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Draft Whole-Genome Sequences of 51 *Campylobacter jejuni* and 12 *Campylobacter coli* Clinical Isolates from Chile

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ABSTRACT *Campylobacter* species are the leading cause of gastroenteritis worldwide and an emerging threat in developing countries. Here, we report the draft whole-genome sequences of 51 *Campylobacter jejuni* and 12 *Campylobacter coli* strains isolated from patients with gastroenteritis in Santiago, Chile.

Human campylobacteriosis has been recognized as an important public health problem worldwide (1, 2). In developing countries such as Chile, diarrheal illness caused by *Campylobacter* species are emerging as an important cause of childhood morbidity (3–5). Over a 2-year period (2017 to 2019), 51 *Campylobacter jejuni* and 12 *Campylobacter coli* strains were isolated from acquired enteric infections by the clinical laboratory of Clinica Alemana in Santiago, Chile. The samples consisted of fresh stool, transported at room temperature and processed within 2 h of collection. Sample swabs were plated onto *Campylobacter* selective chromogenic (CASA) medium (bioMérieux, Marcy-l'Étoile, France), streaked into 4 quadrants with a sterile loop, and incubated for 48 h at 42°C under microaerobic conditions (Anaerocult C; Merck, Darmstadt, Germany). *Campylobacter* plates were analyzed after 48 h, and suspicious colonies were further identified through matrix-assisted laser desorption–ionization time of flight (MALDI-TOF) mass spectrometry using a Vitek MS instrument (bioMérieux). Following surveillance regulations, *Campylobacter* strains were sent to the National Reference Laboratory at the Chilean Institute of Public Health for further confirmation.

The *Campylobacter* strains were grown overnight on 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, Hilden, Germany). The 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. Sequencing libraries 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 instrument and 1 ng DNA for the Nextera XT kit for the NextSeq instrument. The strains were sequenced using both the MiSeq and NextSeq sequencers (Illumina). For the MiSeq, we used a MiSeq v3 kit with 2 × 250-bp paired-end chemistry, according to the manufacturer's instructions, with >100× average coverage. For the NextSeq, we used a NextSeq 500/550 high-output kit v2.5 (300 cycles) with 2 × 150-bp paired-end chemistry, according to the manufacturer's instructions, with >300× average coverage. Default parameters were used for all software unless otherwise specified. The Illumina reads were managed with the CLC Genomics

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TABLE 1 Metadata for the *Campylobacter jejuni and Campylobacter coli* strains reported in this study

