

Introduction

Historical perspective:

- DNA is first discovered in 1860
- Friedrich Miescher Swiss scientist from Basel
- DNA called "Blueprint of Life"

The development of various methods:

- Chromatography (1950)
- EtBr-CsCl Gradient Centrifugation (1957)
- Silica Column-Based (1980)
- Salting-Out (1988)
- Magnetic Beads (1998)



Method: ZymoBIOMICS™ DNA Miniprep Kit for

DNA extraction

1. Mechanical lysis to release DNA

- Bead beating
- Centrifugation

2. Filtration process

- Get rid of contaminants
- Humic substances inhibit PCR

3. Binding of the DNA to a purification matrix

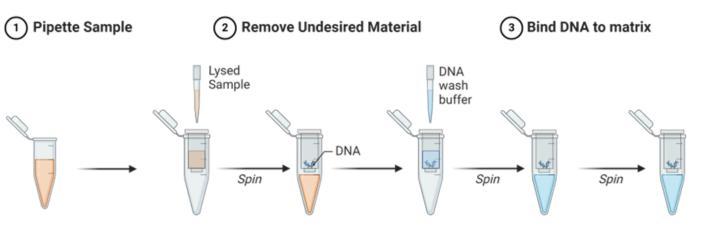
• Binding depending on the affinity of the matrix

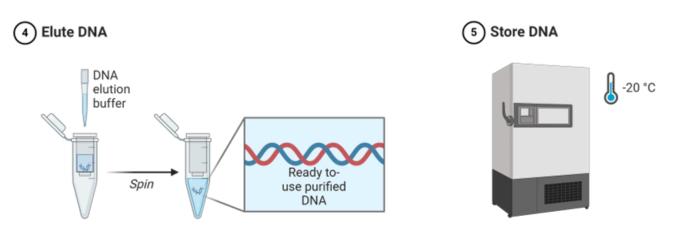
4. Washing processes

- Release DNA from the matrix
- Remove additional contaminants









Published Study

Research Open access | Published: 27 December 2022

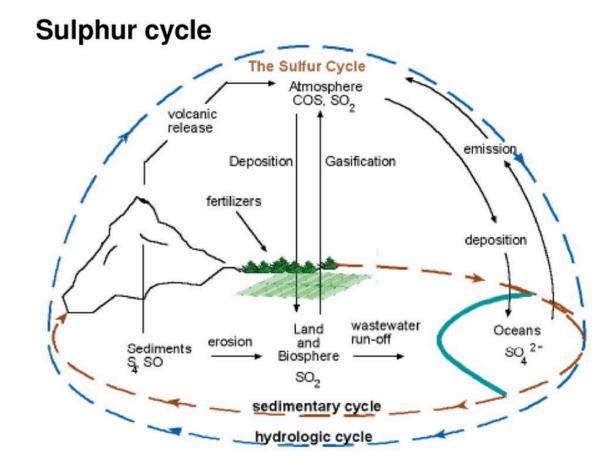
Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits

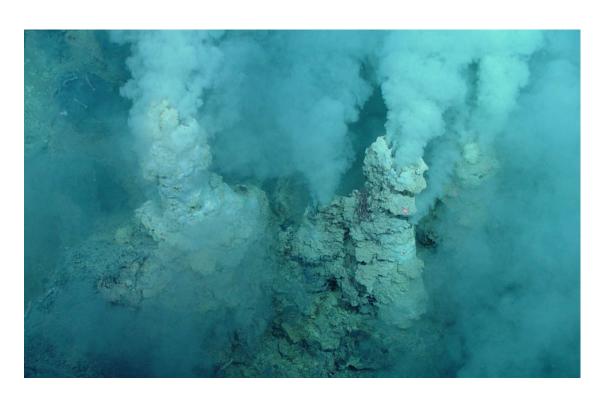
Microbiome 10, Article number: 241 (2022) Cite this article

10k Accesses | 32 Citations | 129 Altmetric | Metrics

Goals

- Explore **genomic diversity** of thermophilic microorganisms living on the deep-sea hydrothermal deposits
- Learn about their possible implications in biogeochemical cycles



