuel N_2 fixation. The ability to reduce N_2O indicates a potential role of this Eremiobacterota population in mitigating the emission of this potent greenhouse gas, as has been shown for other non-denitrifying N_2O reducers [19].

After more than 20 years since the first description of Eremiobacterota as "candidate phylum WPS-2" from contaminated soil [20], the recovery of a MAG harbouring *nifH* homologs suggests that N_2 fixation might also be a part of the metabolic repertoire of this phylum. At present, it remains unclear if the genomic organisation of KWL-0264 can lead to a nitrogenase with function in N_2 fixation. Further studies should focus on isolating this population, recovering other closely related genomes (preferentially using long read sequencing technologies), and providing evidence of N_2 fixation activity using, for example, rate measurements coupled with (meta)transcriptomics and/or stable isotope probing.

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Competing interests

The authors declare no competing interests.

Data availability

Raw metagenomic data and MAGs can be found in the European Nucleotide Archive (ENA) under the project PRJEB41762.

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Figures

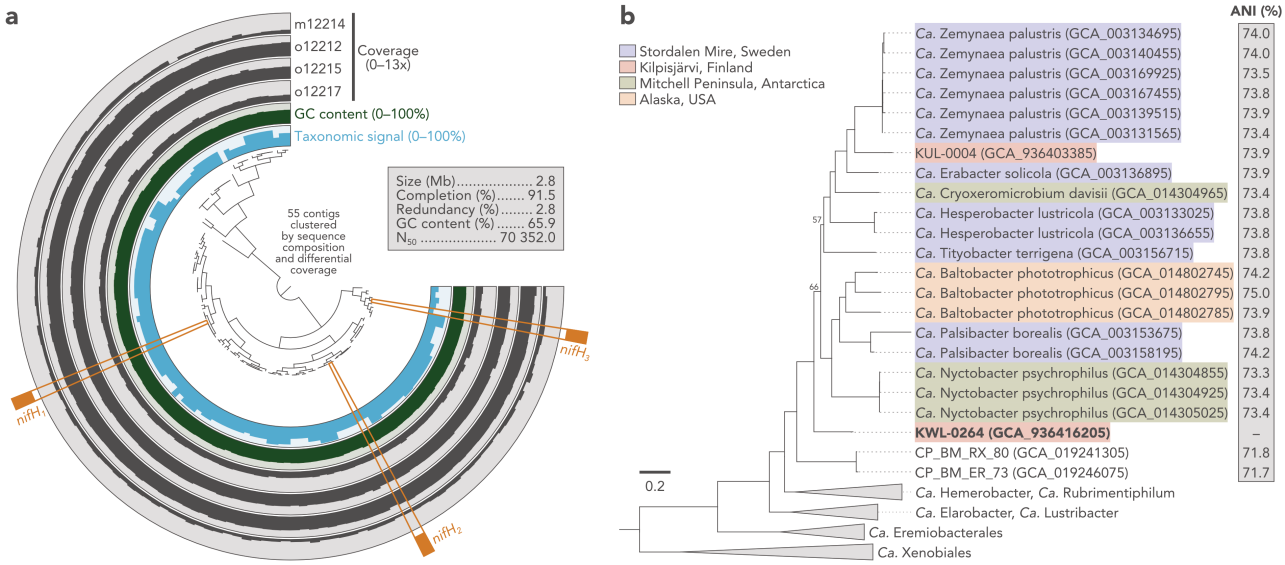

Fig. 1. a) Representation of the metagenome-assembled genome (MAG) KWL-0264. The four external rings show the mean coverage of each contig across four fen metagenomes from Kilpisjärvi, northern Finland [7]. The innermost blue ring (taxonomic signal) represents the proportion of genes in each contig that had the best match with another Eremiobacterota sequence in GenBank (*nr* database, *blastp*, highest bitscore). The three contigs harbouring the *nifH* homologs are indicated. **b)** Phylogenomic analysis of the MAG KWL-0264 alongside other Eremiobacterota genomes available in GenBank (n=176, accessed on 16th December 2022). Maximum-likelihood tree (LG+I+G model) based on a concatenated alignment of 71 single-copy genes. Average nucleotide identity (ANI) values between the KWL-0264 genome and its neighbours are indicated. Bootstrap support is ≥95% unless shown.

