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GENOME SEQUENCES

Draft Genome Sequences of Three Strains of *Campylobacter jejuni* Isolated from Patients with Guillain-Barré Syndrome in Bangladesh

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ABSTRACT *Campylobacter jejuni* is the pathogen most commonly associated with Guillain-Barré syndrome (GBS). The present work describes the draft genome sequences of 3 *C. jejuni* strains, BD39, BD67, and BD75, isolated from stool specimens of patients with *C. jejuni*-triggered GBS using Illumina technologies.

Campylobacter jejuni is one of the prevailing diarrheal pathogens worldwide and causes Guillain-Barré syndrome (GBS) as a postinfection sequel (1, 2). Molecular mimicry between *C. jejuni* outer membrane lipooligosaccharides and host peripheral nerve gangliosides is widely postulated as the mechanism that triggers this autoimmunity (3–5). The interrelation between the microbial factors and host immunity that trigger autoreactivity is still unclear. Genome profiling of *C. jejuni* isolated from fecal samples from patients with GBS can unfold its genetic information and create a platform for comparison with other *C. jejuni* strains causing campylobacteriosis, which will help to reveal the detailed mechanisms and pathogenesis of GBS and other sequelae of *Campylobacter*-associated diarrhea. The study was approved by the institutional review board (IRB) of icddr,b, Bangladesh.

C. jejuni strains BD39, BD67, and BD75 were isolated from stool specimens from GBS patients using standard microbiological procedures (3). The *C. jejuni* isolates were enriched at 42°C for 48 h in blood agar with 5% sheep blood, and genomic DNA was extracted from the *C. jejuni* strains using the Wizard genomic DNA purification kit (Promega) following the manufacturer's instructions (3). The DNA quality was determined using a NanoDrop spectrophotometer (Thermo Scientific, USA) and quantified using a Quantus fluorometer with the QuantiFluor ONE double-stranded DNA (dsDNA) system in order to fulfill sample quality requirements (quantity, 10 μg; concentration, N_{50}, $<$200 ng/μg). Next-generation genome sequencing of the three *C. jejuni* strains was performed using the NextSeq 500 system (Illumina platform). The Illumina Nextera XT DNA library preparation kit (catalog number FC-131-1024) was used to prepare the sequencing library, and the NextSeq v2.5 reagent kit was used for sequencing. Quality checks on the paired-end sequencing reads (150 bp) were performed using FastQC v0.11.5 (6). Trimmomatic v0.36 was used for adapter trimming based on quality scores of Q30 with the following parameters applied: SLIDINGWINDOW:4:15, HEADGROUP:15, TRAILING:3, and MINLEN:36 (7). *De novo* assembly was performed using SPAdes v3.9.0 (8). Genome annotation was accomplished by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.1 (9). CRISPRCasFinder (https://crisprcas.i2bc.paris-saclay.fr/CrisprCasFinder/Index) and the CRISPRTarget Web tool (http://crispr.otago.ac.nz/CRISPRTarget/crispr_analysis.html) were used to find and analyze clustered regularly interspaced short palindromic repeats (CRISPR) arrays. Default parameters were applied for all software unless otherwise specified.

The obtained genomic sequences had coverages of $>$200 for each strain. The guanine and cytosine (G+C) contents and genome sizes for these strains were found to be

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TABLE 1 Genome features and accession numbers for *Campylobacter jejuni* strains BD-39, BD-67, and BD-75

								PGAP[a] annotation						Read information			
										No. of rRNAs							
Strain	LOS[b,c]	Penner type[c,d]	GenBank assembly accession no.	Genome size (bp)	G+C content (mol%)	No. of contigs	N_{50} (bp)	GenBank accession no.	Total no. of genes	5S	16S	23S	No. of tRNAs	SRA[e] accession no.	No. of reads	Avg length (bp)	Genome coverage (×)
BD-39	A	HS:19	GCA_003048165.1	1,599,909	32.3	35	145,897	NGUG00000000	1,660	1	1	1	40	SRR5363131	5,030,760	300	393
BD-67	B	HS:23	GCA_003048115.1	1,778,638	31.8	62	129,048	NGUF00000000	1,866	1	1	1	40	SRR5363132	11,984,930	300	842
BD-75	A	HS:55	GCA_003048185.1	1,651,474	32.0	18	183,845	NGUI00000000	1,734	1	1	1	40	SRR5363133	6,078,678	300	460

[a] PGAP, NCBI Prokaryotic Genome Annotation Pipeline.
[b] LOS, lipooligosaccharide.
[c] This information comes from Islam et al. (10).
[d] Penner heat-stable (HS) serotypes.
[e] SRA, Sequence Read Archive.

31.8% to 32.3% and 1.59 Mbp to 1.77 Mbp (Table 1). From PGAP annotation, the *C. jejuni* strains have a total of 1,660 to 1,866 genes, including 46 RNAs for each strain. Moreover, CRISPR arrays were found in *C. jejuni* strains BD-39 and BD-67. The spacer sequences of these two strains target the protospacers of different plasmids and phages, but *Campylobacter phage* DA10 (GenBank accession number MN530981) was the common phage targeted by both strains (three protospacers targeted by one spacer sequence of BD-39 and two spacer sequences of BD-67). It is possible that the pathophysiology of *C. jejuni* is affected by the CRISPR-*cas9* system, which distinctively links *C. jejuni* bacteriophage defense, virulence, and GBS (11, 12).

Data availability. All accession numbers are provided in Table 1.

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