AMERICAN SOCIETY FOR MICROBIOLOGY genomeAnnouncements™

PROKARYOTES

Draft Genome Sequences of 116 *Campylobacter jejuni* Strains Isolated from Humans, Animals, Food, and the Environment in Brazil

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ABSTRACT *Campylobacter jejuni* is a major zoonotic pathogen that causes foodborne gastroenteritis worldwide. However, clinical cases of campylobacteriosis have been underreported and underdiagnosed in Brazil. Herein, we describe the draft genome sequences of 116 *C. jejuni* strains isolated from diverse sources in Brazil.

Campylobacter jejuni has emerged as the most common bacterial cause of foodborne disease in humans in many countries (1, 2). In the United States, *C. jejuni* is the most common cause of diarrhea in humans, which affects over 1.3 million people each year (https://www.cdc.gov/campylobacter/index.html). According to the European Food Safety Authority (EFSA), in 27 European countries in 2016, campylobacteriosis was the most commonly reported gastrointestinal bacterial pathogen in humans, with approximately 246,000 cases reported (3). However, in Brazil, clinical cases of campylobacteriosis have been underreported and underdiagnosed, and large-scale whole-genome sequencing (WGS) data are currently somewhat limited in strains isolated in that country. Here, we announce 116 draft genome sequences from a collection of *C. jejuni* strains isolated from humans, animals, food, and the environment between 1996 and 2016 in some states of Brazil.

DNA from each strain was extracted according to Frazão et al. (4). Libraries were prepared using 1 ng of genomic DNA with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA). WGS was carried out on a MiSeq or a NextSeq Illumina instrument using a 2 × 250-bp or a 2 × 150-bp paired-end MiSeq or NextSeq reagent kit, respectively (Illumina), according to the manufacturer's instructions. *De novo* assemblies were generated from all raw sequence data. The Illumina reads were assembled using CLC Genomics Workbench version 10.0.1 (CLC Bio, Aarhus, Denmark). The contigs for each isolate (draft genomes) were annotated with NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) (5). The total lengths of the genomes ranged from 1.6 to 1.8 Mb, with an average G+C content of 30.35%, and the number of contigs per assembly for each isolate ranged from 24 to 338.

These data are the first announcements of *C. jejuni* genomes sequenced from strains isolated in Brazil. Therefore, the data provided will help in understanding the molecular epidemiology of this species isolated from different sources in Brazil. It will also provide support in future research of *C. jejuni* phylogenetics. More information about the genomic features of those *C. jejuni* strains will be detailed in future publications.

Received 26 February 2018 **Accepted** 22 March 2018 **Published** 19 April 2018

Citation Frazão MR, Cao G, Medeiros MIC, Duque SDS, Leon MS, Allard MW, Falcão JP. 2018. Draft genome sequences of 116 *Campylobacter jejuni* strains isolated from humans, animals, food, and the environment in Brazil. Genome Announc 6:e00250-18. https://doi.org/10.1128/genomeA.00250-18.

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TABLE 1 Metadata of the 116 *C. jejuni* strains isolated from humans, animals, food, and the environment between 1996 and 2016 in Brazil