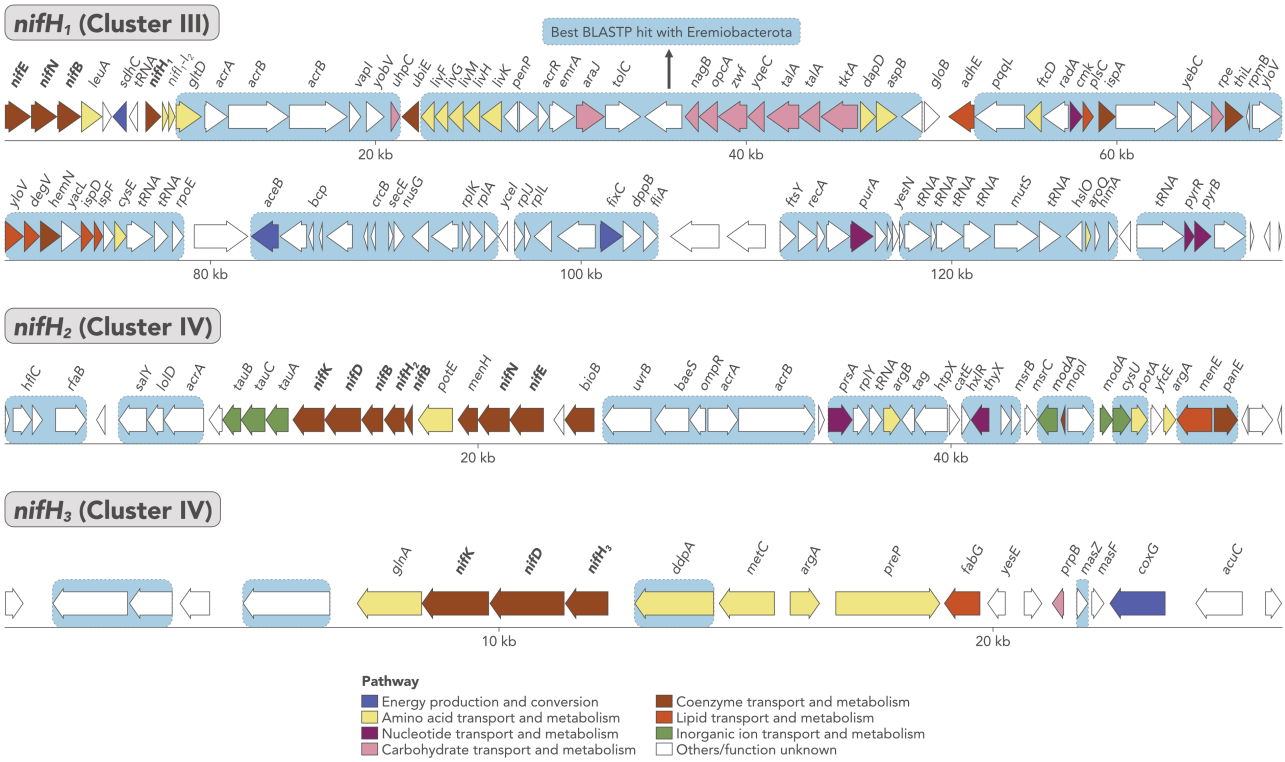

Fig. 2. Representation of the three contigs harbouring *nifH* homologs in the metagenome-assembled genome (MAG) KWL-0264. Genes highlighted with a blue rectangle had the best match with another Eremiobacterota sequence in GenBank (*nr* database, *blastp*, highest bitscore).