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GENOME SEQUENCES

Complete Genome Sequence of the *Arcobacter skirrowii* Type Strain LMG 6621

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ABSTRACT *Arcobacter skirrowii* is a species of veterinary importance, originally recovered from the feces, aborted fetuses, and preputial fluids of livestock. We present here the whole-genome sequence of the *A. skirrowii* type strain LMG 6621 (= 449/80^T = CCUG 10374^T), isolated in the United Kingdom from a lamb diarrheal fecal sample.

Arcobacter skirrowii is a member of a related group of taxa, including *Arcobacter trophiarum*, *Arcobacter cibarius*, *Arcobacter cryaerophilus*, and *Arcobacter thereius* (1), that are recovered from pigs, cattle, and poultry (2). *A. skirrowii* was isolated originally from veterinary samples, e.g., bovine preputial fluid and aborted bovine and porcine fetuses (3). Subsequently, *A. skirrowii* has also been recovered from pork and beef (4, 5), poultry (6), fish (7), and milk and cheese (8). Additionally, two reports of *A. skirrowii* isolated from human stool samples have been published (9, 10). In this study, we report the first closed genome sequence of the *A. skirrowii* type strain LMG 6621 (= 449/80^T = CCUG 10374^T) (3), which was isolated in the United Kingdom from lamb feces.

A. skirrowii strain LMG 6621^T was grown aerobically at 30°C for 48 h on anaerobe basal agar (Oxoid) plus 5% horse blood. An approximately 5-μl loop of cells was taken from a plate, and genomic DNA was prepared using the Wizard genomic DNA kit (Promega, Madison, WI). Shotgun and paired-end Roche 454 libraries were constructed as described previously (11) and sequenced on a GS-FLX+ instrument, using the Titanium chemistry and standard protocols. The reads from both 454 libraries were assembled together, using Newbler version 2.6 (Roche) and default settings, into 52 contigs and a single chromosomal scaffold of 16 unique contigs. Low-quality contigs were deleted, and placement of the remaining 20 contigs at one or more positions within the scaffold was accomplished with the custom Perl script contig_extender3 (11). PacBio libraries were prepared as described previously (11) and sequenced on an RS II instrument using standard methodology. Read assembly was performed using RS_HGAP_Assembly version 3 (Pacific Biosciences) with default settings. A single chromosomal contig was obtained, which was quality trimmed to a *Q* score of 40 and circularized using Geneious (version 11.0; Biomatters Ltd., Auckland, New Zealand). This contig and the 454 scaffold contigs were assembled together with SeqMan Pro (version 8.0.2; DNASTAR, Madison, WI), with the repeat 454 contigs added manually, to create a composite 454/PacBio assembly. Illumina HiSeq reads were obtained from SeqWright (Houston, TX) and used to verify and error correct the base calls within the 454/PacBio assembly, as described previously (12). The final coverage across the genome was 1,821×. Chromosomal assembly was also validated using an optical restriction map (restriction enzyme XbaI; OpGen, Gaithersburg, MD).

Sequencing metrics and genomic data for *A. skirrowii* strain LMG 6621^T are presented in Table 1. Protein-, rRNA-, and tRNA-encoding genes were identified as described previously (13) using GeneMark, RNAmmer, and ARAGORN, respectively

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TABLE 1 Sequencing metrics and genomic data for *A. skirrowii* strain LMG 6621^T

Feature	Data[a]
Sequencing metrics by platform	
454 (shotgun)	
No. of reads	77,166
No. of bases	31,779,672
Average length (bases)	411.8
Coverage (×)	16.1
454 (paired-end)	
No. of reads	135,775
No. of bases	46,030,534
Average length (bases)	339.0
Coverage (×)	23.4
Illumina HiSeq 2000	
No. of reads	18,024,500
No. of bases	1,820,474,500
Average length (bases)	101
Coverage (×)	924.2
PacBio	
No. of reads	252,507
No. of bases	1,689,600,967
Average length (bases)	6,691.3
Coverage (×)	857.7
Genomic data	
Chromosome	
Size (bp)	1,969,846
G+C content (%)	27.75
No. of CDS[b]	1,957
Assigned function (%)	868 (44.4)
General function annotation (%)	634 (32.4)
Domain/family annotation only (%)	134 (6.8)
Hypothetical (%)	321 (16.4)
No. of pseudogenes	20
Genomic islands/CRISPR	
No. of genetic islands	3
No. of CDS in genetic islands	146, [5]
CRISPR-Cas loci	Type III
Gene content/pathways	
Signal transduction	
Che proteins	*cheABDRVW*$(Y)_2$
No. of methyl-accepting chemotaxis proteins	17
No. of response regulators	20, [1]
No. of histidine kinases	21, [1]
No. of response regulator/histidine kinase fusions	1
No. of diguanylate cyclases	9
No. of diguanylate phosphodiesterases (HD-GYP, EAL)	2, 1
No. of diguanylate cyclase/phosphodiesterases	6
No. of other	8
Motility	
Flagellin genes	*flaAB*
Restriction/modification	
No. of type I systems (*hsd*)	0
No. of type II systems	6
No. of type III systems	0
Transcription/translation	
No. of transcriptional regulatory proteins	35
Non-ECF[c] σ factors	σ^{70}
No. of ECF σ factors	0
No. of tRNAs	48
No. of ribosomal loci	4
Nitrogen fixation (*nif*)	No
Osmoprotection	BCCT, *ectABCD*
Pyruvate → acetyl coenzyme A	
Pyruvate dehydrogenase (E1/E2/E3)	Yes
Pyruvate:ferredoxin oxidoreductase	No
Urease	No
Vitamin B_{12} biosynthesis	No

[a]Numbers in square brackets indicate pseudogenes or fragments.
[b]Numbers do not include pseudogenes. CDS, coding sequences.
[c]ECF, extracytoplasmic function.

(14–16). These features and the genome sequence were used to create a preliminary GenBank-formatted file, which was entered into Artemis version 16 (17) to manually curate the start codon of each putative coding sequence and identify putative pseudogenes. Annotation was accomplished through a BLASTP comparison of the strain LMG 6621^T proteome against proteins in the following two databases: the NCBI nonredundant (nr) database and a custom database that includes proteomes from all completed *Arcobacter* and *Campylobacter* genomes. Annotation calls were also verified through an analysis of Pfam motifs (18). Three genomic islands encoding type IIP restriction/modification systems were identified in the LMG 6621^T chromosome. Two islands (~97.9 kb and ~42.8 kb) are predicted to also encode a type VI secretion system and a P-type type IV conjugative transfer system, respectively. The third island (~23 kb) also contains four transposition-related genes, suggesting that this island may be a mobile element. The LMG 6621^T genome is predicted to encode a type III CRISPR-Cas system. No plasmids were identified in the LMG 6621^T genome.

Data availability. The complete genome sequence of *A. skirrowii* strain LMG 6621^T has been deposited in GenBank under the accession number CP032099. The 454, HiSeq, and PacBio sequencing reads have been deposited in the NCBI Sequence Read Archive (SRA) under the accession number SRP155172.

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