

Poison + water = hydrogen. New microbial genome shows how

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Take a pot of scalding water, remove all the oxygen, mix in a bit of poisonous carbon monoxide, and add a pinch of hydrogen gas. It sounds like a recipe for a witch's brew. It may be, but it is also the preferred environment for a microbe known as *Carboxydotherrnus hydrogenoforrnans*.

In a paper published in the November 27th issue of *PLoS Genetics*, a research team led by scientists at The Institute for Genomic Research (TIGR) report the determination and analysis of the complete genome sequence of this organism. Isolated from a hot spring on the Russian volcanic island of Kunashir, this microbe lives almost entirely on carbon monoxide. While consuming this normally poisonous gas, the microbe mixes it with water, producing hydrogen gas as waste.

As the world increasingly considers hydrogen as a potential biofuel, technology could benefit from having the genomes of such microbes. "*C. hydrogenoforrnans* is one of the fastest-growing microbes that can convert water and carbon monoxide to hydrogen," remarks TIGR evolutionary biologist Jonathan Eisen, senior author of the PLoS Genetics study. "So if you're interested in making clean fuels, this microbe makes an excellent starting point."

In sequencing the microbe's genome, Eisen and his collaborators discovered why *C. hydrogenoforrnans* grows more rapidly on carbon monoxide than other species: The bug boasts at least five different forms of a protein machine, dubbed carbon monoxide dehydrogenase, that is

able to manipulate the poisonous gas. Each form of the machine appears to allow the organism to use carbon monoxide in a different way. Most other organisms that live on carbon monoxide have only one form of this machine. In other words, while other organisms may have the equivalent of a modest mixing bowl to process their supper of carbon monoxide, this species has a veritable food processor, letting it gorge on a hot spring buffet all day.

"The findings show the continued value of microbial genome sequencing for exploring the useful capabilities of the vast realm of microbial life on Earth," says Ari Patrinos, director of the Office of Biological and Environmental Research, part of the U.S. Department of Energy's (DOE) Office of Science. DOE, which funded the study, is pursuing clean fuel technologies.

Little was known about this hydrogen-breathing organism before its genome sequence was determined. By utilizing computational analyses and comparison with the genomes of other organisms, the researchers have discovered several remarkable features. For example, the genome encodes a full suite of genes for making spores, a previously unknown talent of the microbe. Organisms that make spores have attracted great interest recently because this is a process found in the bacterium that causes anthrax. Sporulation allows anthrax to be used as a bioweapon because the spores are resistant to heat, radiation, and other treatments.

By comparing this genome to those of other spore-making species, including the anthrax pathogen, Eisen and colleagues identified what may be the minimal biochemical machinery necessary for any microbe to sporulate. Thus studies of this poison eating microbe may help us better understand the biology of the bacterium that causes anthrax.

Building off this work, TIGR scientists are leveraging the information from the genome of this organism to study the ecology of microbes

living in diverse hot springs, such as those in Yellowstone National Park. They want to know what types of microbes are found in different hot springs--and why. To find out, the researchers are dipping into the hot springs of Yellowstone, Russia, and other far-flung locales, to isolate and decipher the genomes of microbes found there.

"What we want to have is a field guide for these microbes, like those available for birds and mammals," Eisen says. "Right now, we can't even answer simple questions. Do similar hot springs, a world apart, share similar microbes? How do microbes move between hot springs? Our new work will help us find out."

Source: The Institute for Genomic Research

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