



Conference Abstract

Integrative Genomics Sheds Light on Global Deep Terrestrial Biosphere Communities

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Abstract

Active microbial lineages inhabit the deep terrestrial subsurface (Fry et al. 1997, Lopez-Fernandez et al. 2018) with estimates suggesting deep subsurface ecosystems to host ca. 90% of the total bacterial and archaeal biomass on Earth and about 10-20% of all terrestrial biomass (McMahon and Parnell 2014, Bar-On et al. 2018, Magnabosco et al. 2018, Drake and Reiners 2021). This highlights deep subsurface ecosystems as a vast reservoir of genetic innovation that remains poorly characterized. The biological diversity of deep subsurface ecosystems seem to be influenced by parameters such as temperature, pressure, water residence times, and geochemistry (Drake and Reiners 2021).

The deep subsurface environment remains underrepresented in metagenomic databases, and yet the publicly available datasets are not synoptically analyzed in an integrated way. In this project, we collected a large set of publicly available and published metagenomes, published metagenome assembled genomes (MAGs) as well as single cell amplified genomes (SAGs) originating from global deep oligotrophic terrestrial subsurface samples (>70 m). Reconstructed MAGs/SAGs from this survey were integrated in to our own existing *Fennoscandian Shield Genomic Database* (FSGD) (Holmfeldt et al. 2021, Mehrshad et al. 2021). This expanded global database of the deep oligotrophic terrestrial subsurface contains >4000 MAGs/SAGs. In this dataset, representatives of phyla Firmicutes, Desulfobacterota, Patescibacteria, and Chloroflexota were the most prevalent

taxa. The presence of *Candidatus Desulforudis audaxviator* across different continents and samples highlighted its adaptation to different deep biosphere environments. In addition, novel bacterial lineages at the class level were identified in several locations, pointing to the importance and necessity of further studies to characterize deep biosphere microbial diversity.

This extensive study of the global deep oligotrophic terrestrial subsurface will reveal whether deep terrestrial populations are ubiquitous and how their distribution patterns are affected by different physicochemical variables such as water types and geology. By identifying key populations present across multiple global groundwaters, our study will advance our understanding of the global diversity hosted in deep oligotrophic terrestrial subsurface ecosystems.

Keywords

deep terrestrial biosphere, (meta)genomic, extremophiles

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Conflicts of interest

The authors have declared that no competing interests exist.

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