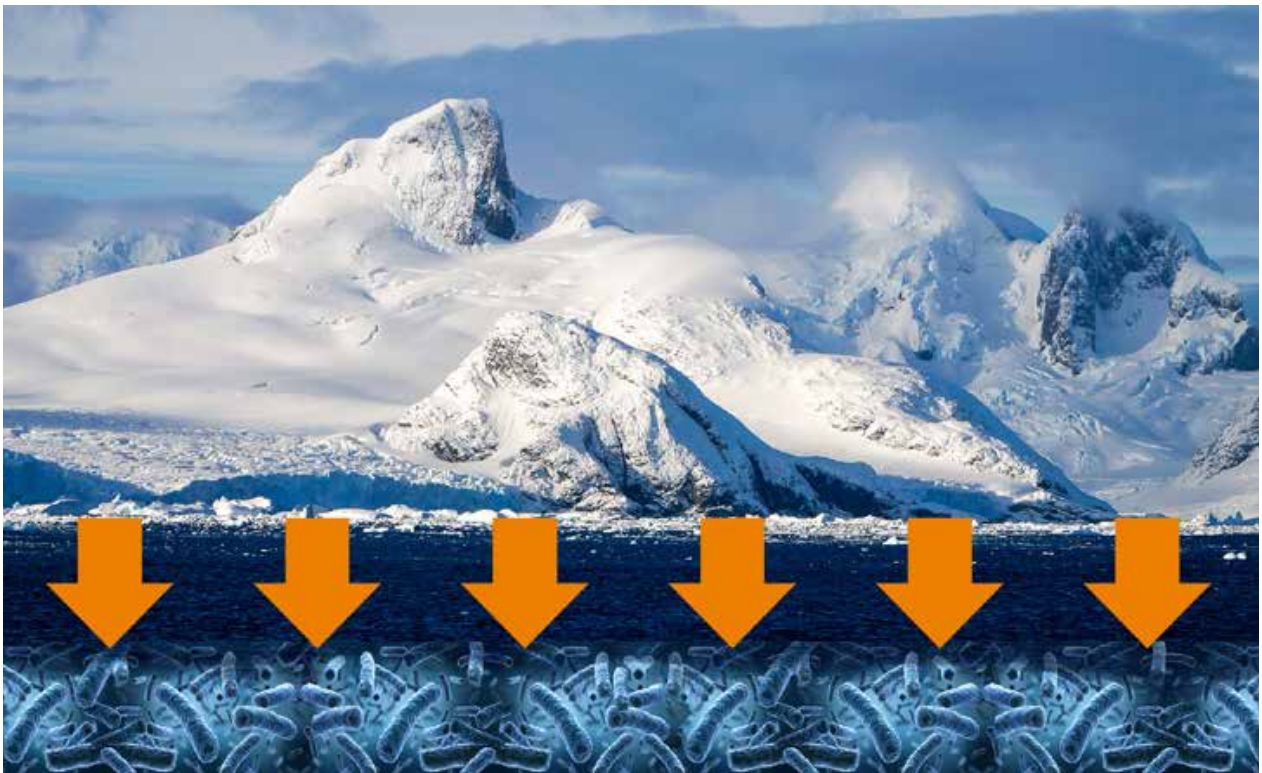


Microbiota in permafrost play an important role in climate change

Jenni Hultman, Senior Scientist at the Natural Resources Institute Finland (Luke), is interested in microbiota in cold climates that may also have an effect on the global climate. For example, there are bacteria and archaea on the tundra that eat methane, a potent greenhouse gas.



It has been discovered that the tundra is also a major source of other greenhouse gases, such as nitrous oxide. However, the diversity of micro organisms that contribute to generating nitrous oxide, is largely unknown to science yet. Even if we found out which types of microbes are involved, it is also important to know what kind of processes their genes are actually involved.

Metagenomics means the study of microbial DNA directly in their natural living environment. The term generally refers to bacterial genomes in a sample, but it also means the genomes of other micro organisms, such as those of archaea and fungi and

also the genomes of the eukaryotes inhabiting the sample of interest. Metagenomics can thus be used to study and sequence multiple organisms simultaneously from a single sample. Hultman and her colleagues sequenced millions of genomes from tundra soil microbiomes. To do this, they needed the computing power of the Finnish ELIXIR Node CSC – IT Center for Science, because the volume of data in the materials runs in terabytes.

“We have learned what kind of microbes live in the subarctic area and what they do. Processing the data material has taken up an incredible amount of computing power.

We discovered several previously unknown microbiota and genomes.”

