

Draft Genome Sequence of *Ardenticatena maritima* 110S, a Thermophilic Nitrate- and Iron-Reducing Member of the *Chloroflexi* Class *Ardenticatenia*

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We report here the draft genome sequence of *Ardenticatena maritima* 110S, the first sequenced member of class *Ardenticatenia* of the phylum *Chloroflexi*. This thermophilic organism is capable of a range of physiologies, including aerobic respiration and iron reduction. It also encodes a complete denitrification pathway with a novel nitric oxide reductase.

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Ardenticatena maritima 110S was originally isolated from an iron-rich coastal hydrothermal field in the Kirishima Volcanic Belt of Japan (1). Closely related strains have been reported from hot springs (2) and hydrothermal vents (3). *A. maritima* is a filamentous nonmotile organism that can facultatively reduce nitrate and iron (1). It grows optimally at 50 to 70°C and pH 7.0 (pH range, 5.5 to 8.0).

The genome of *A. maritima* 110S (DSM 23922) was sequenced as part of a project to expand the phylogenetic breadth of *Chloroflexi* genomes. Genome sequencing was performed at SeqMatic using the Illumina MiSeq sequencing platform. SPAdes 3.1.1 (4) was used to assemble the genome. The genome was screened for contaminants based on sequence coverage, G+C composition, and BLAST hits of conserved single-copy genes. Genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline. The draft genome is 3.62 Mb in size, assembled into 12 contigs. It contains 3,041 genes, 2,578 coding sequences (CDSs), 2 16S RNAs, 46 tRNAs, and 10 clustered regularly interspaced short palindromic repeat (CRISPR) arrays. It is estimated to be ~99% (111/111) complete based on conserved single-copy genes.

Analysis of the *A. maritima* genome revealed the presence of many genes responsible for its physiological breadth. *A. maritima* encodes a branched aerobic respiratory chain, including complex I (NADH dehydrogenase), complex II (succinate dehydrogenase), complex III (cytochrome *bc* complex), and three oxygen reductases (A- and B-family heme-copper oxygen reductases and *bd* oxidase). B-family heme-copper oxygen reductases are commonly found in aerobic thermophiles, enabling growth with the low oxygen levels found in thermal systems (5). *A. maritima* also encodes a complete denitrification pathway composed of nitrate reductase (NapA), nitrite reductase (NirK), a novel nitric oxide reductase (eNOR) (6), and nitrous oxide reductase (NosZ). Interestingly, the eNOR is found in an operon with NirK, suggesting that these genes are coregulated. No genes were found for either lipopolysaccharide (LPS) biosynthesis or outer membrane proteins, consistent with the proposal that *Chloroflexi* have only one membrane (7).

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. [LGKN00000000](https://www.ncbi.nlm.nih.gov/nuclink/LGKN00000000).

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REFERENCES

- Kawaichi S, Ito N, Kamikawa R, Sugawara T, Yoshida T, Sako Y. 2013. *Ardenticatena maritima* gen. nov., sp. nov., a ferric iron- and nitrate-reducing bacterium of the phylum “*Chloroflexi*” isolated from an iron-rich coastal hydrothermal field, and description of *Ardenticatenia classis* nov. *Int J Syst Evol Microbiol* 63:2992–3002. <http://dx.doi.org/10.1099/ijs.0.046532-0>.
- Kormas KA, Tamaki H, Hanada S. 2009. Apparent richness and community composition of Bacteria and Archaea in geothermal springs. *Aquat Microb Ecol* 57:113–122.
- Meyer-Dombard DR, Amend JP, Osburn MR. 2013. Microbial diversity and potential for arsenic and iron biogeochemical cycling at an arsenic rich, shallow-sea hydrothermal vent (Tutum Bay, Papua New Guinea). *Chem Geol* 348:37–47. <http://dx.doi.org/10.1016/j.chemgeo.2012.02.024>.
- Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prjibelski AD, Pyshkin A, Sirotkin A, Sirotkin Y, Stepanauskas R, Clingenpeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA. 2013. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. *J Comput Biol* 20:714–737. <http://dx.doi.org/10.1089/cmb.2013.0084>.
- Chang H-Y, Hemp J, Chen Y, Fee JA, Gennis RB. 2009. The cytochrome *ba3* oxygen reductase from *Thermus thermophilus* uses a single input channel for proton delivery to the active site and for proton pumping. *Proc Natl Acad Sci U S A* 106:16169–16173. <http://dx.doi.org/10.1073/pnas.0905264106>.
- Hemp J, Gennis RB. 2008. Diversity of the heme-copper superfamily in archaea: insights from genomics and structural modeling. *Results Probl Cell Differ* 45:1–31.
- Sutcliffe IC. 2011. Cell envelope architecture in the *Chloroflexi*: a shifting frontline in a phylogenetic turf war. *Environ Microbiol* 13:279–282. <http://dx.doi.org/10.1111/j.1462-2920.2010.02339.x>.