Complete Genome Sequence of the *Arcobacter marinus* Type Strain JCM 15502

William G. Miller,a Emma Yee,a Steven Huynh,a Craig T. Parkera

aProduce Safety and Microbiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Albany, California, USA

**ABSTRACT** *Arcobacter* species are often recovered from marine environments and are isolated from both seawater and shellfish. *Arcobacter marinus* was recovered from the homogenate of a sample containing surface seawater, seaweed, and a starfish. This study describes the whole-genome sequence of the *A. marinus* type strain JCM 15502 (= CL-S1T = KCCM 90072T).

*Arcobacter* species have been isolated from a diverse group of land animals (1, 2). However, other arcobacters are more free living and are often associated with aquatic marine environments. Four *Arcobacter* species were recovered from either seawater (3–5) or hypersaline lagoon water in the Hawaiian Islands (6). A fifth species, *Arcobacter marinus*, was isolated from the homogenate of a sample containing surface seawater from the Sea of Japan (East Sea), seaweed, and a starfish (7). In this study, we report the first closed genome sequence of the *A. marinus* type strain JCM 15502 (= CL-S1T = KCCM 90072T).

*A. marinus* strain JCM 15502T was grown under the same conditions as *Arcobacter mytili* (8), and genomic DNA was isolated as described (9). Sequencing was first performed on a Roche GS-FLX+ instrument, with libraries constructed using standard protocols. Shotgun and paired-end 454 reads were assembled (Newbler; Roche, version 2.6) into a single chromosomal scaffold of 28 unique contigs. Un scaffolded contigs that were determined to be of low quality (i.e., small contigs containing multiple bases with a quality score of <20 and comprised generally of <20 reads) were deleted. The Perl script contig_extender3 (9) was used to place the remaining 16 contigs at one or more locations within the scaffold. PacBio and Illumina MiSeq sequencing were also performed using standard protocols, with libraries constructed as described (9). The PacBio chromosomal contig and the 454 scaffold contigs were assembled together using SeqMan Pro (version 8.0.2; DNASTAR, Madison, WI), with the remaining 454 contigs added to the assembly manually, using the placement determined above. The Illumina MiSeq reads were assembled using Newbler version 2.6 with default settings. These contigs were also quality controlled (10) and added to the 454/PacBio SeqMan assembly. The MiSeq reads and contigs were used to error correct base calls within the JCM 15502T sequence, in the same manner as described previously for HiSeq reads (10). Briefly, base calls within contigs at a single location within the assembly were adjusted to the Illumina consensus sequence; single nucleotide polymorphisms within each repeat contig and sequences between the Illumina contigs were addressed by assembling the MiSeq reads onto these regions using Geneious (version 8.1; Biomatters, Auckland, New Zealand) and using the “find variations/SNPs” module, with a default minimum variant frequency parameter of 0.3. The final coverage across the genome was 611×. Chromosomal assembly was also validated using an optical restriction map (restriction enzyme AflII; OpGen, Gaithersburg, MD).

Sequencing metrics and genomic data for *A. marinus* strain JCM 15502T are presented in Table 1. Strain JCM 15502T has a circular genome of 2,917,098 bp, with an
TABLE 1 Sequencing metrics and genomic features of A. marinus strain JCM 15502<sup>T</sup>