DNA sequences obtained from the samples have been analysed, aiming to identify new species and their relationships. By analysing RNA sequences, they have learned what the microbiota were doing at the time of sampling.

“What I’m particularly excited about is being able to visit the same sites in winter-time. Now we are able to learn about seasonal variation, that is, what takes place in the microbiota in the summer and winter and how warm autumns contribute to the microbial activity.”



Micro organisms that contribute to generating green house gases, is largely unknown to science yet. It is also important to know what kind of processes their genes are actually involved.

Hultman compared the sequence fragments found in the microbiota to those available in the databases.

“Most of the time, we could not find the same sequences in the databases. More than 90 per cent of the identified genes were unknown to us.”

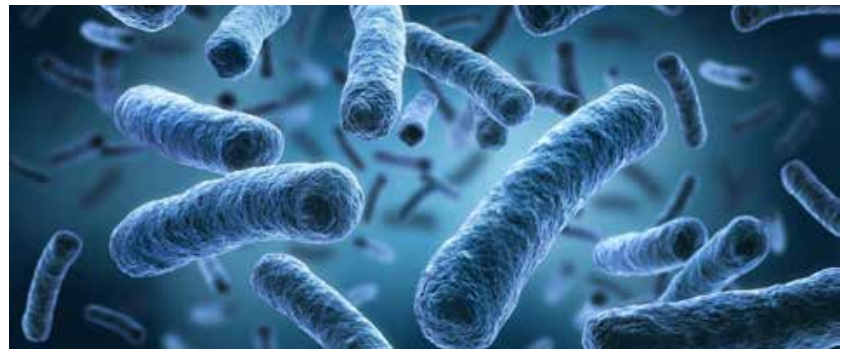
Industrially useful microbe species

Microbial data found in Kilpisjärvi and Pallas in Finnish Lapland was compared to other data sources, such as findings in Alaska and Sweden. Most of the Earth’s organisms are microbes. Although they occur everywhere and in all conditions, most of them are difficult to cultivate in laboratories. New techniques are required for their study, one of them being assembly of the metagenomic sequences. The metagenome-assembled genome, or MAG, is binned from metagenomic data. In other words, using a sample that contains a number of genomes, the genome of an individual species is pieced together.

This MAG data gives us new information about microbes that have not been cultured and subsequently sequenced, stored and annotated in databases.

Jenni Hultman’s study found more than 800 different MAGs, and only a small fraction of them were known previously. One interesting MAG was a species of archaea that oxidises ammonia. Ammonia-oxidising microbes play an important role in the nitrogen cycle.

“We first looked for the unknown archaea species in two datasets, from Norway and Kilpisjärvi, Finland. Once we started finding out where similar sequences could be found, we discovered them in Canada and Abisko, Sweden. Following a more detailed study, the particular archaeal genus was eventually found on both polar regions of the globe. It’s a fascinating thought that this archaea is specialised in living in polar regions. It is important to note that this





Lake Kilpisjärvi in Finnish Lapland is situated at 69° north. The Arctic Circle is situated 278 kilometers south from Kilpisjärvi.

discovery was made thanks to openness of data and the availability of databases. Arctic regions may be found to have plenty of microbes that can be useful in biochemical cycles.”

These include enzymes – proteins that speed up chemical reactions – that are created by microbes.

“Microbes are efficient in creating enzymes in cold conditions. These are biotechnically interesting communities. We create large, open databases about these species, sequencing them all. We have already discovered more than a thousand genomes. Enzyme processes can be interesting, because in cold conditions it can be more economical to grow microbes that produce enzymes.”

As a case in point, Hultman mentions genes found in microbes that can break down lignin. One potential application is the replacement of fossil materials.

Other interesting targets of study are fungi and actinobacteria.