CFSAN no.	GenBank accession no.	Isolate name	No. of contigs	Coverage (×)	Genome size (Mb)
CFSAN065294	PIBJ00000000	Cj 01	49	209	1,678,925
CFSAN065295	PIBI00000000	Cj 02	42	96	1,652,297
CFSAN065296	PIBH00000000	Cj 03	48	209	1,668,078
CFSAN065297	PIBG00000000	Cj 04	51	179	1,707,150
CFSAN065298	PIBF00000000	Cj 06	55	306	1,804,215
CFSAN065299	PIBE00000000	Cj 07	49	216	1,802,410
CFSAN065300	PIBD00000000	Cj 09	46	220	1,687,215
CFSAN065301	PIBC00000000	Cj 11	68	263	1,806,596
CFSAN065302	PIBB00000000	Cj 12	48	269	1,734,641
CFSAN065303	PIBA00000000	Cj 13	27	237	1,702,285
CFSAN065305	PIAZ00000000	Cj 15	48	239	1,761,819
CFSAN065306	PIAY00000000	Cj 16	77	275	1,803,006
CFSAN065307	PIAX00000000	Cj 17	118	154	1,769,104
CFSAN065308	PIAW00000000	Cj 18	47	156	1,771,462
CFSAN065309	PIAV00000000	Cj 19	24	242	1,705,617
CFSAN065310	PIAU00000000	Cj 20	51	216	1,772,036
CFSAN065312	PIAT00000000	Cj 22	37	130	1,658,649
CFSAN065313	PIAS00000000	Cj 23	39	166	1,636,095
CFSAN065314	PIAR00000000	Cj 24	37	222	1,637,517
CFSAN065315	PIAQ00000000	Cj 25	190	221	1,654,857
CFSAN065316	PITT00000000	Cj 26	31	176	1,595,918
CFSAN065317	PIAP00000000	Cj 27	33	192	1,596,189
CFSAN065319	PIAO00000000	Cj 29	67	68	1,727,160
CFSAN065320	PIAN00000000	Cj 30	29	158	1,594,811
CFSAN065321	PIAM00000000	Cj 31	36	258	1,636,720
CFSAN065322	PIAL00000000	Cj 32	35	300	1,636,458
CFSAN065323	PIAK00000000	Cj 33	31	250	1,637,414
CFSAN065324	PIAJ00000000	Cj 34	42	231	1,683,573
CFSAN065325	PIAI00000000	CCAMP 81	47	88	1,635,800
CFSAN065326	PIAH00000000	CCAMP 159	38	156	1,812,324
CFSAN065327	PIAG00000000	CCAMP 162	35	271	1,599,331
CFSAN065328	PIAF00000000	CCAMP 163	38	292	1,599,208
CFSAN065329	PIAE00000000	CCAMP 470	41	260	1,760,234
CFSAN065330	PIAD00000000	CCAMP 471	46	148	1,759,697
CFSAN065331	PIAC00000000	CCAMP 472	40	207	1,760,447
CFSAN065332	PIAB00000000	CCAMP 473	42	184	1,713,063
CFSAN065333	PIAA00000000	CCAMP 476	29	197	1,704,094
CFSAN065334	PHZZ00000000	CCAMP 478	31	160	1,703,651
CFSAN065335	PHZY00000000	CCAMP 479	37	184	1,706,050
CFSAN065336	PHZX00000000	CCAMP 480	26	96	1,651,015
CFSAN065337	PHZW00000000	CCAMP 481	25	159	1,649,512
CFSAN065338	PHZV00000000	CCAMP 487	63	117	1,685,038
CFSAN065339	PHZU00000000	CCAMP 488	109	66	1,683,207
CFSAN065340	PHZT00000000	CCAMP 489	34	95	1,685,408
CFSAN065341	PHZS00000000	CCAMP 493	38	101	1,611,209
CFSAN065342	PHZR00000000	CCAMP 497	116	77	1,716,424
CFSAN065343	PHZQ00000000	CCAMP 501	49	163	1,689,341
CFSAN065344	PHZP00000000	CCAMP 506	53	90	1,687,457
CFSAN065345	PHZO00000000	CCAMP 512	35	163	1,611,698
CFSAN065346	PHZN00000000	CCAMP 588	65	317	1,634,101
CFSAN065347	PHZM00000000	CCAMP 594	80	330	1,748,723
CFSAN065348	PHZL00000000	CCAMP 601	58	401	1,768,624
CFSAN065349	PHZK00000000	CCAMP 612	61	337	1,694,670
CFSAN065350	PHZJ00000000	CCAMP 621	74	341	1,785,086
CFSAN065351	PHZI00000000	CCAMP 672	81	407	1,735,916
CFSAN065352	PHZH00000000	CCAMP 674	75	419	1,735,575
CFSAN065353	PHZG00000000	CCAMP 675	79	318	1,734,937
CFSAN065354	PHZF00000000	CCAMP 678	54	343	1,767,906
CFSAN065355	PHZE00000000	CCAMP 685	67	418	1,634,518
CFSAN065356	PHZD00000000	CCAMP 687	185	79	1,727,948
CFSAN065357	PHZC00000000	CCAMP 689	101	343	1,738,975
CFSAN065358	PHZB00000000	CCAMP 696	83	410	1,728,963
CFSAN065360	PHZA00000000	CCAMP 699	244	240	1,778,240
CFSAN065361	PHYZ00000000	CCAMP 700	89	233	1,783,490
CFSAN065362	PHYY00000000	CCAMP 730	43	405	1,683,506

(Continued on next page)

TABLE 1 (Continued)

