

# **Novel bacteria hiding in the deep**

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Much of our knowledge concerning microbial diversity comes from culturing, or the growing of microorganisms under laboratory conditions. However, the vast majority of microbial life is unable to be grown in this way, due to our inability to effectively replicate many natural environments. This uncultured diversity that permeates our world is referred to as microbial dark matter. The sequencing of genetic material directly from an environment is a way in which we can explore such diversity without the need to directly grow an organism in the lab. A metagenome, for instance, refers to sequence data of all of the genetic material from an environmental sample, which gives us access to the genomes of microbes living in this location. From such genomic information we can explore gene content, thus gaining insight into the lifestyle and metabolism of various organisms that would otherwise remain invisible to us.

Deep below the oceans surface (3000m) in the frigid waters North of Norway and Iceland, the 'towers' of Loki's Castle lay. At this hydrothermal vent, minerals carried by super heated water escape from fissures in the ocean floor and are deposited over time, forming the towering chimney-like black smokers found here. Representing nutrient-rich meccas in the middle of the desert of the ocean floor, such locations are hotspots for biological activity. The area surrounding Loki's Castle played host to past bouts of such activities over thousands of years. It was here, 15km from today's vents, that we discovered large amounts of novel major bacterial lineages.

I have studied the abundance and diversity of these novel bacterial groups present in different samples from Loki's Castle hydrothermal vent field sediments. All copies of a gene, called the 16S/18S rRNA gene, present in environmental samples taken from near Loki's Castle were sent for sequencing. This gene is found in all known cellular life forms (including *Homo sapiens*) and allows us to determine the identity of organisms and their evolutionary relationship to each other.

Furthermore, using state-of-the-art bioinformatics tools, I extracted genomic data of three novel microbes found in a large metagenome derived from a particular Loki's Castle sediment sample. I will explore the gene content of these novel organisms to learn more about their lifestyle, metabolism and evolutionary history. Initial analyses have already shown, that they might yield novel insights into the evolution of some important pathogens.

Altogether, this study revealed an unprecedented abundance and hereto-unknown diversity of novel bacterial lineages that evolved hundreds of millions of years ago. Certainly, prospective analyses will yield exciting new insights into such microbial dark matter hiding in the deep oceans.

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