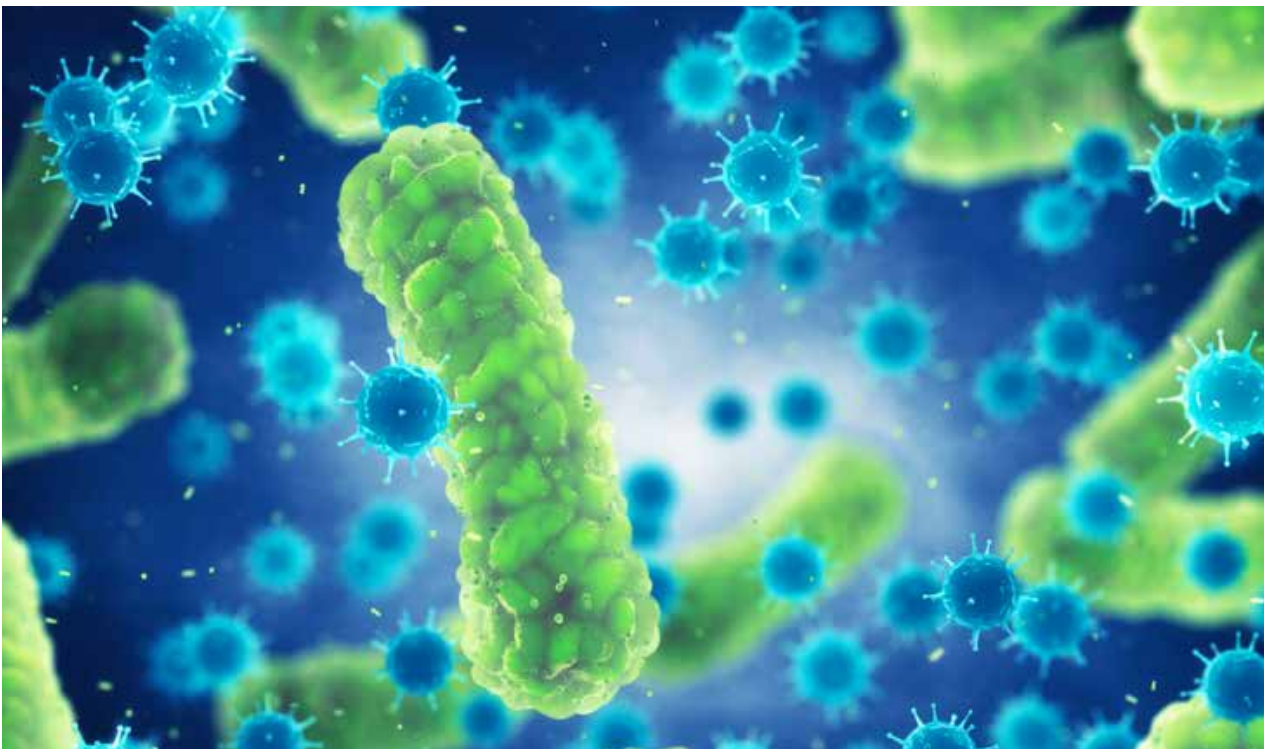


Microbes and Climate Change

Genetic research has revealed that there are a lot more microbes with much more diverse communities than we even knew about. Studying the genetics of microbial communities gave rise to a new branch of life sciences, metagenomics. Jenni Hultman studies the significance of the microflora in Arctic regions on climate change.



Microbes, or microorganisms, are what single-celled organisms or life forms consisting of a few cells are commonly referred to as. These include bacteria, protozoa, viruses and unicellular algae. Although microbes exist everywhere in our environment and even in extreme conditions, their genetic origin and function remain poorly understood. The vast majority of microbes are unknown.

The term metagenome references the idea that a collection of genes picked up and sequenced from the environment could be analysed in a way analogous to the study of the genome of a single species. With metagenomics, it is possible to investigate changes in microflora during the course of various diseases and, after

treatment, find new pathogens and obtain information about their function during medication, for example. Metagenomics can also be used to study how microbes affect our environment.

Arctic microbiology

Jenni Hultman is holding a sample that contains tens of thousands of different microbes.

In metagenomics, DNA is isolated from the microbial community. This has been relatively easy when microbes have been studied in the intestines and bodies of water, for example.

The examination of soil is considerably more challenging due to the large number of microbes in a single sample. One sample

may include up to 10,000 different species. Since new technologies allow the DNA of different microbes to be isolated from the soil, microbial research is under constant change. New information about organisms as well as the origin of life on Earth is obtained all the time. However, microbial communities are challenging as research subjects. Microbial diversity is very high and microbes also affect each other in ways that are not well known yet.

“Microbes have traditionally been grown in petri dishes. But we are now talking about a huge number to be studied because the research subjects are microbial communities where the different microbes are dependent on other microbes or nutrients. Such communities cannot be grown in

dishes. Now, the aim is to sequence the majority of the genes in the soil sample. Even if you find out what the species is, it is also important to know what the genes do. Since up to millions of genes are sequenced from a microbial community, this requires computing capacity”, says Academy Research Fellow Jenni Hultman.