CFSAN no.	GenBank accession no.	Isolate name	No. of contigs	Coverage (×)	Genome size (Mb)
CFSAN065363	PHYX00000000	CCAMP 764	69	473	1,676,314
CFSAN065364	PHYW00000000	CCAMP 770	73	419	1,784,355
CFSAN065365	PHYV00000000	CCAMP 789	93	271	1,859,503
CFSAN065366	PHYU00000000	CCAMP 828	66	521	1,688,461
CFSAN065367	PHYT00000000	CCAMP 830	53	422	1,610,333
CFSAN065368	PHYS00000000	CCAMP 845	81	412	1,732,437
CFSAN065369	PHYR00000000	CCAMP 980	60	438	1,610,707
CFSAN065370	PHYQ00000000	CCAMP 991	53	321	1,621,260
CFSAN065371	PHYP00000000	CCAMP 1013	71	239	1,676,660
CFSAN065372	PHYO00000000	CCAMP 1014	70	271	1,736,018
CFSAN065373	PHYN00000000	CCAMP 1015	48	163	1,712,819
CFSAN065374	PHYM00000000	CCAMP 1016	46	221	1,713,751
CFSAN065375	PHYL00000000	CCAMP 1018	338	248	1,841,107
CFSAN065376	PHYK00000000	CCAMP 1019	73	260	1,618,523
CFSAN065377	PHYJ00000000	CCAMP 1020	60	342	1,718,399
CFSAN065378	PHYI00000000	CCAMP 1021	53	412	1,715,372
CFSAN065379	PHYH00000000	CCAMP 1023	74	429	1,620,071
CFSAN065380	PHYG00000000	CCAMP 1024	67	428	1,619,031
CFSAN065381	PHYF00000000	CCAMP 1025	61	178	1,716,643
CFSAN065382	PHYE00000000	CCAMP 1032	69	194	1,619,042
CFSAN065383	PHYD00000000	CCAMP 1039	86	288	1,763,753
CFSAN065384	PHYC00000000	CCAMP 1047	59	133	1,614,893
CFSAN065385	PHYB00000000	CCAMP 1048	78	344	1,760,602
CFSAN065386	PHYA00000000	CCAMP 1050	72	441	1,737,009
CFSAN065387	PHXZ00000000	CCAMP 1051	74	486	1,739,722
CFSAN065388	PHXY00000000	CCAMP 1052	78	396	1,740,214
CFSAN065389	PHXX00000000	CCAMP 1053	86	247	1,682,879
CFSAN065390	PHXW00000000	CCAMP 1054	87	327	1,681,930
CFSAN065391	PHXV00000000	CCAMP 1055	87	431	1,685,406
CFSAN065392	PHXU00000000	CCAMP 1056	83	393	1,742,202
CFSAN065393	PHXT00000000	CCAMP 1057	94	350	1,745,619
CFSAN065394	PHXS00000000	CCAMP 1058	75	468	1,680,673
CFSAN065395	PHXR00000000	CCAMP 1059	81	435	1,680,464
CFSAN065396	PHXQ00000000	CCAMP 1060	59	456	1,735,059
CFSAN065397	PHXP00000000	CCAMP 1061	81	314	1,731,243
CFSAN065399	PHXO00000000	CCAMP 1080	308	489	1,852,898
CFSAN065400	PHXN00000000	CCAMP 1140	66	239	1,608,933
CFSAN065401	PHXM00000000	CCAMP 1266	64	353	1,698,726
CFSAN065402	PHXL00000000	CCAMP 1466	80	419	1,641,107
CFSAN065403	PHXK00000000	CCAMP 1478	109	93	1,708,613
CFSAN065404	PHXJ00000000	CCAMP 1491	105	128	1,729,770
CFSAN065405	PHXI00000000	CCAMP 1493	126	350	1,632,513
CFSAN065406	PHXH00000000	CCAMP 1497	115	178	1,663,987
CFSAN065407	PHXG00000000	CCAMP 1518	124	159	1,805,069
CFSAN065408	PHXF00000000	CCAMP 1519	132	190	1,767,168
CFSAN065409	PHXE00000000	CCAMP 1520	217	168	1,836,048
CFSAN065410	PHXD00000000	CCAMP 1521	185	116	1,819,069
CFSAN065411	PITS00000000	CCAMP 1523	185	153	1,816,718
CFSAN065412	PHXC00000000	CCAMP 1538	241	163	1,855,211
CFSAN065413	PHXB00000000	CCAMP 1555	236	215	1,806,342
CFSAN065414	PHXA00000000	CCAMP 1574	192	163	1,806,801

Accession number(s). The draft genome sequences for the 116 *Campylobacter jejuni* isolates reported here are available in GenBank under the accession numbers listed in Table 1.

ACKNOWLEDGMENTS

This study was supported by an FDA/Center for Food Safety and Applied Nutrition (CFSAN) research grant under the supervision of Marc William Allard and a grant from the Sao Paulo Research Foundation (FAPESP) (no. 2014/13029-0) under the supervision of Juliana Pfrimer Falcão. During the course of this work, Miliane Rodrigues Frazão was supported by a scholarship from Coordination for the Improvement of the Higher Education Personnel (CAPES/PDSE) (no. 88881.133716/2016-01).

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