Strain no.[a]	Species	SRA accession no.	GenBank accession no.	CC[b]	ST[c]	Genome size (bp)	GC content (%)	No. of contigs	No. of reads	Coverage (×)
CFSAN093225	*C. jejuni*	SRR10860994	JAAMXD000000000	48	475	1,680,704	30.35	29	1,324,624	180
CFSAN093228	*C. jejuni*	SRR10860964	JAAMXC000000000	21	1359	1,781,797	30.32	39	1,057,805	140
CFSAN093229	*C. jejuni*	SRR10860963	JAAMXB000000000		468	1,587,226	30.39	27	1,133,889	137
CFSAN093231	*C. jejuni*	SRR10860962	JAAMXA000000000	21	1359	1,697,519	30.37	31	1,475,962	162
CFSAN093232	*C. jejuni*	SRR10860961	JAAMWZ000000000	52	52	1,595,492	30.49	25	1,465,907	196
CFSAN093233	*C. jejuni*	SRR10860960	JAAMWY000000000	257	257	1,773,175	30.24	21	1,205,773	148
CFSAN093234	*C. jejuni*	SRR10860959	JAAMWX000000000	21	1359	1,760,698	31.06	60	882,983	23
CFSAN093235	*C. jejuni*	SRR10860993	JAAMWW000000000	21	1359	1,695,455	30.38	31	1,045,271	141
CFSAN093236	*C. jejuni*	SRR10860992	JAAMWV000000000	353	**10197**	1,698,351	30.25	39	1,023,125	141
CFSAN093237	*C. jejuni*	SRR10860991	JAAMWU000000000	206	**10193**	1,671,646	30.35	29	1,121,441	155
CFSAN093239	*C. jejuni*	SRR10860989	JAAMWT000000000	353	**10198**	1,681,217	30.28	28	1,329,238	179
CFSAN093240	*C. jejuni*	SRR10860988	JAAMWS000000000	21	1359	1,744,288	30.36	32	1,255,094	148
CFSAN093242	*C. jejuni*	SRR10860986	JAAMWR000000000	21	1359	1,658,077	30.37	33	1,073,048	108
CFSAN093243	*C. jejuni*	SRR10860985	JAAMWQ000000000	52	52	1,636,882	30.41	26	1,115,084	159
CFSAN093244	*C. coli*	SRR10860984	JAAMWP000000000	828	829	1,672,819	31.36	21	1,254,542	155
CFSAN093245	*C. jejuni*	SRR10860982	JAAMWO000000000	206	**10193**	1,672,029	30.35	30	1,125,976	159
CFSAN093247	*C. jejuni*	SRR10860980	JAAMWN000000000	52	52	1,604,559	30.48	26	1,375,114	195
CFSAN093249	*C. jejuni*	SRR10860979	JAAMWM000000000	443	51	1,626,108	30.33	19	1,091,724	153
CFSAN093250	*C. jejuni*	SRR10860978	JAAMWL000000000	48	475	1,712,809	31.08	30	1,002,658	53
CFSAN093251	*C. coli*	SRR10860977	JAAMWK000000000	828	1173	1,748,418	31.24	40	1,013,159	135
CFSAN093253	*C. coli*	SRR10860976	JAAMWJ000000000	1150	**10203**	1,786,483	31.16	29	993,128	101
CFSAN093254	*C. coli*	SRR10860975	JAAMWI000000000	828	1173	1,690,423	31.27	27	1,287,195	175
CFSAN093255	*C. jejuni*	SRR10860974	JAAMWH000000000	21	883	1,670,465	30.45	33	1,015,414	140
CFSAN093258	*C. jejuni*	SRR10860970	JAAMWG000000000	48	475	1,645,019	30.41	27	1,065,408	148
CFSAN093261	*C. jejuni*	SRR10860967	JAAMWF000000000	353	**10198**	1,682,616	30.28	28	1,056,783	142
CFSAN093262	*C. coli*	SRR10860966	JAAMWE000000000	828	**10201**	1,678,889	31.36	26	1,055,784	147
CFSAN093263	*C. coli*	SRR10860965	JAAMWD000000000	828	829	1,672,987	31.37	23	1,251,285	172
CFSAN096299	*C. jejuni*	SRR10859487	AANORF000000000	464	464	1,718,277	30.2	43	5,476,280	465
CFSAN096304	*C. jejuni*	SRR10868852	AANHWB000000000	21	883	1,671,524	30.43	36	4,419,880	381
CFSAN096308	*C. jejuni*	SRR10859598	AANOWN000000000	49	3720	1,601,057	30.41	19	5,861,201	361
CFSAN096310	*C. jejuni*	SRR10859577	AANOUI000000000	48	475	1,674,594	30.35	66	1,753,261	155
CFSAN096311	*C. jejuni*	SRR10859580	AANCIZ000000000	508	508	1,647,086	30.44	33	4,708,076	423
CFSAN096312	*C. jejuni*	SRR10859610	AANOQP000000000	45	137	1,633,626	30.41	18	5,353,374	483
CFSAN096313	*C. jejuni*	SRR10859488	AANOPZ000000000	21	883	1,620,403	30.46	34	3,177,773	287
CFSAN096315	*C. jejuni*	SRR10859588	AANOQR000000000	21	50	1,695,902	30.69	42	3,791,069	300
CFSAN096316	*C. jejuni*	SRR10859605	AANHVC000000000	443	**10200**	1,669,068	30.34	22	5,679,390	469
CFSAN096317	*C. jejuni*	SRR10859607	AANHUM000000000	21	883	1,624,970	30.47	35	5,730,522	340
CFSAN096318	*C. coli*	SRR10859593	AANHVQ000000000	828	1556	1,739,084	31.33	34	5,897,351	366
CFSAN096319	*C. jejuni*	SRR10859596	AANORO000000000	21	8938	1,751,744	30.25	54	4,898,705	394
CFSAN096320	*C. jejuni*	SRR10859484	AANHVM000000000	48	475	1,718,157	30.42	30	4,360,492	355
CFSAN096321	*C. jejuni*	SRR10859579	AANOQK000000000	42	3997	1,639,939	30.5	25	4,791,209	374
CFSAN096322	*C. coli*	SRR10859575	AANORL000000000		**10202**	1,686,003	31.28	19	5,638,361	435
CFSAN096323	*C. jejuni*	SRR10859576	AANOQD000000000	45	137	1,628,880	30.51	22	5,964,128	514
CFSAN096324	*C. jejuni*	SRR10868843	AANOFK000000000	21	883	1,617,745	30.47	45	6,814,094	608
CFSAN096325	*C. jejuni*	SRR10859491	AANOQN000000000	21	50	1,624,655	30.43	39	5,580,427	498
CFSAN096326	*C. coli*	SRR10859578	AANOQJ000000000		**10204**	1,560,320	31.79	20	5,267,801	496
CFSAN096327	*C. coli*	SRR10859608	AANOQZ000000000	828	828	1,826,387	31.05	69	7,193,183	536
CFSAN096328	*C. jejuni*	SRR10859486	AANHUK000000000		8941	1,573,428	30.53	25	3,972,658	371
CFSAN096329	*C. jejuni*	SRR10859490	AANOQL000000000		6091	1,644,013	30.39	19	7,719,809	640
CFSAN096330	*C. jejuni*	SRR10859571	AANOQF000000000	48	475	1,638,878	30.43	34	5,762,736	511
CFSAN096331	*C. jejuni*	SRR10859601	AANHVB000000000	353	4053	1,704,061	30.32	25	4,438,611	381
CFSAN096332	*C. jejuni*	SRR10859606	AANOQH000000000	607	1510	1,681,507	30.22	49	8,590,010	745
CFSAN096333	*C. jejuni*	SRR10859599	AANHUZ000000000	21	50	1,700,375	30.48	38	5,241,779	288
CFSAN096334	*C. jejuni*	SRR10859600	AANCJA000000000	48	475	1,638,392	30.44	32	7,357,763	627
CFSAN096335	*C. coli*	SRR10868836	AANORE000000000		**10204**	1,561,235	31.81	21	4,668,764	410
CFSAN096336	*C. jejuni*	SRR10859481	AANOQM000000000	353	4053	1,735,932	30.28	34	2,937,522	230
CFSAN096337	*C. jejuni*	SRR10859483	AANOED000000000	21	1359	1,740,390	30.37	33	6,008,099	417
CFSAN096339	*C. coli*	SRR10859485	AANOQC000000000	828	1556	1,735,795	32.79	37	7,891,488	664
CFSAN096340	*C. jejuni*	SRR10859492	AANOEA000000000	21	1359	1,693,355	30.38	33	6,779,991	550
CFSAN096341	*C. jejuni*	SRR10859477	AANOEB000000000	21	1359	1,696,562	30.37	53	5,452,622	456
CFSAN096343	*C. jejuni*	SRR10859474	JAAMWC000000000	206	**10192**	1,746,366	30.44	37	6,525,453	549
CFSAN096344	*C. jejuni*	SRR10859586	AANOQG000000000		3573	1,603,229	30.41	30	5,346,306	494
CFSAN096345	*C. jejuni*	SRR10859604	AANOQO000000000	48	38	1,693,493	30.38	29	7,799,266	676