Hultman is particularly interested in the microflora of Arctic regions. As microbes act as decomposers in nature, they may play a significant role in the formation of greenhouse gases, such as carbon dioxide and methane. In the short term, the impact of methane on the greenhouse effect is several dozen times that of carbon dioxide.

“The microbes in the Arctic environment are not well known. They can have an effect on how the climate and conditions change. There are many questions. How is nature adapting to climate change? What do species do when the climate changes?”

The melting of peat bogs under the permafrost especially generates methane emissions. But what is the significance of microbes in this process? That is what Hultman wants to find out.

Hultman, who works at the Department of Food and Environmental Sciences of the University of Helsinki, collects research data on microbes in different parts of the Northern hemisphere. In her research, Hultman analyses soil samples in Kilpisjärvi, Alaska and Greenland. She is now looking for a survey site in Siberia, after which the samples she has collected would well represent the entire Northern hemisphere.

“20% of the Earth’s land surface is covered by permafrost. Within the permafrost are huge stores of carbon diox-



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ide. The melting of permafrost may release the highest amounts of carbon dioxide ever measured into the atmosphere. This process is dependent on a microbial response but, at present, we know rather little about the activity of microbes under permafrost.”

Data for climate models

ELIXIR is participating in the Tara Oceans project studying oceanic microbes. It is easy to filter microbes from water and obtain a comprehensive sample. However, when collecting soil samples, it is necessary to perform parallel isolations due to the heterogeneity of the soil in order to obtain a sufficient number of decent samples.

Hultman is interested in the activity of microbial communities and especially in what the genes of the microbial communi-

ties do (metagenomics) and how active the genes of the communities are at a given time (metatranscriptomics).

Hultman isolates the total DNA and RNA from the soil samples of the field area in Kilpisjärvi, divides them into smaller pieces and sequences them. She isolates the DNA and RNA from samples of 0.5 grams. The number of sampling points is over a hundred. The area has a microclimate, allowing Hultman to take into account various factors, such as humidity, pH and temperature. This makes it possible to study the significance of the activity of microbial communities on climate change on the scale of “mini climate change.”

“A high number of parallel samples weighing half a gram are needed because the microflora of the soil is diverse and because the soil itself varies greatly. Microbes can be present in stone, a dead worm, the root of a plant or just in a place that is more humid than another. So there is a lot to dig up and isolate.”

The essential thing is to know what the genes of the microbes are actively doing and how they affect climate change.

“I am studying what is happening in the soil sample at this moment. Which genes are active? Are some microbes accelerating climate change and some slowing it down? Do microbes just produce methane or do they utilise it?”

One important goal of Hultman’s research is to produce data obtained from metagenomics also for climate models. This





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may potentially improve the reliability of climate models.

Only 1% can be made to grow in laboratories

One gram of soil may contain up to ten billion different microbes. When microbial ecology research truly started in the late 1970s and microbial samples from the environment were compared with cultured microbial samples, it was found that the samples from the environment contained up to 99% more new and unknown microbes than the cultured samples.

Traditionally, the sequencing of genes is started by growing cells in a Petri dish. When DNA from the cells is placed in a DNA sequencer, it determines the order of the DNA base pairs: adenine, guanine, cytosine and thymine. However, early metagenomic studies revealed that there are large groups of microorganisms that cannot be grown in laboratories and that, therefore, cannot be sequenced.

The early studies focused on the sequences produced by the 16S rRNA gene. The function of the 16S rRNA gene, which is found in all living creatures, is to pro-

duce the ribosomes in which protein synthesis occurs. In 1977, microbiologist Carl Woese started the sequencing of this gene when studying microbes. Because the gene is always slightly different in different microbes, Woese noticed that it can be used to study the development history of the microflora in the samples. However, Woese and his colleague George E. Fox were surprised when many of the isolated 16S rRNA sequences did not belong to any known species. The discoveries made with the 16S rRNA gene revolutionised microbial research.

Woese and Fox observed that the samples also contained unicellular, but anucleate microorganisms that externally resembled bacteria but were not. They called this group the archaea.

Archaea are involved in metabolism and affect the functioning of enzymes. Archaea were initially observed only in extreme conditions, such as hot springs and salt lakes, but have since also been found in different soil types, marshlands, oceans and even human intestines, for example.

Organisms could thus be divided into three categories. Eukaryota, i.e. multisel-

lular plants, fungi and animals, have nuclei. Bacteria and archaea, in turn, are anucleate microbes that make up most of the world's biodiversity.

"As the sequencing of DNA is becoming cheaper all the time, metagenomics allows microbes to be studied on a much larger scale and in more detail than before", Jenni Hultman says.

The mysterious archaea may play a greater role in the formation of methane than has previously been known. Some archaea break down organic carbon into methane. But how many of such archaea are there and how effective are they as decomposers?

The data on the secrets of the microbiome collected by Jenni Hultman and other researchers is stored in the public information resources maintained by ELIXIR, the European life sciences infrastructure for bioinformatics.

Ari Turunen

FURTHER INFORMATION:

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builds infrastructure in support of the biological sector. It brings together the leading organisations of 21 European countries and the EMBL European Molecular Biology Laboratory to form a common infrastructure for biological information. CSC - IT Center for Science is the Finnish centre within this infrastructure.

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