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Hyperthermophile genome

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Abstract

The complete genome sequence of *Pyrobaculum aerophilum* reveals clues to how organisms can adapt to extreme temperatures

Significance and context

Pyrobaculum aerophilum is a hyperthermophilic archaeon that grows optimally at a temperature of 100°C. Taxonomically, *P. aerophilum* is most closely related to *Thermoproteus* species and belongs to the crenarchaea, a group of archaea that can survive at extreme temperatures. In contrast to most other hyperthermophiles described so far, *P. aerophilum* can survive under microaerobic conditions (<3% oxygen), but growth is completely inhibited when the element sulfur is present in the medium. *P. aerophilum* strain IM2, isolated from a boiling marine water-hole at Maronti beach, Italy, was used by Fitz-Gibbon *et al.* to determine the complete genome sequence. This study reveals clues to how this bacterium adapts to its hyperthermophilic environment and contributes to our understanding of life under extreme conditions.

Key results

The genome of *P. aerophilum* IM2 is relatively small, consisting of 2,222,430 base-pairs (bp), and has a G+C content of 51%. It contains 2,587 coding sequences, of which 38% showed similarity to known proteins, 22% to proteins with unknown function, 40% had no similarity to any proteins in the database. Interesting observations were made concerning DNA repair in archaea. Most commonly, replication mistakes in bacteria and other organisms are repaired immediately by polymerases or shortly after replication by a mismatch-repair system. No homologs of the mismatch-repair genes could be detected in the *P. aerophilum* genome, suggesting that such a DNA repair system is not present. This was further supported by the fact that certain regions within the genome exhibit fluctuations in DNA length. Fitz-Gibbon *et al.* suggest that *P. aerophilum* may have a permanent 'mutator' lifestyle, which may have severe consequences for its evolution if deleterious mutations continue to accumulate. Remarkably, *P. aerophilum* mRNAs generally lack a 5' untranslated region, suggesting that the mechanism of translation-initiation is different from that in which ribosomes recognize a typical bacterial Shine-Dalgarno sequence upstream of the translation start site.

Study of the genome sequence also explains why the presence of sulfur is lethal for *P. aerophilum*. Three genes involved in sulfate reduction or sulfur oxidation were found intact, but genes encoding both subunits of the adenylylsulfate reductase, acting in the middle of the pathway involved in sulfur metabolism, were mutated. Furthermore, some distantly related protein families were found in *P. aerophilum* that contain sequences of 8 to 11 adenines or thymines within the 24 bp preceding their start codons. Genome organization-wise, it was striking to observe that all runs of adenines were present in one half of the genome, whereas all runs of thymines were found in the other half of the genome. Many of the associated genes showed similar characteristics and are part of gene pairs, the downstream genes of which also share similarities, but the function of the respective proteins remains to be determined.

Links

An electron microscopic image of *P. aerophilum* is presented on the website of the [Department of Microbiology and Archaeenzentrum, University of Regensburg](#). Information about ongoing proteomics studies on this organism is available on the webpage for [The proteome of *Pyrobaculum aerophilum*: A pilot study in genomic-scale structural analysis](#).

Reporter's comments

The study by Fitz-Gibbon *et al.* reveals interesting observations of this particular bacterium, which belongs to a group of organisms that need to be studied in depth, since they represent life under extreme and unusual conditions. The availability of the genome sequence will facilitate further study of *P. aerophilum*. Future work should include attempts to answer questions such as the following: How does *P. aerophilum* prevent DNA and proteins from denaturing at a temperature of 100°C? How do proteins within *P. aerophilum* interact with each other and with DNA or RNA molecules? What is the composition of the *P. aerophilum* cell envelope, and which, if any, proteins and/or other factors are secreted by which mechanisms, and what is their role?

Table of links

[Proceedings of the National Academy of Sciences of the United States of America](#)

[Department of Microbiology and Archaeenzentrum, University of Regensburg](#)

[The proteome of *Pyrobaculum aerophilum*: A pilot study in genomic-scale structural analysis](#)

References

1. Fitz-Gibbon ST, Ladner H, Kim U-J, Stetter KO, Simon MI, Miller JH: Genome sequence of the hyperthermophilic crenarchaeon *Pyrobaculum aerophilum*. Proc Natl Acad Sci USA. 2002, 99: 984-989. 0027-8424