Complete Genome Sequences of \textit{Campylobacter jejuni} Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barré Syndrome

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Infections with \textit{Campylobacter jejuni} subsp. \textit{jejuni} are a leading cause of foodborne gastroenteritis and the most prevalent infection preceding Guillain-Barré syndrome (GBS). This study describes the genomes of \textit{C. jejuni} subsp. \textit{jejuni} HS:41 strains RM3196 (233.94) and RM3197 (308.95) that were isolated from patients with GBS in Cape Town, South Africa.

Received 21 September 2015 Accepted 28 September 2015 Published 5 November 2015

Citation Parker CT, Huynh S, Heikema AP, Cooper KK, Miller WG. 2015. Complete genome sequences of \textit{Campylobacter jejuni} strains RM3196 (233.94) and RM3197 (308.95) isolated from patients with Guillain-Barré syndrome. Genome Announc 3(6):e01312-15. doi:10.1128/genomeA.01312-15.

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The majority of \textit{Campylobacter jejuni} subsp. \textit{jejuni} infections result in an acute self-limited gastrointestinal illness; however, in a small number of patients, \textit{C. jejuni} subsp. \textit{jejuni} infection is followed by the development of the autoimmune neuropathy Guillain-Barré syndrome (GBS) (1). GBS can be triggered by sialylated lipooligosaccharides (LOS) on the cell surface of \textit{C. jejuni} that exhibit molecular similarity with gangliosides on human peripheral nerves (2–4). In \textit{C. jejuni} subsp. \textit{jejuni} strains isolated from stool samples from patients with GBS in Cape Town, South Africa, the Penner serotype HS:41 was overrepresented (5, 6). Previously, we observed that 13 distinct clinical \textit{C. jejuni} subsp. \textit{jejuni} HS:41 strains from South Africa were indistinguishable by microarray-based genomic indexing (7). To further explore the genomic similarities between these GBS-related strains, we report the genomic sequences of two \textit{C. jejuni} subsp. \textit{jejuni} strains, RM3196 (233.94) and RM3197 (308.95), which were isolated from patients with GBS in 1994 and 1995, respectively.

Genome sequencing was performed on an Illumina MiSeq desktop sequencer using shotgun library reads. A total of 2,188,526 (RM3196) and 2,153,596 (RM3197) reads, with an average read length of 300 nucleotides (nt), were assembled \textit{de novo} using the Roche Newbler assembler (version 2.3) and resulted in 100 total contigs (>100 bp) and 40 large contigs (5 to 77 kb) for each strain. Reference assemblies for each strain against the \textit{C. jejuni} NCTC 11168 genome were performed within the Geneious. The NCTC 11168 genome were performed within the Geneious.

Acknowledgments

This work was supported by USDA-ARS CRIS project 2030-42000-047-00D.

We thank Al Lastovica at University of the Western Cape, South Africa, for providing strains. We also thank Anne Bates and Robert Mandrell for curation of the Produce Safety and Microbiology Research Unit strain collection.

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