



#FEMSmicroBlog: Finding antibiotic resistance genes in the arctic permafrost

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Global climate change is particularly noticeable in the Arctic since it is warming twice as fast as temperate regions. The permanently frozen ground makes up 90% of Siberia so that the melting of permafrost reactivates microbial populations that contribute to the emission of greenhouse gases and the periodic resurgence of zoonotic diseases. In [this work](#), published in the journal *microLife*, an international team shows that these permafrost microbes also constitute an enormous reservoir of antibiotic resistance genes. #FascinatingMicrobes

Linking frozen microbes to current challenges

In 2014 and 2015, the Information Génomique et Structurale (IGS) laboratory from the Aix-Marseille University and the Centre national de la recherche scientifique (CNRS, France) isolated and reactivated two previously unknown viruses, Pithovirus and Mollivirus. These giant DNA viruses had remained infectious after 30,000 years of freezing in the Siberian permafrost.

Similarly, in 2016, during an unusual summer season in Northwest Siberia, the upper layer of thawed soil exhumed infectious *Bacillus anthracis* endospores. These used to result in frequent outbreaks of anthrax killing 1.5 million reindeers in the Russian North during the last century.

These and other discoveries received a lot of media attention as they added the possible release of “zombie” microbes to already known challenges like global warming and thawing. As such, the permafrost represents an extensive library of frozen but useful genetic elements that can be brought back to life. On the other hand, reviving these elements can be potential threats to today’s society, animals or plants.

The possible release of “zombie” microbes adds to already known challenges like global warming and thawing.

Finding microbes in the cold

This is why the study [“Metagenomic survey of the microbiome of ancient Siberian permafrost and modern Kamchatkan cryosols”](#) published in *microLife* aimed to obtain a complete picture of possible microbial dangers associated with the warming of the Siberian permafrost. For this project, the same research group assembled an international team from the North Eastern Federal University in Russia and Alfred Wegener Institute in Germany to carry out a large scale metagenomic analysis of various soil samples collected in the Yakutsk region and in Kamchatka.

Metagenomics consists of the extraction of total DNA from soils followed by massive sequencing that was performed at the French National Sequencing Centre (“Genoscope”, Evry, France). Bioinformatic methods allowed the detailed characterization of nearly 1000 billion nucleotides, a massive amount of genetic data. The detection of unknown, possibly pathogenic microorganisms was thus carried out in complete safety, without them ever being put into culture.



Drilling and

deep sample collection from permafrost in central Yakutia (Sakha Republic). Credit: Guido Grosse, Alfred Wegener Institute.

Interestingly, the microbial communities were found to be highly variable from one sample to another, regardless of their temporal or geographical distances. Yet, a more refined analysis revealed an unexpected property shared by these microbial communities. While these bacteria are certainly different, most of them carry genes for the enzyme β -lactamase causing the inactivation of penicillin-derived antibiotics.

Reviving new (or old?) Antibiotic Resistance Genes

The constant emergence of new versions of extended-spectrum β -lactamases from the environment is a major public health problem. As such, more and more multidrug-resistant bacteria emerge whose infections cause more than one million deaths per year.

The high proportion of bacteria carrying beta-lactamases in pristine soils untouched by human activity was totally unexpected and for the moment unexplained. Indeed, such a phenomenon is expected from microbial communities in agricultural or farming soils where heavy antibiotic usage would select resistances. One possibility is that competition among soil microorganisms – for instance between bacteria and/or fungi – might involve the natural synthesis of beta-lactam-related signaling/inhibitory compounds.

In addition to the prehistoric viruses it contains, permafrost thus seems to constitute an enormous reservoir of antibiotic resistance genes that could be put back into service either in revived ancient bacteria or by the transformation of contemporary bacteria when it thaws.

The permafrost constitutes an enormous reservoir of antibiotic resistance genes that could be revived.

With this work, the inexorable melting of the Siberian permafrost is now associated with two of the major challenges threatening the future of our society: global warming and the return of infectious diseases beyond our therapeutic arsenal.

- Read the paper “[Metagenomic survey of the microbiome of ancient Siberian permafrost and modern Kamchatkan cryosols](#)” by Rigou *et al.* (2022).

About the authors of this blog



[Dr. Jean-Michel Claverie](#) is Emeritus Professor of Genomics and Bioinformatics at the School of Medicine of Aix-Marseille University. Until recently, he directed the Mediterranean Institute of Microbiology and was the head of the [Structural and Genomic Information Laboratory](#), a unit of the French National Research Center (CNRS) that he founded in 1996. During his career, he occupied positions in various French CNRS laboratories, the Salk Institute (La Jolla, CA), The Pasteur Institute (Paris), NIH (Bethesda, MD), and Incyte Pharmaceuticals (Palo Alto, CA). In the last 15 years, he discovered and studied several new families of giant viruses, some of them revived from ancient (>30,000 y) Siberian permafrost layers. His main research goal is now to evaluate the microbial threats that may arise from the thawing of ancient arctic permafrost.

About this blog section

The section **#FascinatingMicrobes** for the **#FEMSmicroBlog** explains the science behind a paper and highlights the significance and broader context of a recent finding. One of the main goals is to share the fascinating spectrum of microbes across all fields of microbiology.