

The First Sequenced Extremophile

What scientists have learned from the *M. jannaschii* genome

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featured article

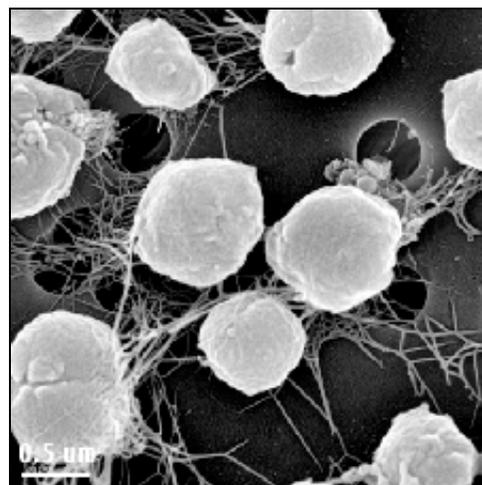
Extremophiles are the rule breakers of biology. These organisms live in the harshest environments on earth—boiling water holes in Italy, the ice of Antarctic seas, and hydrothermal vents at the bottom of the ocean. They not only survive but also thrive under conditions previously thought to prohibit all forms of life. In recent years, scientists have begun to mine the genomes of extremophiles for information that might lead to new technologies, such as heat-resistant molecules for commercial uses, and to breakthroughs in medicine and the environmental sciences.

The first extremophile to be sequenced was *Methanococcus jannaschii*, an organism straight out of science fiction. The single-celled microbe lives near hydrothermal vents 2,600 meters below sea level, where temperatures approach the boiling point of water and the pressure is sufficient to crush an ordinary submarine. There, *M. jannaschii* survives on carbon dioxide, hydrogen and a few mineral salts. It cannot tolerate oxygen and takes care of its energy needs by producing methane.

The weirdness of this creature intrigued scientists at The Institute for Genome Research (TIGR) in Rockville, Maryland, who, in the mid-nineties, decided to sequence *M. jannaschii*. They saw the project as an opportunity to explore a new theory about evolution. The genome sequence, which was published in 1996, has helped scientists draw more accurately the evolutionary tree and sparked the current fascination with extremophile genomes.

Until the 1970s, biologists placed living things into two broad categories, or domains, based on the structure of their cells. These were the eukaryotes—mainly plants and animals, whose cells had a nucleus—and the prokaryotes, such as bacteria, whose cells did not. In 1977, a microbiologist at the University of Illinois at Urbana-Champaign, Carl Woese, challenged the status quo. He proposed that there are actually three domains of life rather than two.

The third domain, known today as the archaea, is made up of single-celled organisms that lack a nucleus. Woese argued that despite a superficial resemblance to bacteria, archaeons have a distinct evolutionary heritage and therefore belong in a separate category.



Methanococcus jannaschii
©UC Berkeley Electron Microscope Lab



Methanococcus jannaschii was isolated near a "smoker," a hydrothermal vent 2,600 meters deep in the Pacific Ocean.
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Woese had wanted to sequence an archaeal genome since the early 1980s. "Having been discovered rather late in the game, the archaea were not very well understood organisms," he says. "You could use genome sequencing to give you a jump-start on characterizing the archaea."

TIGR sequenced the *M. jannaschii* genome in order to provide "a much more comprehensive view of the relationship between organisms of these three domains of life," recalls Claire Fraser, a member of the TIGR sequencing team. Until then, the evidence for the existence of a new biological domain had been largely based on studies of small numbers of genes.

Methanococcus jannaschii was first plucked from the edge of a sea-floor chimney known as a white smoker off the coast of Mexico in 1982. It was named for Holger Jannasch of the Woods Hole Oceanographic Institute in Massachusetts, the microbiologist who led the research expedition that identified the organism.

