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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Variant of *Campylobacter jejuni* NCTC 11168

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***Campylobacter jejuni* NCTC 11168 is widely used in research, but at least two variants have been reported. The available genome was sequenced from a variant which later showed a different phenotype and gene expression profile. Here we present the complete genome sequence of a second variant of *C. jejuni* NCTC 11168.**

The first *Campylobacter jejuni* genome was sequenced from a clone of the NCTC 11168 strain (11168-GS) (8). This clone was found to colonize 1-day-old chicks (1, 2) and invade tissue culture cells less efficiently (2, 4) and to be less motile (2, 4) than the original *C. jejuni* variant isolated in 1977 and to display a straight rod shape (4). These findings suggest that *C. jejuni* NCTC 11168 variants from different laboratories not only may display phenotypic differences but can have a genetic variability which can adversely affect the results and reproducibility of experiments.

Here we present the genome sequence of a *C. jejuni* strain variant of NCTC 11168 (NCTC 11168-BN148), obtained in 1979 from the collection of the Centers for Disease Control and Prevention (CDC) (Atlanta, GA). According to its invasion, motility, and morphology, NCTC 11168-BN148 is similar to the original clinical isolate.

The genome sequence of *C. jejuni* NCTC 11168-BN148 was determined using Illumina sequencing technology (100 cycles, paired-end library, 860× coverage; performed by Base-Clear BV, Leiden, The Netherlands). Reads were filtered using the Condetri Perl script (10) (default settings, minimum read length of 75 nucleotides), and only sequences passing the quality threshold in both paired reads were aligned to the *C. jejuni* NCTC 11168-GS NCBI entry using the Burrows-Wheeler aligner (7).

In addition, all reads were assembled using Velvet v1.2.03 (11), and the resulting contigs of >500 nucleotides could be completely aligned to 11168-GS. No additional DNA regions or extrachromosomal material was detected. Gene calling and annotation were transferred from NC_002163.1 (5) using Artemis (9). The *C. jejuni* NCTC 11168-BN148 genome differed from that of 11168-GS by a total of seven point mutations. The genes used in the multilocus sequence typing (MLST), *gltA* and *porA*, were mutated at A242T and E180G, respectively. Although the mutation in *gltA* did not change the allele number and consequently the ST, this was not the case for the major outer membrane proteins (MOMPs) (PorA). According to pubMLST (6), 11168GS has the allele *porA34* (MOMP-31) while 11168-BN148 has *porA27* (MOMP-10).

Further changes were observed in BN1480276 (*mreB*; D48G), BN1480284c (*cheA*; I290T), and BN1480807 (7-α-hydroxysteroid dehydrogenase; K198E). In addition, mutations in BN1480431 (periplasmic ATP/GTP binding protein; *205K [where the asterisk represents the stop codon]) and BN1480455c (hypothetical protein; *115Q) extended the correspondent proteins of 41 and 61 amino acids, respectively. Based on the BLASTP homology search, these genes appear to be highly conserved in *Campylobacter jejuni* strains, but both Cj0431 and Cj0455c are fragmented in 11168-GS. As a consequence of the mutation observed in BN1480455c, we reannotated the start codon of the downstream gene (BN1480454c) using Glimmer v3.02 (3). The new start codon corresponds to the methionine at position 18 of Cj0454c.

All together, the mutations reported here in strain 11168-BN148 may contribute to the phenotypic differences, and we propose sequencing of *porA* as a tool for elucidating the diversity of variants present among different laboratories.

Nucleotide sequence accession number. The complete genome sequence of the *C. jejuni* strain NCTC 11168-BN148 has been deposited in EMBL under the accession number HE978252 (project identification, PRJEB175).

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