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GENOME SEQUENCES

Complete Genome Sequence of the *Arcobacter mytili* Type Strain LMG 24559

William G. Miller,[a] Emma Yee,[a] James L. Bono[b]

[a]Produce Safety and Microbiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Albany, California, USA

[b]Meat Safety and Quality Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Clay Center, Nebraska, USA

ABSTRACT Multiple *Arcobacter* species have been recovered from fresh and contaminated waters, marine environments, and shellfish. *Arcobacter mytili* was recovered in 2006 from mussels collected from the Ebro River delta in Catalonia, Spain. This study describes the complete whole-genome sequence of the *A. mytili* type strain LMG 24559 (=F2075^T =CECT 7386^T).

Arcobacter species are commonly encountered components of the microflora of marine environments. Several species have been isolated from both seawater (1–4) and shellfish, such as mussels and clams (2, 5–7). *Arcobacter mytili* is an indoxyl acetate hydrolysis-negative arcobacter that was isolated originally from mussels and brackish water from Catalonia, Spain (8). In this study, we report the first closed genome sequence of the *A. mytili* type strain LMG 24559 (=F2075^T =CECT 7836^T), recovered in September 2006 from mussels from the Ebro River delta (8).

Arcobacter mytili was grown at 30°C aerobically for 48 h on anaerobe basal agar (Oxoid) amended with 5% horse blood, and genomic DNA was extracted as described previously (9) from a 5-μl loop of cells. The genomic DNA was first sequenced using the Roche GS-FLX+ system, and 86 total contigs were generated following Newbler (version 2.6) assembly of shotgun and paired-end Roche 454 reads. Two scaffolds containing 38 and 3 unique contigs were obtained. These scaffolds were closed, using the remaining 45 contigs that represent repeated regions within the genome and a custom Perl script (9), into two circular, contiguous sequences presumably representing the chromosome and an ~170-kb megaplasmid. 454 assembly of the chromosome was also validated using an optical restriction map (restriction enzyme XbaI; OpGen, Gaithersburg, MD). PacBio sequencing was performed and generated two circular, closed sequences of 2.87 Mb and 170 kb, following assembly and end trimming of the contig sequences; the long PacBio reads were also necessary to resolve two large repeat regions within the chromosome. The sequences generated by the 454 and PacBio platforms were further verified using Illumina HiSeq reads (SeqWright, Houston, TX) as described previously (9). The HiSeq reads provided an additional 793× coverage across the genome with a final coverage of 995×.

Genome features for *A. mytili* strain LMG 24559^T are presented in Table 1. LMG 24559^T has a single circular chromosome of 2,867,150 bp with an average GC content of 26.65%. Protein-, rRNA-, and tRNA-encoding genes were identified as described previously (10). The LMG 24559^T genome is predicted to encode 2,672 putative protein-coding genes, 21 pseudogenes, 6 rRNA operons, and 63 tRNA-encoding genes. A 31.4-kb integrated Mu phage was identified in the LMG 24559^T chromosome, as well as a putative type II-C CRISPR-Cas system and four genomic islands of 6.9, 14.4, 16.9, and 17.8 kb. *A. mytili* strain LMG 24559^T also contains the 170,445-bp plasmid pAMYT;

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Address correspondence to William G. Miller, william.miller@ars.usda.gov.

TABLE 1 Genomic features of *Arcobacter mytili* strain LMG 24559^T

Feature	Value(s)
Size (bp)[a]	2,867,150/170,445
G+C content (%)[a]	26.65/24.93
No. of CDS[a,b]	2,672/208
Assigned function (% CDS)	990 (37.1)/2 (1)
General function annotation (% CDS)	1,075 (40.2)/35 (16.8)
Domain/family annotation only (% CDS)	173 (6.5)/3 (1.4)
Hypothetical (% CDS)	434 (16.2)/168 (80.8)
No. of pseudogenes	21/2
Genomic islands/CRISPR[c,d]	
No. of prophage/genetic islands	5; 0
No. of CDS in genetic islands	99 [1]; 0
CRISPR/Cas loci	II-C; 0
Gene content/pathways[c,d]	
Signal transduction	
Che proteins	*cheABCDRVW*(*Y*)$_2$
No. of methyl-accepting chemotaxis proteins	25; 0
No. of response regulators	60; 0
No. of histidine kinases	75, [1]; 0
No. of response regulator/histidine kinase fusions	3; 0
No. of diguanylate cyclases	22; 0
No. of diguanylate phosphodiesterases (HD-GYP, EAL)	9, 6; 0, 0
No. of diguanylate cyclase/phosphodiesterases	12; [1]
No. of others	12; 0
Motility	
Flagellin genes	*fla1* to *fla4*
Restriction/modification	
No. of type I systems (*hsd*)	0
No. of type II systems	2; 0
No. of type III systems	1; 0
Transcription/translation	
No. of transcriptional regulatory proteins	68; 3
Non-ECF σ factor	σ^{70}
No. of ECF σ factors	0
No. of tRNAs	63; 0
No. of ribosomal loci	6; 0
Nitrogen fixation (*nif*)	No
Osmoprotection	BCCT, *betA*, *ectABC*
Pyruvate → acetyl-CoA[e]	
Pyruvate dehydrogenase (E1/E2/E3)	Yes
Pyruvate:ferredoxin oxidoreductase	*por*, *porABDG*
Urease	No
Vitamin B_{12} biosynthesis	Yes

[a]Values before the backslash are for the chromosome, while values after the backslash are for the pAMYT plasmid.
[b]Numbers do not include pseudogenes. CDS, coding DNA sequence.
[c]Numbers after the semicolon indicate plasmid-borne features.
[d]Numbers in square brackets indicate pseudogenes/fragments.
[e]CoA, coenzyme A.

pAMYT is presumably conjugative, because it encodes several genes for an F-type type IV conjugative transfer system.

The *A. mytili* genome contains five genes larger than 11 kb. Two genes, *amyt2456* (15,222 bp) and *amyt2527* (18,810 bp), encode a large adhesive protein and a von Willebrand A domain-containing protein, respectively. These genes are distinguished by the presence of internal, tandemly repeated motifs, 25 copies of a 269-bp repeat in *amyt2456* and 27 copies of a 337-bp repeat in *amyt2527*. The remaining three genes (*amyt1680*, 32,355 bp; *amyt1888*, 12,267 bp; and *amyt1611*, 11,142 bp) encode putative RTX toxin-related calcium-binding proteins; however, these genes do not contain any large, repeated internal domains.

Data availability. The complete genome sequence of *A. mytili* strain LMG 24559^T has been deposited in GenBank under the accession numbers CP031219 (chromosome)

and CP031220 (pAMYT). 454, HiSeq, and PacBio sequencing reads have been deposited in the NCBI Sequence Read Archive (SRA; accession number SRP155023).

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