[a] Strains in bold were sequenced on the NextSeq platform.

[b] CC, clonal complex.

[c] ST, sequence type. Entries in bold are novel STs.

Workbench v9.5.2 (Qiagen), assessed for quality (Q, >30) with the quality control tool, and trimmed (adapter trimming, quality trimming, and length trimming) with the trim sequences tool. The trimmed data for each strain were *de novo* assembled using CLC Genomics Workbench and a minimum contig size threshold of 500 bp.

The assembly and annotation metrics of the draft whole-genome sequences are listed in Table 1. This study reports the draft genomes of 51 *C. jejuni* and 12 *C. coli* strains from Chile. Currently, there are only 3 draft genomes of *C. jejuni* from this country available at NCBI (6); thus, this release increases by 17-fold the number of available *C. jejuni* genomes from Chile. *In silico* multilocus sequence typing (MLST) analysis using the MLST *Campylobacter jejuni/coli* database (http://pubmlst.org/campylobacter) identified that clonal complex 21 (CC-21) was the most common among the reported *C. jejuni* strains (35.3%). In the case of *C. coli*, 66.7% of strains belonged to CC-828. Our study presents genomic data that will be useful for understanding the genetic diversity, virulence potential, and antimicrobial resistance of clinical *Campylobacter* strains from Chile and the region.

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

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