

Genome Sequence of *Halorhabdus tiamatea*, the First Archaeon Isolated from a Deep-Sea Anoxic Brine Lake

André Antunes, Intikhab Alam, Vladimir B. Bajic and Ulrich
Stingl

J. Bacteriol. 2011, 193(17):4553. DOI: 10.1128/JB.05462-11.
Published Ahead of Print 24 June 2011.

Updated information and services can be found at:
<http://jb.asm.org/content/193/17/4553>

	<i>These include:</i>
REFERENCES	This article cites 12 articles, 5 of which can be accessed free at: http://jb.asm.org/content/193/17/4553#ref-list-1
CONTENT ALERTS	Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

Genome Sequence of *Halorhabdus tiamatea*, the First Archaeon Isolated from a Deep-Sea Anoxic Brine Lake[∇]

André Antunes,^{1*} Intikhab Alam,² Vladimir B. Bajic,² and Ulrich Stingl¹

Red Sea Research Center, King Abdullah University of Science and Technology (KAUST), 23955-6900 Thuwal, Kingdom of Saudi Arabia,¹ and Computational Bioscience Research Center (CBRC), King Abdullah University of Science and Technology (KAUST), 23955-6900 Thuwal, Kingdom of Saudi Arabia²

Received 4 June 2011/Accepted 13 June 2011

We present the draft genome of *Halorhabdus tiamatea*, the first member of the *Archaea* ever isolated from a deep-sea anoxic brine. Genome comparison with *Halorhabdus utahensis* revealed some striking differences, including a marked increase in genes associated with transmembrane transport and putative genes for a trehalose synthase and a lactate dehydrogenase.

Halorhabdus tiamatea is the first archaeon isolated from deep-sea brines (2, 3), specifically, from Shaban Deep. The genome of the type species of this genus (11) has recently been sequenced (1).

Cells were grown under optimal conditions (2). Genomic DNA was extracted with a blood & cell culture DNA minikit (Qiagen), following the manufacturer's instructions. The *Halorhabdus tiamatea* genome was sequenced using the Roche 454 GS (FLX Titanium) and Illumina sequencing platforms (single and paired end). A total of 93,895,127 bp (mean read length, 306 bp) was obtained from Roche 454, providing approximately 22-fold genome coverage. Single and paired-end Illumina data provided 5,816,168 bp (mean read length, 30 bp) and 5,220,362 bp (mean read length, 35 bp), corresponding to 420-fold coverage. Roche 454 sequencing data were assembled using Newbler Assembler version 2.5 (Roche), while Illumina data were assembled with SOAPdenovo (<http://soap.genomics.org.cn/soapdenovo.html>). The resulting assemblies were merged using AMOS Minimus2 (<http://sourceforge.net/apps/mediawiki/amos/index.php?title=Minimus2>).

The sequences were assembled into 76 scaffolds, with an N50 contig size of approximately 88.6 kb (where N50 is the contig length such that at least 50% of the bases of the assembly are contained within contigs of this size or greater). Genes were identified using Prodigal software (<http://compbio.ornl.gov/prodigal/>) followed by mpiBLAST (<http://www.mpiblast.org/>) and Interproscan (<http://www.ebi.ac.uk/InterProScan/>) annotation. This approach provided annotation for 89% of all 4,034 predicted genes. Additional analysis was done using the RAST server (4). The draft genome has a G+C content of 62%.

Genome comparison with *Halorhabdus utahensis* (1, 12) revealed some striking differences, namely, a marked increase in genes associated with transport across the membrane, mainly transport and utilization of phosphonate, di- and oligopeptides, maltose, and maltodextrin.

While phosphonate transport and utilization is frequent for

Bacteria, it seems to be quite rare for *Archaea* (6). Genes involved in phosphonate utilization are subjected to extensive lateral gene transfer (9) and are likely transferred in this manner from *Bacteria* to *Archaea*. The use of phosphonates is associated with adaptations to phosphate-limited environments, which is in agreement with data from Shaban Deep (11).