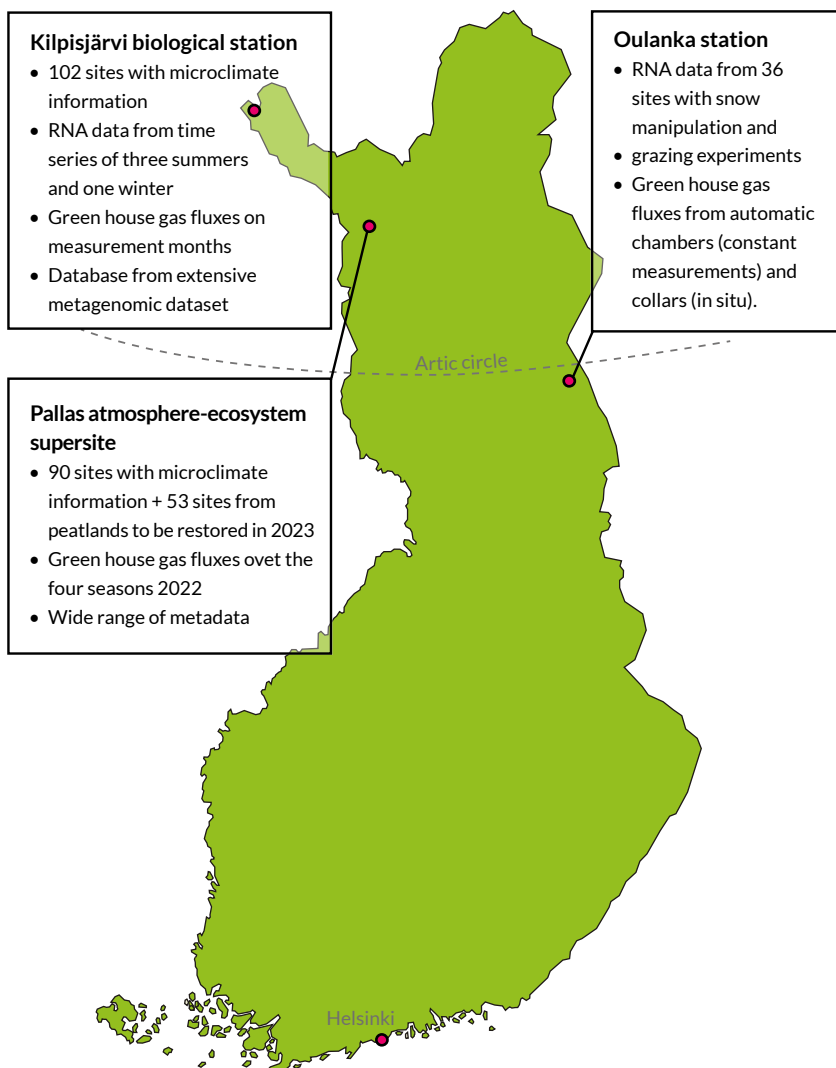
“We have found fungal families new to science – yet actually very common in our northern samples – which contain genes related to breaking up carbohydrates. Actinobacteria, known decomposers, occur in composts, for example, but there are also plenty of actinobacteria that live in cold conditions but still manage to be very active.

Methane-eating microbes

Methane is one of the most significant greenhouse gases. A Tampere University study in which sequencing data was analysed using CSC’s computing power, it was discovered that methane-eating bacteria, or methanotrophs, can be utilised for the manufacture of inexpensive bioproducts. Methanotrophs consume methane for their growth extremely efficiently.

Previously only individual species of microbes were studied, and the assumption was that a specific species only operates in a specific way. According to Hultman, these new findings have disproved this idea. For example, methane-eating microbes can be found among many species, not only in bacteria but also in archaea.

“Some can operate in both aerobic and anaerobic conditions. Previously it was thought that methane is created in anaerobic conditions and consumed in aerobic conditions. Deeper layers of soil contain methanogenic archaea that produce methane, while layers closer to the surface contain methanotrophs which oxidise methane and to which methane is key energy source. How to find the conditions in which these methane-eating methanotrophs thrive and how to make them multiply?”



Metagenomics and meteorology

Jenni Hultman did her thesis on composts and then moved on from such warm environments to the permafrost and Arctic areas. She is interested in how much the Arctic areas are warming and how much carbon is released into the atmosphere, but also how microbes work in carbon sequestration. Microbes play an important role in this.

“At high latitudes, the climate is warming four times as fast as previously thought. Once we learn how Arctic microbiota function, we can improve the climate-change prediction models. This data should be included in the climate models in order to better predict what the changes will cause. Metagenomics and climate sciences are actually rather closely linked. Microbes produce greenhouse gases and also consume them.”

In her work Hultman has been using the Sequence Read Archive (SRA) database, an open-access database composed of DNA sequences. They are maintained by the National Center for Biotechnology Information (NCBI), the European Bioinformatics Institute (EBI) and the DNA Data Bank of Japan (DDBJ).

“Researchers produce a huge amount of data all the time, and it is vital that we have access to databases. I hope ELIXIR can offer us up-to-date databases. When I find a new sequence fragment and I want to know what it is, I don’t have to download all new databases. Instead, they would be offered by ELIXIR. ELIXIR enables a large network that can help researchers to make open publications.

Ari Turunen

MORE INFORMATION:

Natural Resources Institute Finland (Luke)
<https://www.luke.fi/en>

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