| Feature                  | Value(s)<sup>b</sup> |
|--------------------------|----------------------|
| **Sequencing metrics**   |                      |
| 454 (shotgun) platform   |                      |
| No. of reads             | 255,668              |
| No. of bases             | 115,346,816          |
| Average length (bases)   | 451.2                |
| Coverage (×)             | 39.5                 |
| 454 (paired-end) platform|                      |
| No. of reads             | 58,215               |
| No. of bases             | 21,224,999           |
| Average length (bases)   | 364.6                |
| Coverage (×)             | 7.3                  |
| Illumina MiSeq platform   |                      |
| No. of reads             | 2,524,304            |
| No. of bases             | 746,008,863          |
| Average length (bases)   | 296                  |
| Coverage (×)             | 255.7                |
| PacBio platform          |                      |
| No. of reads             | 89,384               |
| No. of bases             | 900,973,905          |
| Average length (bases)   | 10,079.8             |
| Coverage (×)             | 308.9                |
| **Genomic data**         |                      |
| **Chromosome**           |                      |
| Size (bp)                | 2,917,098            |
| G=C content (%)          | 27.19                |
| No. of CDS<sup>c</sup>   | 2,717                |
| Assigned function (% CDS)| 1,046 (38.5)         |
| General function annotation (% CDS) | 1,077 (39.6) |
| Domain/family annotation only (% CDS) | 181 (6.7) |
| Hypothetical (% CDS)     | 413 (15.2)           |
| No. of pseudogenes       | 25                   |
| **Genomic islands/CRISPR**|                     |
| No. of genetic islands   | 3                    |
| No. of CDS in genetic islands | 78, [1] |
| No. of CRISPR/Cas loci   | 0                    |
| **Gene content/pathways**|                      |
| **Signal transduction**  |                      |
| Che proteins             | cheABCDRIW(Y)         |
| No. of methyl-accepting chemotaxis proteins | 29, [1] |
| No. of response regulators| 59                   |
| No. of histidine kinases  | 75                   |
| No. of response regulator/histidine kinase fusions | 3 |
| No. of diguanylate cyclases | 21                  |
| No. of diguanylate phosphodiesterases (HD-GYP, EAL) | 7, 6 |
| No. of diguanylate cyclase/phosphodiesterases | 12 |
| No. of other             | 14                   |
| **Motility**             |                      |
| Flagellin genes          | fla1 to fla7         |
| **Restriction/modification**|                    |
| No. of type I systems (hsd) | 1                   |
| No. of type II systems   | 1                    |
| No. of type III systems  | 0                    |
| **Transcription/translation**|                   |
| No. of transcriptional regulatory proteins | 73 |
| Non-ECF α factors        | α<sup>b</sup>         |
| No. of ECF α factors     | 0                    |
| No. of tRNAs             | 63                   |
| No. of ribosomal loci    | 6                    |
| **CO dehydrogenase (coxSUF)** | No              |
| Ethanolamine utilization (eutBCH) | No |
| **Nitrogen fixation**    | no                   |
| **Osmoprotection**       | BCCT<sub>r</sub>, cali, fix, betA, ectABC |
| **Pyruvate to acetyl-CoA**|                      |
| Pyruvate dehydrogenase (E1/E2/E3) | Yes             |
| Pyruvate/ferredoxin oxidoreductase | por           |
| Urease                   | No                   |
| Vitamin B<sub>12</sub> biosynthesis | Yes |

<sup>a</sup>CDS, coding sequences; ECF, extracytoplasmic function; acetyl-CoA, acetyl coenzyme A.

<sup>b</sup>Numbers in square brackets indicate pseudogenes or fragments.

<sup>c</sup>Numbers do not include pseudogenes.
average GC content of 27.2%. Protein-, rRNA-, and tRNA-encoding genes were identified (11) and annotated (12) as described. The genome is predicted to encode 2,717 putative protein-coding genes, 25 pseudogenes, 6 rRNA operons, and 63 tRNA-encoding genes. Three genomic islands (19.5, 26.6, and 35.3 kb) were identified in the JCM 15502\(^T\) chromosome, with the 35.3-kb island putatively encoding a type VI secretion system.

A noteworthy feature of the \textit{A. marinus} genome is the presence of genes associated with DNA phosphorothioation, in which a nonbridging oxygen in the DNA sugar-phosphate backbone is replaced with sulfur, forming a phosphorothioate linkage (13). In \textit{Streptomyces} spp., this modification involves the \textit{dndABCDE} genes (14). Although \textit{dndBCDE} orthologs are present in strain JCM 15502\(^T\), the cysteine desulfurase \textit{dndA} was not identified; however, in \textit{Escherichia coli}, \textit{IscS} (present in \textit{A. marinus}) provides the cysteine desulfurase activity for phosphorothioation (15). The function of phosphorothioation in \textit{A. marinus} is unknown but is linked to restriction/modification (16) and resistance to reactive oxidative species (17) in other organisms.

**Data availability.** The complete genome sequence of \textit{A. marinus} strain JCM 15502\(^T\) was deposited in GenBank under the accession number CP032101. The 454, MiSeq, and PacBio sequencing reads were deposited in the NCBI Sequence Read Archive (SRA; accession number SRP155050).

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