**Draft Genome of *Halomonas* Species Strain GFAJ-1 (ATCC BAA-2256)**

Le T. Phung, Simon Silver, William L. Trimble, and Jack A. Gilbert

Department of Microbiology and Immunology, University of Illinois, Chicago, Illinois, USA; Institute for Genomics and Systems Biology, Argonne National Laboratory, Argonne, Illinois, USA; and Department of Ecology and Evolution, University of Chicago, Chicago, Illinois, USA

*Halomonas* strain GFAJ-1 was reported in *Science* magazine to be a remarkable microbe for which there was “arsenate in macromolecules that normally contain phosphate, most notably nucleic acids.” The draft genome of the bacterium was determined (NCBI accession numbers AHBC01000001 through AHBC01000103). It appears to be a typical gamma proteobacterium.

*Halomonas* is a diverse genus of halophilic, alkalophilic gammaproteobacteria. Strain GFAJ-1 has not been assigned a species name. The motivation for isolation of strain GFAJ-1 was to find “shadow life,” which is defined in *Wikipedia* (http://en.wikipedia.org/wiki/Shadow_life) as life on earth “which has no evolutionary connection with life currently known to science” (perhaps cells without DNA or ribosomes). There is no evidence for “shadow life.”

When the initial report on strain GFAJ-1 was published (13), there was an immediate negative reaction (e.g., references 4, 7, 10, and 12) to the claim of “arsenate in macromolecules that normally contain phosphate, most notably nucleic acids,” arguing about the inadequacy of the data supporting the claim and the expected instability of arsenate diester bonds. No progress has occurred on these matters since the initial publication. The Oremland laboratory has published on novel arsenic metabolism of other species (5, 6, 11). The genome of strain GFAJ-1 was determined in an effort toward further understanding. The genome indicates that the strain is a gammaproteobacterium, the same class that includes *Escherichia coli*. There is no indication in the genome of any unusual or unexpected metabolism. However, the genome does not directly address the basic problem.

*Halomonas* strain GFAJ-1 was grown in the medium described previously (13), with 1.5 mM phosphate but no added vitamins or tungsten. The medium was supplemented with 0.2 g/liter yeast extract, 10 mM KCl, and 10 mM potassium glutamate. The strain grows rapidly, with a doubling time of 2.5 h and approximately 10^6 cells/ml after overnight incubation at 29°C (data not shown). Cells in late-log-phase growth were harvested and lysed by EDTA, lysozyme, and detergent treatment, followed by proteinase K and RNase digestion. DNA isolation was by phenol-chloroform or isopropanol-ethanol precipitation (8). DNA purity was measured as the A_260/A_280 ratio, and a single DNA band more than 20 kbp in size was observed (data not shown) after agarose gel electrophoresis. The genome was sequenced using the Illumina HiSeq 2000 sequencing platform, with a random subset of 3.5 million paired-end reads (175 times coverage) used for assembly with MIRA version 3.4.2c into 103 contigs that were submitted to GenBank.

Strain GFAJ-1 was initially (13) placed in genus *Halomonas* based on the sequence of its 16S rRNA gene; the genome sequence includes a sequence (GenBank accession number AHBC01000061) that is identical to that in reference 13, with a single exception in the 5' PCR primer that was used (13). The draft genome comprises 3,624,896 nt in 103 contigs, with 3,341 coding sequences plus 68 RNAs totaling 3,409 genes. The *Halomonas* strain genome projects currently published are for *Halomonas* sp. strain TD01 (3) (GenBank accession number AFQW00000000.1) and *H. elongata* strain DSM 2581 (9) (RefSeq number NC_014532.1); the genome of strain GFAJ-1 appears closely related to that of *Chromohalobacter salexigens* strain DSM 3043 (1). It is of interest to analyze potential genes involved in arsenic metabolism and resistance. The predicted protein-encoding genes do not include the now-standard *ars* gene operon of other proteobacteria, including *E. coli*. In particular, the genes for the ArsB arsenite efflux membrane protein and the ArsC arsenate reductase enzyme appear to be absent.

**Nucleotide sequence accession numbers.** The draft genome of *Halomonas* strain GFAJ-1 was deposited in GenBank (http://www.ncbi.nlm.nih.gov/projects/WGS/WGSprojectlist.cgi) under accession numbers AHBC01000001 through AHBC01000103.

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**REFERENCES**


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Address correspondence to Simon Silver, simon@uic.edu, or Jack A. Gilbert, gilbertjack@anl.gov.

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