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Insights into an extreme lifestyle

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Summary

Sequencing *Thermoanaerobacter tengcongensis* reveals clues as to how this thermophile manages to live an extreme lifestyle

Significance and context

Thermoanaerobacter tengcongensis was isolated from a freshwater hot spring in Tengchong, China, and is a Gram-negative rod-shaped bacterium belonging to the anaerobic Eubacteria. The optimal growth temperature and pH are 75°C and 7-7.5, respectively. Bao *et al.* demonstrated that although *T. tengcongensis* has some features in common with other *Thermoanaerobacter* species, it also has some more peculiar characteristics, illustrating the heterogeneity within this taxonomic group. Determination of the entire genome sequence of *T. tengcongensis* adds to our understanding of how micro-organisms can survive at extreme high temperatures and how they have adapted during evolution to these exceptional environmental conditions, at the molecular level.

Key results

The genome of *T. tengcongensis* contains 2,689,445 base-pairs and the average G+C content is 37.6%. Coding DNA sequences with an average length of 905 base-pairs comprise 87.1% of the genome. A total of 2,588 coding DNA sequences were identified, the products of 57.8% of which show significant similarity to proteins present in public databases; in addition, 10.4% contain known protein domains; 11.6% showed similarity to hypothetical proteins; and 20.2% did not show any similarity to proteins present in databases. The G+C content of the rDNA and tDNA gene clusters is significantly higher than that of the genome as a whole, being 58.2-60.3% and 52.6-69.3%, respectively. This feature is common to all thermophiles sequenced so far. Repetitive elements, with a length that varies between a few tens up to hundreds of base-pairs, comprise 9.1% of the *T. tengcongensis* genome. To the latter type belong sequences encoding, for instance, transposases, ATP-binding cassette transporters, and hypothetical proteins. Interestingly, the genome contains 305 copies of a small 30 base-pair AT-rich repeat. High-abundance, small, repetitive elements have also been found in other thermophilic Archaea and Eubacteria. On the basis of a genome-wide comparison of proteins it was found that *T. tengcongensis* was most closely related to *Bacillus halodurans*, *Clostridium acetobutylicum*, and *B. subtilis*.

Previously, it has been demonstrated that *T. tengcongensis* can use thiosulfate or elemental sulfur but not sulfate to obtain energy. This property is reflected in the genome sequence, because the genes encoding sulfate transporters or enzymes involved in sulfate reduction are lacking, and a gene encoding a rhodanese-related sulfurtransferase, which uses thiosulfate as its electron acceptor, was identified. *T. tengcongensis* is able to metabolize monosaccharides and polysaccharides, including starch, to yield H₂, CO₂ and acetate. It contains many genes with products related to transport systems, for example transporters for monovalent, divalent and heavy-metal cations and transporters for carbohydrates. Although flagella were not noticed on cultured *T. tengcongensis* cells, by far the majority of genes required for flagellar synthesis and chemotaxis were present. Furthermore, the bacterium has 23 coding DNA sequences related to sporulation, although spore formation was not noticed in cultured cells.

On the basis of its Gram staining pattern, *T. tengcongensis* belongs to the Gram-negative bacteria. Some genes involved in the synthesis of lipopolysaccharides (LPSs), characteristic of Gram-negative bacteria, are present, but crucial genes are missing, including genes encoding an LPS-glycosyltransferase, two genes related to LPS transport, and four major genes involved in the synthesis of lipid A, the part of LPS that is localized to the bacterial outer membrane. In addition, coding DNA sequences for porins, typically present in Gram-negative bacteria, are absent. Interestingly, only 15 coding DNA sequences in the genome are unique to thermophiles. These comprise a single copy of a reverse gyrase, particular ATPase-encoding genes, a methyltransferase-encoding gene, and a metal-dependent hydrolase. A strong correlation was found between the G+C contents of tDNA/rDNA gene clusters and the optimal growth temperature for all 12 sequenced thermophilic Archaea and Eubacteria.

Links

The entire genome sequence of *T. tengcongensis* is available. More information about the genome sequence can be obtained from the Human Genome Project's (Beijing, China) [Thermoanaerobacter tengcongensis](#) website and from Indiana University's [The tmRNA website](#).

Reporter's comments

The study by Bao *et al.* on the genome sequence of *T. tengcongensis* definitely adds to our understanding of how bacteria adapt to extreme high temperatures. Now that several entire genome sequences of thermophilic bacteria are available, characteristic features of these genomes, including the tDNA/rDNA G+C contents and the presence of small abundant sequences, should be further exploited on a molecular level. Adaptation to life under extreme (temperature) conditions may indeed be an evolutionary question, but uncovering the molecular tools that enable bacteria to survive under these extraordinary conditions may have useful applications. The constitution of the *T. tengcongensis* surface remains an open question. It would be interesting to perform an in-depth study of the surface polysaccharides and get a clear picture of how the bacterial envelope is built up. One might expect an exceptionally rigid network of surface polysaccharides to provide the bacterial body with thorough protection against such severe environmental conditions.

Table of links

Genome Research

[NCBI bacterial genomes ftp site](#)

Thermoanaerobacter tengcongensis

[The tmRNA website](#)

References

1. Bao Q, Tian Y, Li W, Xu Z, Xuan Z, Hu S, Dong W, Yang J, Chen Y, Xue Y, et al: A complete sequence of the *T. tengcongensis* genome. *Genome Res.* 2002, 12: 689-700.