Genes related to the transport and utilization of maltose and maltodextrins are associated with genes for transport of other sugars, and, most notably, with a trehalose synthase (likely using maltose as a substrate). Trehalose synthases have only been reported in few *Archaea* (e.g., *Sulfolobus*) and, to our knowledge, have never been detected in members of *Halobacteriaceae*. Trehalose has several possible functions in cells, namely, structural or protection against oxidic, thermal, or osmotic stress (10). In halophilic microbes, trehalose is most often used as a compatible solute for coping with osmotic stress. However, haloarchaea are traditionally associated with the “salt-in” strategy, which is thought to preclude the use of compatible solutes, with few exceptions (7). Additional studies are necessary to clarify the role of trehalose in *H. tiamatea*.

An additional interesting feature of this genome is the presence of a gene coding for an L-lactate dehydrogenase (LDH), which might provide a new fermentative pathway within the *Halobacteriaceae*. Although LDH activity has previously been reported in *Halobacterium salinarum* cell extracts (5), no clear LDH homologues had been reported in any haloarchaeal genomes (8).

Nucleotide sequence accession number. Nucleotide sequences are available in GenBank under the project identification number 66979, with accession number AFNT00000000.

This work was partially supported by the External Lab Access program of the King Abdullah University of Science and Technology Global Collaborative Research (GCR).

We also acknowledge the support of R. Huber and that of G. Gmeinwieser, H. Huber, M. Thomm, and the rest of the former and current team at the Lehrstuhl für Mikrobiologie und Archaeenzentrum, University of Regensburg.

REFERENCES

- Anderson, I., et al. 2009. Complete genome of *Halorhabdus utahensis* type strain (AX-2^T). *Stand. Genomic Sci.* 1:218–225.
- Antunes, A., et al. 2008. *Halorhabdus tiamatea* sp. nov., a non-pigmented, extremely halophilic archaeon from a deep-sea hypersaline anoxic basin of

* Corresponding author. Mailing address: Red Sea Research Center, King Abdullah University of Science and Technology (KAUST), 23955-6900 Thuwal, Kingdom of Saudi Arabia. Phone: 966-2-8082365. Fax: 966-2-8020152. E-mail: andre.antunes@kaust.edu.sa.

[∇] Published ahead of print on 24 June 2011.

- the Red Sea, and emended description of the genus *Halorhabdus*. *Int. J. Syst. Evol. Microbiol.* **58**:215–220.
3. **Antunes, A., D. Kamanda Ngugi, and U. Stingl.** Microbiology of the Red Sea (and other) deep-sea anoxic brine lakes. *Environ. Microbiol. Rep.*, in press. doi:10.1111/j.1758-2229.2011.00264.x.
 4. **Aziz, R. K., et al.** 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* **9**:75.
 5. **Bhaumik, S. R., and H. M. Sonawat.** 1994. Pyruvate metabolism in *Halobacterium salinarium* studied by intracellular ¹³C nuclear magnetic resonance spectroscopy. *J. Bacteriol.* **176**:2172–2176.
 6. **Bolhuis, H., et al.** 2006. The genome of the square archaeon “*Haloquadratum walsbyi*”: life at the limits of water activity. *BMC Genomics* **7**:169.
 7. **Desmarais, D., P. E. Jablonski, N. S. Fedarko, and M. F. Roberts.** 1997. 2-Sulfotrehalose, a novel osmolyte in haloalkaliphilic archaea. *J. Bacteriol.* **179**:3146–3153.
 8. **Falb, M., et al.** 2008. Metabolism of halophilic archaea. *Extremophiles* **12**:177–196.
 9. **Huang, J., Z. Su, and Y. Xu.** 2005. The evolution of microbial phosphonate degradative pathways. *J. Mol. Evol.* **61**:682–690.
 10. **Murphy, H. N., et al.** 2005. The OtsAB pathway is essential for trehalose biosynthesis in *Mycobacterium tuberculosis*. *J. Biol. Chem.* **280**:14524–14529.
 11. **Oudin, E., and A. Cocherie.** 1988. Fish debris record the hydrothermal activity in the Atlantis II Deep sediments (Red Sea). *Geochim. Cosmochim. Acta* **52**:177–184.
 12. **Wainø, M., B. J. Tindall, and K. Ingvorsen.** 2000. *Halorhabdus utahensis* gen. nov., sp. nov., an aerobic, extremely halophilic member of the Archaea from Great Salt Lake, Utah. *Int. J. Syst. Evol. Microbiol.* **50**:183–190.