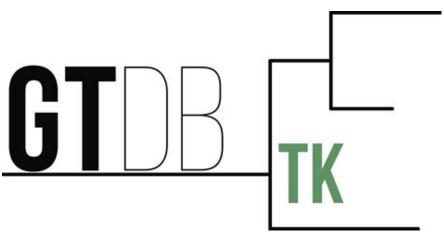


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Methods

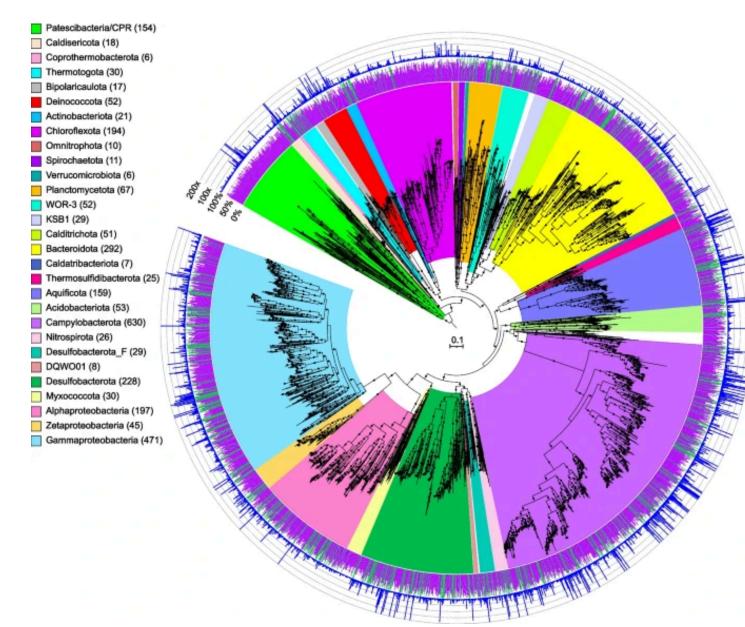
- Samples from 4 deep-sea hydrothermal vent fields + 1 deep sea volcano
- DNA extraction + sequencing
- Generation of metagenome-assembled genomes (MAG)
- Phylogenetics inferences : Genome Taxonomy Database Toolkit (GTDB-Tk)
- Trophic and energy metabolism analysis





Results & Findings

- 2983 bacterial and 652 archaeal draft MAGs
- Discovered a large diversity for Thermoproteia, Patescibacteria and Chloroflexota
- 2 potentially novel phyla: JALSQH01 and JALWCF01
- New assembled genomes
- Ecology side: metabolic "handoffs", functionnal redonduncy & importance of geochemical caracteristics of the site

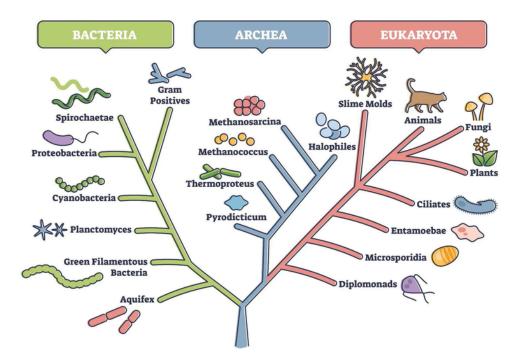


Maximum-likelihood phylogenomic tree of bacterial metagenome-assembled genomes, constructed using 120 bacterial marker genes in GTDB-Tk

Conclusion

- DNA extraction methods have become more effective
- ZymoBIOMICS™ (cell extraction method) is divided into 4 consecutive steps
- Used to explore the genomic diversity in harsh environments
- Helps understanding their implications in geochemical cycles & interactions with other organisms

PHYLOGENETIC TREE





Sources

- [1] https://fr.wikipedia.org/wiki/Friedrich_Miescher
- [2] https://zymoresearch.eu/products/zymobiomics-dna-miniprep-kit
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Study Article:

• Zhou, Z., St. John, E., Anantharaman, K. et al. Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits. Microbiome 10, 241 (2022). https://doi.org/10.1186/s40168-022-01424-7