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The genome of a green sulfur bacterium

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Summary

The complete genome sequence of the photosynthetic anaerobe *Chlorobium tepidum* will help us to understand the evolution of photosynthesis

Significance and context

The Gram-negative bacterium *Chlorobium tepidum*, originally isolated from a hot spring in New Zealand, belongs to the group of green sulfur bacteria. These are anaerobic photosynthetic bacteria that live in anoxic and sulfide-rich waters, mud or sediments under very low light levels. Light harvesting occurs in specialized organelles called chlorosomes, which contain bacteriochlorophyll *a* and c, carotenoids, isoprenoid quinone, and proteins, the most abundant of which is the bacteriochlorophyll *a*-binding protein. Transmission electron microscopy shows the chlorosomes of *C. tepidum* as bodies of low electron density attached to the cell membrane. One of the unique features of *C. tepidum* is that, in contrast to plants and green algae, it photosynthesizes in anoxygenic conditions. Eisen *et al*. have now determined the entire genome sequence of *C. tepidum*, which should eventually reveal some interesting clues about the evolution and mechanisms of photosynthesis.

Key results

The genome of *C. tepidum* consists of a single circular DNA molecule of 2,154,946 base-pairs (bp) with a G+C content of 56.5%. The total number of predicted coding sequences is 2,288, with an average individual length of 837 bp. The predicted protein sequences of 1,315 of these open reading frames showed similarity to proteins of known function. Around 12% of the total number of predicted *C. tepidum* proteins are highly similar to archaeal proteins, and 31 protein sequences are similar to sequences from the plant *Arabidopsis thaliana*. Only a few regulatory proteins could be identified, including, for instance, 20 putative transcriptional regulators, a few proteins involved in sensing particular environmental conditions, and five RNA polymerase sigma factors. All the genes involved in photosynthesis in *C. tepidum* were identified, including a set of genes that encode ferrodoxins and Fe-S or flavin-containing electron-transport proteins, which participate in electron transfer during photosynthesis. Analysis of the genome sequence confirms that *C. tepidum* has a limited capacity to assimilate organic compounds. Compared to other bacteria for which the complete genome sequence is known, the genome contains a large set of genes encoding transporters of inorganic compounds, for example, metal ions, and also transporters of amino acids, peptides, purines, pyrimidines, and drugs. *C. tepidum* synthesizes three chlorophylls, including bacteriochlorophylls *a* and *c*, four versions of heme, and cobalamin. A pathway for chlorophyll synthesis in *C. tepidum* was proposed on the basis of the genome sequence. Finally, all the genes needed for the synthesis of the precursors of all isoprenoid compounds from pyruvate and glyceraldehyde 3-phosphate were identified.

Links

The entire genome sequence of *C. tepidum* can be accessed at the Microbial Genomes Blast Databases.

Reporter's comments

The complete genome sequence of *C. tepidum* provides the opportunity to study genes involved in photosynthesis in an organism with a very different metabolism from the well-studied purple bacteria and the oxygen-evolving cyanobacteria, algae and plants. This should provide clues about the evolution of photosynthesis in both bacteria and plants. Large-scale expression analyses will be useful in determining environmental signals or mechanisms that control the expression of particular sets of genes.

Table of links

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

Microbial Genomes Blast Databases

References

1. Eisen JA, Nelson KE, Paulsen IT, Heidelberg JF, Wu M, Dodson RJ, Deboy R, Gwinn ML, Nelson WC, Haft DH, et al: The complete genome sequence of *Chlorobium tepidum* TLS, a photosynthetic, anaerobic, green-sulfur bacterium. Proc Natl Acad Sci USA. 2002, 99: 9509-9514.