



Complete Genome Sequence of the *Campylobacter helveticus* Type Strain ATCC 51209

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ABSTRACT *Campylobacter helveticus* has been isolated from domestic dogs and cats. Although *C. helveticus* is closely related to the emerging human pathogen *C. upsaliensis*, no *C. helveticus*-associated cases of human illness have been reported. This study describes the whole-genome sequence of the *C. helveticus* type strain ATCC 51209 (=CCUG 30682^T).

Campylobacter helveticus is a catalase-negative, thermotolerant campylobacter that is generally isolated from cats and occasionally from dogs (1–4). However, although it is isolated from pets and is related to the human emerging pathogen *C. upsaliensis* (5), there have been no reports of *C. helveticus*-associated human disease (5, 6). The *C. helveticus* type strain ATCC 51209 was isolated in Switzerland from a domestic cat with diarrheal illness (7). In this study, we report the first closed genome sequence of strain ATCC 51209^T.

The Roche GS-FLX, Illumina HiSeq, and PacBio RS next-generation sequencing platforms were used to complete the strain ATCC 51209^T genome. Shotgun and paired-end Roche 454 reads were assembled (using Newbler version 2.6) into 6 scaffolds (1 chromosomal and 5 plasmid) of 46 contigs interspersed with unique and repeat contigs. Three plasmid scaffolds contained a single contig each and were closed/circularized using HiSeq reads (SeqWright, Houston, TX, USA). Two of the remaining three scaffolds were closed into a single contig using a combination of PCR amplification/Sanger sequencing across the contig gaps and PacBio sequencing. Base calls on all six final contigs were validated using HiSeq reads. The final coverage across the genome was 1,314×. Assembly of the chromosome was further validated using an optical restriction map (restriction enzyme *NheI*; OpGen, Gaithersburg, MD, USA).

C. helveticus strain ATCC 51209^T has a circular genome of 1,759 kb with an average GC content of 34.6%. Protein-, rRNA- and tRNA-encoding genes were identified as previously described (8). The genome contains 1,698 putative protein-coding genes and 75 pseudogenes. Three rRNA operons were identified; however, all three operons are split, where the 23S and 16S ribosomal RNA genes are separated by 21, 353, or 4 kb. Two large genetic islands of 107 and 83 kb were identified in the ATCC 51209^T chromosome, as well as three smaller elements of 4, 6, and 10 kb. The chromosome also contains 82 GC tracts ≥ 8 bp.

Five plasmids were identified in the *C. helveticus* type strain: two large plasmids of 72 (pHELV-1) and 34 (pHELV-2) kb (GC = 30.1%), and three small plasmids of 3.3 (pHELV-3), 1.7 (pHELV-4), and 1.8 (pHELV-5) kb (GC = 30.5 to 32.8%). The pHELV-1 sequence could not be circularized using reads from any of the next-generation platforms. Furthermore, pHELV-1 contains a perfect 606-bp terminal inverted repeat, suggesting that pHELV-1 is a linear plasmid (9). pHELV-3 is a *repAB* family theta-replicating, iteron-containing plasmid (10). pHELV-5 is a RepL family plasmid; however,

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pHELV-5 RepL is more similar to RepL proteins in *Firmicutes* spp., with no similarity to RepL proteins identified previously in *Campylobacter* spp. (10).

A noteworthy feature of the *C. helveticus* type strain genome is the presence of a large suite of restriction/modification (R/M) genes. The ATCC 51209^T genome is predicted to encode seven R/M systems: one type I, four type II, and two type III; two additional type II systems are also encoded, although in each case the R subunit is predicted to be a pseudogene. Besides these systems, 10 DNA methyltransferases, 2 restriction endonucleases, and 10 R/M-associated putative pseudogenes were identified.

Accession number(s). The complete genome sequence of *C. helveticus* strain ATCC 51209^T has been deposited in GenBank under the accession numbers CP020478 (chromosome) and CP020479 to CP020483 (plasmids pHELV-1 to pHELV-5).

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REFERENCES

1. Acke E, McGill K, Golden O, Jones BR, Fanning S, Whyte P. 2009. A comparison of different culture methods for the recovery of *Campylobacter* species from pets. *Zoonoses Publ Health* 56:490–495. <https://doi.org/10.1111/j.1863-2378.2008.01205.x>.
2. Bojanić K, Midwinter AC, Marshall JC, Rogers LE, Biggs PJ, Acke E. 2016. Isolation of *Campylobacter* spp. from client-owned dogs and cats, and retail raw meat pet food in the Manawatu, New Zealand. *Zoonoses Public Health* [Epub ahead of print.]. <https://doi.org/10.1111/zph.12323>.
3. Koene MG, Houwers DJ, Dijkstra JR, Duim B, Wagenaar JA. 2009. Strain variation within *Campylobacter* species in fecal samples from dogs and cats. *Vet Microbiol* 133:199–205. <https://doi.org/10.1016/j.vetmic.2008.06.022>.
4. Rossi M, Hänninen ML, Revez J, Hannula M, Zanoni RG. 2008. Occurrence and species level diagnostics of *Campylobacter* spp., enteric *Helicobacter* spp. and *Anaerobiospirillum* spp. in healthy and diarrheic dogs and cats. *Vet Microbiol* 129:304–314. <https://doi.org/10.1016/j.vetmic.2007.11.014>.
5. On SLW. 2005. Taxonomy, phylogeny, and methods for the identification of *Campylobacter* species, p 13–42. In Ketley JM, Konkel ME (ed), *Campylobacter: molecular and cellular biology*. Horizon Scientific Press, Norfolk, United Kingdom.
6. Debruyne L, Gevers D, Vandamme P. 2008. Taxonomy of the family *Campylobacteraceae*, p 3–25. In Nachamkin I, Szymanski CM, Blaser MJ (ed), *Campylobacter*, 3rd ed. ASM Press, Washington, DC.
7. Stanley J, Burnens AP, Linton D, On SL, Costas M, Owen RJ. 1992. *Campylobacter helveticus* sp. nov., a new thermophilic species from domestic animals: characterization, and cloning of a species-specific DNA probe. *J Gen Microbiol* 138:2293–2303. <https://doi.org/10.1099/00221287-138-11-2293>.
8. Miller WG, Yee E, Chapman MH, Smith TP, Bono JL, Huynh S, Parker CT, Vandamme P, Luong K, Korlach J. 2014. Comparative genomics of the *Campylobacter lari* group. *Genome Biol Evol* 6:3252–3266. <https://doi.org/10.1093/gbe/evu249>.
9. Stewart P, Rosa PA, Tilly K. 2004. Linear plasmids in bacteria: common origins, uncommon ends, p 291–301. In Funnell BE, Phillips GJ (ed), *Plasmid biology*. ASM Press, Washington, DC.
10. Miller WG, Heath S, Mandrell RE. 2007. Cryptic plasmids isolated from *Campylobacter* strains represent multiple, novel incompatibility groups. *Plasmid* 57:108–117. <https://doi.org/10.1016/j.plasmid.2006.08.005>.