Draft Genome Sequence of a Divergent Anaerobic Member of the Chloroflexi Class Ardenticatenia from a Sulfidic Hot Spring

L. M. Ward,a S. E. McGlynn,b W. W. Fischerc

a Department of Earth and Planetary Sciences, Harvard University, Cambridge, Massachusetts, USA
b Earth-Life Science Institute, Tokyo Institute of Technology, Meguro, Tokyo, Japan
c Division of Geological and Planetary Sciences, California Institute of Technology, Pasadena, California, USA

ABSTRACT Here, we present a draft genome sequence of Nak82, the second genome sequence available for the Chloroflexi class Ardenticatenia and the first from a sulfidic terrestrial hot spring. Nak82 is genetically and metabolically distinct from Ardenticatenia maritima and likely represents a new genus- or family-level lineage lacking high-potential respiratory pathways.

Ardenticatenia is a curious class in the Chloroflexi phylum; it is currently known only as a single isolate from an iron-rich hydrothermal field in Japan (1). Ardenticatenia maritima is unique among the Chloroflexi for its capacity for iron reduction and complete denitriﬁcation (2). Here, we report the ﬁrst genome sequence available from a second Ardenticatenia lineage strain, Nak82, recovered from Nakabusa Onsen in Japan. Nak82 is most closely related to Ardenticatenia maritima but is genetically distinct at the genus or family level and does not share the diverse respiratory pathways that distinguish Ardenticatenia maritima from other Chloroflexi species.

The Nak82 metagenome-assembled genome (MAG) was recovered from sequencing of Nakabusa Onsen, a moderately sulfidic hot spring in Japan. The site and metagenomic sequencing were described previously (3, 4). In brief, the site is a moderately sulfidic and alkaline (pH 8.5 to 9) hot spring with source water near 70°C and containing ~0.1 mM sulfide (5). Samples were collected from microbial mats, and DNA was extracted and submitted to SeqMatic LLC (Fremont, CA) for sequencing with an Illumina HiSeq instrument. Sequences from four samples were coassembled with MEGAHIT v. 1.1.2 (6), and genome bins were constructed based on differential coverage using MetaBAT (7). Genome bins were assessed for completeness and contamination using CheckM (8) and uploaded to the RAST server for overall characterization (9).

The Nak82 MAG totals 3.49 Mb and consists of 2,942 protein-coding sequences across 195 contigs. The genome has a 58.7% GC content and is estimated by CheckM to be 91.74% complete, with 0.64% contamination. Forty-four tRNAs were recovered.

Phylogenetic analysis of Nak82 and other Chloroflexi using the RpoB protein—a valuable single-copy marker (10)—robustly places this organism as a sister taxon to Ardenticatenia maritima; however, the RpoB sequences of these strains are only 72% similar, suggesting divergence to at least the genus level.

Nak82 does not have genes that encode the pathways for aerobic respiration and denitriﬁcation found in Ardenticatenia maritima. The only dioxygen reductase recovered in the Nak82 genome is a bd oxidase, which may be used for oxygen detoxiﬁcation, as it appears in obligate anaerobes, including some members of the phylum Chloroflexi class Anaerolineae (4, 11–14). This distribution of respiration genes is consistent with the acquisition of aerobic respiration and denitriﬁcation by Ardenticatenia maritima via horizontal gene transfer after its divergence with Nak82, a pattern consistent with broader trends in the evolution of metabolic traits in the Chloroflexi (4, 15).
Acknowledgments

L.M.W. acknowledges support from the NASA NESSF (grant number NNX16AP39H), the NSF (grant number OISE 1639454), NSF GROW (grant number DGE 1144469), the Lewis and Clark Fund for Exploration and Field Research in Astrobiology, the Earth-Life Science Institute, the ELSI Origins Network, and the Agouron Institute. S.E.M. acknowledges support from a MEXT KAKENHI grant-in-aid for challenging exploratory research (grant award number 15K14608). W.W.F. acknowledges the support of a NASA Exobiology award (number NNX16AJ57G) and of the David and Lucile Packard Foundation.

We thank Katsumi Matsuura and the Environmental Microbiology Laboratory at Tokyo Metropolitan University for laboratory support. Sequencing was performed at SeqMatic, Fremont, CA.

References