

New key players in the methane cycle

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Hot springs such as the Tengchong Yunnan hot spring in China are a preferred habitat of the investigated microorganisms. Credit: Prof. Wenjun Li

Methane is not only a powerful greenhouse gas, but also a source of energy. Microorganisms therefore use it for their metabolism. They do

so much more frequently and in more ways than was previously assumed, as revealed by a study now published in *Nature Microbiology* by researchers from the Max Planck Institute for Marine Microbiology and Jiao Tong University in Shanghai.

Methane is a very special molecule. It is the main component of natural gas and we heat our apartments with it, but when reaching the atmosphere it is a potent greenhouse gas. It is also central in microbiology: In the absence of oxygen, a special group of microorganisms, the so-called methanogenic archaea, can produce methane. Other microorganisms—archaea living in symbiosis with bacteria—can use methane as a food source.

Regardless of whether methane is produced or consumed, the same enzyme is the key: methyl coenzyme M-reductase (MCR). This enzyme produces methane, but it can also be used to break up this gas. This enzyme produces methane and can break this gas up again. For a long time, scientists believed that only a few species of microbes could convert methane in one way or another. Recently, however, increasing evidence has sprung up that important key players in the methane cycle have been overlooked.

Searching for the genome needle in a sequence haystack

Scientists from Jiao Tong University in Shanghai, China, and the Max Planck Institute for Marine Microbiology in Bremen have now taken a closer look at this. They scoured global genome databases for information on genes of new methane organisms found in the environment. Their trick: They did not look for specific organisms, but for the key enzyme.

In his search for [gene sequences](#) similar to the known MCR genes, first author Yinzhao Wang from Jiao Tong University soon found what he was looking for. He discovered a number of previously unknown genes that carry the necessary information for the production of MCR. "These MCRs can be roughly divided into three groups," says Yinzhao Wang. "One group comprises the known gene sequences. The other two groups are completely new."

The researchers used these new sequences as the first piece of the puzzle to find complete genomes from the vast amount of data available. The results were stunning: The assembled genomes were completely different from those of known methane microbes. "For example, we found MCR in *Archaeoglobi* and in archaea from the TACK superphylum. Such [metabolic pathways](#) have not previously been suspected in these organisms," says Fengping Wang from Jiao Tong University, the initiator of the study.

The results now published show that different variants of the methane metabolism are widespread in archaea. This suggests a greater importance of these microorganisms in global carbon balancing than previously assumed.

New species and metabolic pathways

What the microbes do with these metabolic pathways in detail has not yet been clarified. Some organisms seem to produce methane. Others, on the other hand, seem to oxidize it.

"Our results are very exciting. We presumably discovered the first archaea that can breathe methane with sulfate without partner bacteria," says Gunter Wegener from the Max Planck Institute in Bremen. "Others obviously don't feed on methane, but on higher hydrocarbons." The genomes alone only provide clues to the way of life of these archaea.

"We often do not know in which direction the organisms use the apparently very flexible metabolic pathway of [methane](#) production," Wegener says.

From the database to the lab

In order to understand exactly what the discovered organisms are doing and to test the genome-based hypotheses, the researchers from Bremen and Shanghai will now jointly try to cultivate these [organisms](#). It's not easy, however—they seem to prefer life in [hot springs](#) and in deep subsurface habitats. With material from these places, the scientists will begin their cultivation experiments.

More information: Expanding anaerobic alkane metabolism in the domain of Archaea, *Nature Microbiology* (2019). [DOI: 10.1038/s41564-019-0364-2](#) , www.nature.com/articles/s41564-019-0364-2

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