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### A hyperthermophilic methanogen sequenced

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#### Abstract

The complete genome sequence of *Methanopyrus kandleri* will enhance our understanding of how methanogens live in extreme environmental conditions

# Significance and context

The methanogenic archaeon *Methanopyrus kandleri* was isolated from a hot region at the bottom of the Gulf of California, at a depth of 2,000 meters. It grows at 80-110°C in a H<sub>2</sub>-CO<sub>2</sub> atmosphere, showing that methanogenesis, the production of methane, is possible at a temperature of 100°C. *M. kandleri* is unique, even among the Archaea. Its cell membrane is made of terpenoid lipids, the most primitive lipids in membrane evolution, and its cells contain a high concentration of 2,3-diphosphoglycerate, which is thought to help protect enzymes at extremely high temperatures. It also contains some exceptional enzymes; for example, a unique type 1B DNA topoisomerase. The determination of its genomic sequence should thus increase our understanding of life at extreme temperatures.

## Key results

The genome of *M. kandleri* is 1,694,969 bp in size and contains 1,691 putative protein-coding genes. *M. kandleri* proteins have an exceptionally high ratio of negatively to positively charged residues, which is perhaps correlated with the high intracellular salinity. The genome sequence was compared with those of *Methanothermobacter thermoautotrophicum* and *Methanococcus jannaschii*, two other methanogenic archaea. Previous taxonomic classifications, based on 16S RNA sequences, positioned *M. kandleri* in a deep branch of the archaea; however, on the basis of the current genome comparisons, *M. kandleri* is part of a clade including *M. thermoautotrophicum* and *M. jannaschii*, demonstrating that methanogenic archaea are monophyletic. All three contain several gene clusters that are relatively well conserved among methanogens, including the gene cluster encoding a putative thermophile-specific DNA repair system. Also, these methanogens share gene clusters that are not present in other archaeal genomes. Genes unique tomethanogens include those for membrane proteins involved in methanogenesis and hydrogenogenesis. Overall, conservation was highest between the genomes of *M. kandleri* and *M. thermoautotrophicum*. All three species are hydrogen-dependent autotrophic methanogens and their metabolic pathways are very similar. The predicted proteome of *M. kandleri* contains significantly fewer

membrane transporters than other archaea, but, on the other hand, some new transporter genes were noted. Unique to *M. kandleri* is an operon of 12 genes putatively encoding a type II/IV secretion system, probably involved in the secretion of protein and protein-DNA complexes. Interestingly, the *M. kandleri* genome contains an ortholog of the bacterial P-loop-containing serine kinase, which is involved in the phosphorylation of Hpr, a protein component of the sugar transport phosphotransferase system. This important regulator of carbohydrate metabolism in Gram-positive bacteria had not been found in archaea until now, and is thought to have been acquired by *M. kandleri* by lateral gene transfer.

## Links

Information about the genome of *M. kandleri* and other archaea can be found at the Center for Biological Sequence Analysis, BioCentrum-DTU, Technical University of Denmark.

# Conclusions

The genome of *M. kandleri* comprises all the genes characteristic of archaea. In gene content and organization, it is closely related to other methanogenic archaea, and forms a monophyletic group with them. *M. kandleri* considered a 'minimalist' archaeon because of the small number of genes acquired by gene transfer from other microorganisms, the low diversity of its transport proteins, and the scarcity of regulatory proteins, all of which are probably consequences of the severe environmental conditions of this microorganism's natural habitat.

# Reporter's comments

The determination of the entire genomic sequence of the hyperthermophilic methanogen *M. kandleri* provides extraordinary study material that will enhance our understanding of methanogenesis, of life at extremely high temperatures, and of the archaeal life-style in general. Of especial interest will be the physiological and/or genetic adaptations that this type of microorganism has that prevent the degradation of DNA and protein at such high temperatures. Particularly important proteins may have special conformations or be protected by other heat-stable proteins in order to maintain their activity. It will also be interesting to study gene expression and regulation under these severe conditions.

# Table of links

Proceedings of the National Academy of Sciences of the United States of America

Center for Biological Sequence Analysis, BioCentrum-DTU, Technical University of Denmark

#### References

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