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GENOME SEQUENCES

Draft Genomic Sequences of *Campylobacter coli* Isolates from Chicken Carcasses

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ABSTRACT *Campylobacter* bacteria are one of the leading causes of bacterial foodborne illnesses in the United States. Here, we report the draft genomic sequences of eight *Campylobacter coli* isolates from chicken carcasses, including virulence factors and antibiotic resistance.

Campylobacter bacteria cause a large amount of human disease annually in the United States and are leading causative agents in the 3.6 million bacterial foodborne pathogen illnesses reported annually (1). The consumption of poultry meat contaminated by *Campylobacter* is associated with an estimated 608,231 illnesses, 6,091 hospitalizations, 55 deaths, and a $1,257 million cost of illness annually, which is the top disease burden among 50 pathogen-food combinations (2). Poultry meat can be contaminated by *Campylobacter* during slaughter and carcass processing (3). A better understanding of the mechanisms of survival and infection of *Campylobacter*, including virulence and resistance factors, is needed to develop effective control technologies (4). Toward this end, eight low-passage-number *Campylobacter coli* isolates recovered from chicken carcasses were subjected to genomic sequencing (5, 6).

Frozen (−80°C) cultures were streaked directly onto Brucella agar plates (Becton, Dickinson, Sparks, MD) and incubated for ~16 h at 42°C in a microaerobic (5% O_2, 10% CO_2, 85% N_2) growth chamber (Concept-M; Baker Ruskinn, United Kingdom). Genomic DNA was isolated from a single colony of each of the strains using the MagAttract HMW DNA kit (Qiagen, Hilden, Germany) and quantified in a Qubit 3.0 fluorimeter (Life Technologies, Carlsbad, CA, USA). The genomic DNA library was prepared using the Nextera DNA Flex library prep kit (Illumina, San Diego, CA, USA). Libraries were analyzed for concentration, pooled, and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on the Illumina MiniSeq platform with a 2 × 150-bp paired-end read protocol with more than 400× coverage. Read quality was assessed with FastQC version 1.0.0. (Illumina BaseSpace Labs). The genome was assembled *de novo* using SPAdes (version 3.9.0). Default parameters were used for all software unless otherwise specified. Virulence factors, antibiotic resistance genes, genome size, N_{50} values, paired-end reads, genome coverage, genes, pseudogenes, noncoding RNAs (ncRNAs), rRNAs, tRNAs, and coding sequences (CDSs) were determined using the Illumina Bacterial Analysis Pipeline version 1.0.4 and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 4.3. A description of the characteristics of the eight *Campylobacter coli* strains is presented in Table 1.

Antibiotic resistance includes that to beta-lactams (bla_{OXA-61}) (Illumina Bacterial Analysis Pipeline version 1.0.4). The *Campylobacter coli* strains were positive for most of the virulence factors related to motility, chemotaxis, adhesion, and invasion, including cytolethal distending toxin (*cdtB*), multidrug efflux pumps (*cmeB*, *cmeC*, and *cmeR*), iron uptake regulator (*fur*), chemotaxis proteins (*cheB*, *cheV*, and *cheW*), and flagellar proteins (*flhA*, *flhB*, *flip*, *fliQ*, *fliR*, *fliF*, *fliY*, *fliM*, *fliA*, *fliK*, *flgE*, *flgI*, and *flgH*) (NCBI Sequence Set Browser). This is consistent with recent studies showing that *cmeABC* and *cdtABC* genes

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TABLE 1 Characteristics of eight *Campylobacter coli* strains

Strain name	GenBank accession no.	BioProject no.	SRA accession no.	Genome coverage (×)	Size (bp)	No. of paired-end reads	GC content (%)	No. of contigs	Total no. of genes	No. of pseudogenes	N_{50}[a] (bp)	No. of CDSs	No. of tRNAs	No. of rRNAs	No. of ncRNAs
PSU100	RYEW00000000	PRJNA508208	SRR8321244	741	1,842,077	4,524,912	30.96	117	1,971	61	142,334	1,923	42	3	3
PSU101	RYEX00000000	PRJNA510094	SRR8321238	409	1,838,143	2,491,397	30.96	99	1,960	59	142,334	1,912	42	3	3
PSU116	RYFA00000000	PRJNA510096	SRR8321240	558	1,841,945	3,408,416	30.96	110	1,957	59	142,334	1,909	42	3	3
PSU129	RYEY00000000	PRJNA510100	SRR8321242	482	1,677,628	2,682,276	31.33	49	1,758	40	162,680	1,710	42	3	3
PSU148	RYVW00000000	PRJNA510960	SRR8360371	578	1,823,297	3,491,607	31.13	164	1,962	86	163,420	1,913	42	4	3
PSU150	RYEZ00000000	PRJNA510101	SRR8321246	500	1,696,483	2,812,050	31.34	83	1,780	41	162,680	1,732	42	3	3
PSU165	RYVV00000000	PRJNA510961	SRR8360372	557	1,824,456	3,369,414	31.13	171	1,957	82	163,420	1,911	39	4	3
PSU172	RYVX00000000	PRJNA510962	SRR8360373	604	1,815,101	3,634,447	31.12	127	1,947	75	142,019	1,898	42	4	3

[a] The N_{50} value is the size of the shortest contig in the set of longest contigs that together cover at least 50% of the total genome size.

were detected in *Campylobacter coli* isolates (7, 8). These genomic data sets will be useful for developing methods for the control of *Campylobacter coli* in foods.

Data availability. The whole-genome shotgun projects reported here have been deposited in DDBJ/ENA/GenBank under the accession numbers, BioProject numbers, and Sequence Read Archive (SRA) accession numbers listed in Table 1. The versions described in this paper are the first versions.

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