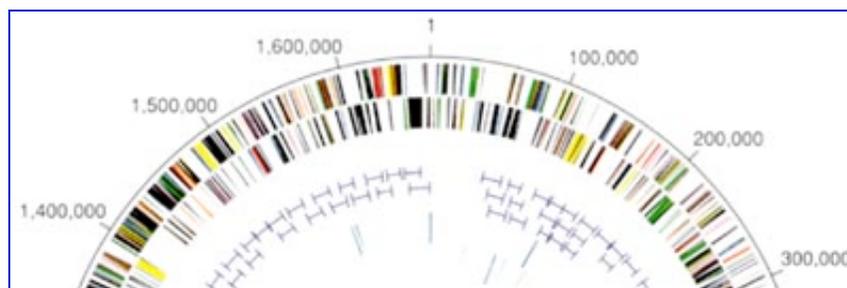
Described as 'raisin-like' in appearance under the microscope, *M. jannaschii* has a thin, tail-like flagellum on one end that gives the cell mobility. It grows in thick mats and shares its habitat near fissures in the Earth's crust with a few other hardy microbes and colonies of giant tube worms. Its genome contains about 1.7 million base pairs arranged in one circular chromosome and two smaller pieces, or extrachromosomal elements. The organism has 1,738 genes.

***M. jannaschii* was like nothing scientists had ever seen before.**

Methanococcus jannaschii was only the fourth free-living organism to be completely sequenced. Researchers at TIGR had previously sequenced two bacteria, *Haemophilus influenzae* and *Mycobacterium genitalium*, and an international consortium had sequenced a eukaryotic genome, *Saccharomyces cerevisiae*, or brewer's yeast. With the genome sequence of *M. jannaschii* in hand, scientists could for the first time compare genomes from all three domains of life.

Methanococcus jannaschii was like nothing scientists had ever seen before—more than half its genes were completely new. Only 44 percent of the genes matched DNA sequences of known genes. For instance, only 11 percent of the genes in *H. influenzae*

and 17 percent of those in *M. genitalium* matched a sequence from *M. jannaschii*. By comparison the two bacteria were very similar: 83 percent of *M. genitalium* genes had a counterpart in *H. influenzae*.



Circular map of the *M. jannaschii* chromosome. [View larger](#)
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The sequencing of *M. jannaschii* was funded by the US Department of Energy (DOE)'s Microbial Genome Project, which, since 1994, has investigated microbes that might be useful in environmental cleanup, energy production, or other aspects of DOE's mission. The agency thought that *M. jannaschii*'s ability to produce methane might be harnessed in the search for renewable energy sources.

But according to Daniel Drell of the DOE Office of Biological and Environmental Research, *M. jannaschii* requires such extreme conditions for growth that it is difficult to develop practical applications using the microbe. "I think the contributions that it will make will tend to be more fundamental," he says.

For example, Sung-Hou Kim and his colleagues at the Lawrence Berkeley National Laboratory in California have been studying *M. jannaschii*'s proteins. They are trying to define the repertoire of protein structural elements, or folds, and understand how protein structure relates to function.

The fact that *M. jannaschii* grows best in extreme environments was an asset in the study. Most of the proteins in *M. jannaschii* crystallize better than their counterparts in organisms that grow at lower temperatures, says Kim. "To function at a hot temperature, their proteins are much sturdier, and thus they crystallize better."

Kim and his colleagues were able to deduce the function of several *M. jannaschii* proteins based on their structures, a strategy that may prove useful in determining the functions of genes and proteins in other sequenced organisms. "The protein fold repertoire is much simpler than the protein sequence repertoire," Kim says. Indeed, new and more efficient strategies are needed to make sense of the data coming out of genome projects.

"I think we were all in those early days perhaps a bit naïve in thinking that once we had the genome sequence we would understand the organism," says Fraser. "Having the parts list is nowhere near enough to figure out the biology. But it's absolutely the right place to start."

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[Zarembinski, T.L. et al. Structure-based assignment of the biochemical function of a hypothetical protein: a test case of structural genomics. *Proc Natl Acad Sci USA* **95**, 15189-15193 \(December 22, 1998\).](#)

[Bult, C.J. *et al.* Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* **273**, 1058-73 \(August 23, 1996\).](#)

Read, T.-A. *et al.* Local endostatin treatment of gliomas administered by microencapsulated producer cells. *Nat Biotechnol* **19**, 29-34 (January 2001).

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