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GENOME SEQUENCES

Complete Genome Sequences of 17 Clinical *Campylobacter jejuni* Strains from Chile

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ABSTRACT *Campylobacter jejuni* is the leading cause of bacterial foodborne disease worldwide. Here, we report the complete annotated genomes and plasmid sequences of 17 *Campylobacter jejuni* strains isolated from patients with gastroenteritis in Santiago, Chile.

Campylobacter spp. are now considered the most common bacterial cause of human gastroenteritis worldwide. Of the 25 *Campylobacter* species, *Campylobacter jejuni* is the most common species associated with human disease (1–3). In Chile, *Campylobacter jejuni* infections are emerging as an important cause of foodborne illnesses (4–7). In this study, we obtained the complete genome sequences of 17 *C. jejuni* strains using a combination of long (Oxford Nanopore) and short (Illumina) reads.

These 17 strains, all belonging to different sequence types, were selected for genome closing out of 81 total strains. These strains were isolated in the laboratory from stool samples from patients with gastroenteritis as previously described (6, 8). These strains were exempt from institutional review board (IRB) review. Strains were grown overnight in Mueller-Hinton 5% sheep blood agar plates at 42°C under microaerobic conditions, and genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen). DNA quality and quantity were assessed using a NanoDrop spectrophotometer and a Qubit fluorometer (Thermo Scientific, Waltham, MA, USA), respectively, following the manufacturer's instructions. The long reads for each strain were generated in a MinION sequencer (Nanopore Technologies, Oxford, UK). The sequencing library was prepared using the rapid barcoding sequencing kit (SQK-RBK004). Every 10 libraries were pooled and run in a FLO-MIN106 (R9.4.1) flow cell, according to the manufacturer's instructions, for 48 h. The run was base called live using default settings (MinKNOW v19.06.8, Guppy v3.0.7). Default parameters were used for all software unless otherwise specified. In total, we conducted 2 Nanopore runs. The sequencing outputs for each of the 2 runs were 2.50 Gb (quality score, 12.41; N_{50}, 3,957 bp; total reads, 300,000) and 7.2 Gb (quality score, 11.46; N_{50}, 6,000 bp; total reads, 569,349), for an estimated average genome coverage of 60 to 90×. Reads of <5,000 bp and with a quality score of <7 were discarded for downstream analysis.

The short-read sequencing libraries for each strain were prepared using 100 ng DNA per strain according to the manufacturer's instructions using the Nextera DNA flex kit (Illumina, San Diego, CA, USA) for the MiSeq sequencing and 1 ng DNA for the Nextera XT kit for the NextSeq sequencing. Strains were sequenced using a MiSeq sequencer and a NextSeq sequencer (Illumina). For the MiSeq sequencing, we used a MiSeq v3 kit using 2 × 250-bp paired-end chemistry, according to the manufacturer's instructions, with >100× average coverage. For the NextSeq sequencing, we used a NextSeq

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TABLE 1 Metadata for the 17 *C. jejuni* strains reported in this study[a]

CFSAN no.[b]	GenBank accession no. for:		GC content (%)	Hybrid assembly genome coverage (×)	Nanopore sequencing depth (×)	MiSeq sequencing depth (×)	Illumina SRA no. (no. of reads)	Nanopore SRA no. (no. of reads)	Yr of isolation	ST[c]
	Chromosome	Plasmid								
CFSAN093260	CP040618 (1,627,779)		30.56	70	72	145	SRR10860968 (1,022,308)	SRR11620707 (4,572)	2018	52
CFSAN093259	CP040617 (1,688,111)		30.51	64	31	135	SRR10860969 (981,408)	SRR11620706 (5,234)	2018	50
CFSAN093257	CP040616 (1,720,666)		30.47	76	20	168	SRR10860971 (1,250,338)	SRR11620698 (2,472)	2018	1359
CFSAN093256	CP040615 (1,653,603)		30.53	84	95	184	SRR10860973 (1,334,060)	SRR11620697 (9,032)	2018	10196
CFSAN093246	CP040613 (1,680,823)	CP040614 (71,914)	30.54	73	20	150	SRR10860981 (1,224,214)	SRR11620696 (2,637)	2018	8938
CFSAN093241	CP040612 (1,662,100)		30.51	66	90	140	SRR10860987 (995,550)	SRR11620695 (9,485)	2018	475
CFSAN093238	CP040611 (1,745,502)		30.35	76	54	160	SRR10860990 (1,187,310)	SRR11620694 (5,587)	2018	353
CFSAN093227	CP040610 (1,824,459)		30.16	66	46	133	SRR10860972 (1,072,404)	SRR11620693 (4,855)	2017	607
CFSAN093226	CP040608 (1,681,003)	CP040609 (39,913)	30.52	71	60	149	SRR10860983 (1,086,354)	SRR11620692 (7,883)	2018	21
CFSAN093224	CP040607 (1,625,593)		30.56	88	78	187	SRR10860995 (1,288,270)	SRR11620691 (7,887)	2018	6091
CFSAN096296[d]	CP047484 (1,635,710)		30.54	296	20	675	SRR10859473 (7,707,678)	SRR11620705 (2,243)	2019	50
CFSAN096297[d]	CP047482 (1,664,471)	CP047483 (48,209)	30.42	210	79	424	SRR10859482 (5,183,902)	SRR11620704 (7,953)	2018	257
CFSAN096301[d]	CP047481 (1,661,307)		30.48	271	200	553	SRR10859574 (6,233,036)	SRR11620703 (48,095)	2019	52
CFSAN096302[d]	CP047480 (1,721,182)		30.47	249	97	510	SRR10859489 (5,972,014)	SRR11620702 (11,058)	2018	1359
CFSAN096305[d]	CP047479 (1,721,265)		30.44	260	58	520	SRR10859603 (6,157,576)	SRR11620701 (6,781)	2019	222
CFSAN096306[d]	CP047478 (1,650,107)		30.51	139	267	285	SRR10859609 (3,157,756)	SRR11620700 (47,192)	2019	50
CFSAN096307[d]	CP047477 (1,720,216)		30.42	81	30	165	SRR10859583 (1,902,526)	SRR11620699 (3,198)	2018	1359

[a] All strains were isolated in Santiago de Chile, Chile, from stools of patients with gastroenteritis.
[b] CFSAN, Center for Food Safety and Applied Nutrition.
[c] ST, sequence type (https://pubmlst.org/campylobacter/).
[d] Sequenced using NextSeq.

500/550 high-output kit v2.5 (300 cycles) using 2 × 150-bp paired-end chemistry, according to the manufacturer's instructions, with >300× average coverage. The reads were trimmed with Trimmomatic v0.36 (9).

The final complete genome sequence (comprising the chromosome and plasmid, when present) for each strain was obtained using a previously described pipeline (10), except that Flye v2.6 (11) was used instead of Canu v1.7 (12) for long-read *de novo* assembling. The genomes were confirmed as circular closed by finding the contig end overlap, which was then manually trimmed. Each closed genome was rotated to start at the *dnaA* gene.

Data availability. The complete genome sequences reported here have been deposited in NCBI GenBank under the accession numbers listed in Table 1.

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