

# Subsurface Nitrospirota Origins

**Website:** <https://www.bco-dmo.org/dataset/933610>

**Data Type:** Synthesis

**Version:** 1

**Version Date:** 2024-07-22

## Project

» [Microbial activity in the crustal deep biosphere](#) (Slow Life in Crust)

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## Abstract

The phyla Nitrospirota and Nitrospinota have received significant research attention due to their unique nitrogen metabolisms important to biogeochemical and industrial processes. These phyla are common inhabitants of marine and terrestrial subsurface environments and contain members capable of diverse physiologies in addition to nitrite oxidation and complete ammonia oxidation. We used phylogenomics and gene-based analysis with ancestral state reconstruction and gene-tree-species tree reconciliation methods to investigate the life histories of these two phyla. This dataset includes list of previously-published sequence datasets that were used for the analysis. The data and interpretations are published at DOI 10.1038/s41396-023-01397-x.

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## Coverage

**Spatial Extent:** N:81.82 E:179.06 S:-77.01 W:-176.57

**Temporal Extent:** 2013-12 - 2024-04

## Methods & Sampling

*Genomic dataset collection, curation and quality control:* This study used publicly available genome assemblies. Existing publicly available genome assemblies were downloaded from the National Center for Biotechnology Investigation (NCBI) and the Integrated Microbial Genomes (IMG) database of the U.S. Department of Energy's Joint Genome Institute in June 2021. The Genome Taxonomy Database (GTDB) website (release 202) was used to access lists of NCBI assembly accession numbers for the following GTDB-assigned phyla: *Nitrospinota*, *Nitrospinota\_A* (now called *Tectomicrobia*), *Nitrospinota\_B*, *Nitrospirota*, *Nitrospirota\_A* (*Leptospirilla*). The IMG assemblies were found using the same GTDB taxonomy classifier using the search function on the IMG website. IMG metagenome assemblies that were designated as "public" and "published" were also downloaded for these phyla. Duplicate entries between IMG and NCBI were manually removed.

## Data Processing Description

Quality control of the assemblies was performed using the CheckM qa workflow (v 1.07) to remove genomes with <50% genome completion and >10% sequence contamination, leaving genomes that fall within the MIMAG categories “medium” (>50% completion, <10% contamination) and “high” (>90% completion, <5% contamination). These resulting genomes were dereplicated with dRep, using default parameters, to remove nearly-identical assemblies. All genomes were then classified using the GTDB-tk classifier tool (v1.5.0, r202). Polyphyletic groups that were once considered a part of *Nitrospirota* and *Nitrospinota* (i.e., *Nitrospirota\_A* (*Leptospirilla*), *Nitrospinota\_A* (*Tectomicrobia*) and *Nitrospinota\_B*) were included only in the phylogenomic trees. These groups were not included in the gene cluster based functional analyses. All code to recreate these processes are available at [https://github.com/ts-dangelo/bioinformatic\\_scripts\\_python](https://github.com/ts-dangelo/bioinformatic_scripts_python).

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## Parameters

*Parameters for this dataset have not yet been identified*

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## Project Information

### Microbial activity in the crustal deep biosphere (Slow Life in Crust)

**Coverage:** Juan de Fuca Ridge flank CORKs, 47N/127W

#### *NSF Award Abstract:*

The marine deep biosphere is the habitat for life existing under the sea floor. The zone has remarkably low energy sources creating a paradox of how life can persist there. Resolving this energy paradox is a grand challenge in deep biosphere research. The Juan de Fuca Ridge flank off the coast of Washington, USA, is an accessible, low energy environment making it an attractive location for addressing this challenge. A series of experiments will be conducted on the seafloor at the Juan de Fuca Ridge flank, using established subseafloor observatories that access the crustal deep biosphere, to provide the first direct in situ measurement of microbial activity in the crustal subsurface. This project will provide essential information about the ability of life to survive under conditions that we are not able to replicate in the laboratory, but that are increasingly important for understanding microbial community interaction in the environment. This information can then be used in models of global microbial activity for estimating the impact of this biosphere on elemental cycling, transforming our understanding of microbial processes within this vast subseafloor habitat. To communicate these discoveries to the public, the project will include a ship-to-shore outreach program during the cruise. In addition public lectures will be presented, and an interactive display of deep-sea video footage will be set up for the annual public Open House at the Bigelow Laboratory for Ocean Sciences in Maine. Diverse undergraduate students and a postdoctoral researcher will be recruited to participate in the research and public outreach activities.

This project proposes to leverage existing subsurface infrastructure on the eastern flank of the Juan de Fuca Ridge with advances in single-cell based molecular and geochemical approaches to make fundamental new discoveries about the activity of life in the deep crustal biosphere. During a two-week research cruise, the research team will incubate crustal fluids in situ and in the laboratory with labeled substrates for tracking single-cell activity, coupled with radioisotope tracer activity and potentiostat measurements, with the objective of determining in situ and potential rates of activity and cellular physiology. The research will also identify which metabolisms active microorganisms utilize under in situ and laboratory conditions, the rates of these processes, and the microorganisms involved. The results are expected to provide explicit hypothesis testing of microbial activity and in situ microbial growth rates from the crustal deep biosphere to transform understanding of microbial activity in the crustal deep biosphere and generate critical information about the ability of life to survive under low energy conditions.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1737017</a>

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