Genome Sequence of *Atlantibacter subterranea* DSM 16208 Isolated from Uranium-contaminated Sediment

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Abstract

We report the whole genome sequence of an antibiotic-resistant strain of *Atlantibacter subterranea* isolated from Uranium-contaminated sediment in Tennessee. The genome sequence of this strain was 4,717,064 bp in length, contained 34 contigs and 29 scaffolds, and with a GC content of 55.17%.

Announcement

Atlantibacter subterranea is a rod-shaped, gram-negative bacterium, found in aquatic areas in North America (1). It is facultatively anaerobic, motile, and may spread in animals by consuming contaminated food (2). The bacterium can reduce hexavalent uranium to tetravalent uranium, later

precipitating to mineral uraninite, effectively immobilizing uranium from radioactive waste (3). This strain was isolated from Uranium (VI)-contaminated subsurface sediment in 2001 in Tennessee, USA using sediment sampling, enrichment, and serial dilutions plated on aerobic agar containing acetate (3). Analysis of *A. subterranea* aids in identifying similarities in specific extracellular polymeric substance secretions (EPS) across bacterial species related to its significance in uranium reduction (3). It was taxonomically identified before genome sequencing and the 16S rRNA gene sequence is found in the NCBI database (accession number AY373829) (3).

Details on organism growth and DNA isolation to be provided by DSMZ. Sequencing was performed at JGI using Illumina HiSeq 2000 platform by creating an Illumina std shotgun library, TSPS, with a read type of 2x150 bp. It resulted in 2,999,762 raw sequence reads and 450 mb DNA sequences. Reads were filtered using DUK to remove known contaminants including Illumina sequencing and library preparation artifacts (4). Genome assembly initially used Velvet (v1.02.07) (parameters: contig length 500, coverage cutoff 10) (5) followed by Allpaths-LG (v46652) (parameters: PHRED 64, PLOIDY=1, COVERAGE=125) (6). The genome was annotated using the JGI Microbial Genome Annotation Pipeline (v5.0.0) (7). CheckM2 (v5.5.2) determined 100% completion and 0.11% contamination (8).

Table 1 - Genomic features of Atlantibacter subterranea DSM 16208	
Feature	**Finding**
length (bp)	4,717,064
status	complete
No. of contigs	34

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Feature	**Finding**
length (bp)	4,717,064
GC content (%)	55.17%
No. of scaffolds	29
Scaffold N50 (bp)	434618
Average fold coverage	0.635938
No. of rRNAs	17
No. of tRNAs	67
No. of genes	4504
No. of coding sequences	4351

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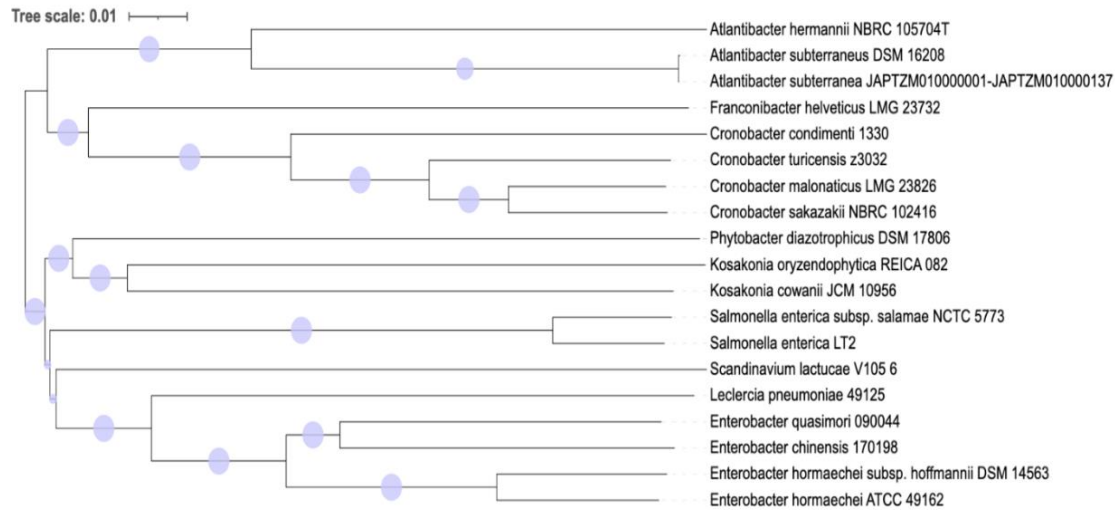
FIG 1 Whole-genome-based phylogenetic classification of *Atlantibacter subterranea*. The genome BLAST distance phylogeny (GBDP) tree was generated with the Type Strain Genome Server accessed 14 March 2025. The tree was inferred with FastME 2.1.6.1 (9) from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of the GBDP distance formula d_5. The numbers at the nodes are GBDP pseudobootstrap support values of >60% from 100 replications. The average branch support was 93.7%. The tree was midpoint rooted (10).

The genome of *A. subterranea* consists of one chromosome measuring 4,717,064 bp with a G+C content of 55.17% (Table 1). Whole-genome-based phylogenetic classification, generated using the Type Strain Genome Server and inferred with FastME 2.1.6.1, shows that A. *subterranea* is most closely related to A. *hermannii* NBRC 105704T, with close proximity to *Franconibacter helvetivus* LMG 23732 (Figure 1). The probability of *A. subterranea* being a human pathogen is 0.702, as determined by PathogenFinder v1.1 (11). Using the Comprehensive Antibiotic Resistance Database (CARD 4.0.0), we confirmed that *A. subterranea* is resistant to various types of antibiotics, including cephalosporin, betalactam, fluoroquinolone, and macrolide (12). CRISPR-Cas Finder version 1.1.2 -I2BC identified 1 CRISPR region (13). AntiSMASH 7.0 software identified the production of secondary metabolites including arylpolyene, NRP metallophore, terpene, thiopeptide, butyrolactone and RiPP like (14).

Data availability statement

This Whole Genome Shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. LC126283. The version described in this paper is the first version, LC126283.1. The data was deposited under the BioProject accession no. PRJDB2388, the BioSample accession no. SAMD00010876, and the Sequence Read Archive accession no. DRR015979.

Acknowledgments

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