



Draft Genome Sequence of *Campylobacter jejuni* Bf, an Atypical Strain Able To Grow under Aerobiosis

Vicky Bronnec, Nabila Haddad, Stéphane Cruveiller, Michel Hernould, Odile Tresse, Monique M. Zagorec

► To cite this version:

Vicky Bronnec, Nabila Haddad, Stéphane Cruveiller, Michel Hernould, Odile Tresse, et al.. Draft Genome Sequence of *Campylobacter jejuni* Bf, an Atypical Strain Able To Grow under Aerobiosis. *Genome Announcements*, 2016, 4 (2), pp.e00120-16. 10.1128/genomeA.00120-16 . hal-02632875

HAL Id: hal-02632875

<https://hal.inrae.fr/hal-02632875>

Submitted on 27 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Draft Genome Sequence of *Campylobacter jejuni* Bf, an Atypical Strain Able To Grow under Aerobiosis

Vicky Bronnec,^{a,b} Nabila Haddad,^{a,b} Stéphane Cruveiller,^c Mathieu Hernould,^{a,b} Odile Tresse,^{a,b} Monique Zagorec^{a,b}

Institut National de Recherche Agronomique, UMR1014, Secalim, Nantes, France^a; LUNAM Université, Oniris, Nantes, France^b; CNRS-UMR 8030 and Commissariat à l'Énergie Atomique CEA/DSV/IG/Genoscope LABGeM, Évry, France^c

In this study, we describe the draft genome sequence of a *Campylobacter jejuni* clinical isolate issued from a French patient suffering from severe campylobacteriosis. This atypical strain is characterized by an unusual resistance to oxygen and the ability to grow under an aerobic atmosphere, a characteristic as-of-yet unique to this species.

Received 27 January 2016 Accepted 24 February 2016 Published 7 April 2016

Citation Bronnec V, Haddad N, Cruveiller S, Hernould M, Tresse O, Zagorec M. 2016. Draft genome sequence of *Campylobacter jejuni* Bf, an atypical strain able to grow under aerobiosis. *Genome Announc* 4(2):e00120-16. doi:10.1128/genomeA.00120-16.

Copyright © 2016 Bronnec et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Monique Zagorec, monique.zagorec@oniris-nantes.fr.

Campylobacter jejuni is among the leading causes of foodborne bacterial enteritis in the world and the most frequently reported in foodborne illness in the European Union since 2005, with 214,779 confirmed cases of human campylobacteriosis in 2013 (1). This zoonosis, which is steadily increasing, is transmitted to humans mainly through the consumption of contaminated food, particularly poultry meat (2). Although *C. jejuni* behavior and virulence have largely been studied, this pathogen remains uncontrolled in the food chain. *C. jejuni* belongs to the *Epsilon-proteobacteria* and is microaerophilic and capnophilic. It can multiply in a variety of ecological niches, and it survives under harsh environmental conditions (3, 4). The *C. jejuni* Bf clinical isolate presents an unusual resistance to oxygen and can grow under an aerobic atmosphere, characteristics that were not previously reported in the *C. jejuni* species (5).

The genomic DNA was sequenced using the Illumina HiSeq 2000 sequencing system, generating ~25,000,000 reads that were assembled *de novo* with the Velvet software (6). Contig sequences were mapped on the reference genome sequence of *C. jejuni* NCTC 11168 (accession no. NC_002163.1) (7, 8). Misassembled regions were checked manually, and PCR amplification products were sequenced for gap filling.

The genome of *C. jejuni* Bf consists of a 1,506,810-bp circular chromosome, with an average G+C content of 30.44%. Annotation performed on the MicroScope platform (MaGe) (9) detected 1,635 coding sequences (CDSs) and 22 tRNAs. The genome contains three rRNA operons. No plasmid-related sequence was noticed.

The comparison of the *C. jejuni* Bf draft sequence with 32 complete and 19 draft *C. jejuni* genome sequences did not reveal any gene unique to *C. jejuni* Bf. However, some CDSs presented putative point mutations or deletions susceptible to affect several functions. Among those, CJBof_v2_160020 and CJBof_v2_160021 may result from a cleavage of the *cj0309c* gene from the reference strain *C. jejuni* NCTC 11168, encoding a multidrug resistance transporter. Interestingly, the *C. jejuni* Bf *oorD* gene encoding one of the 2-oxoglutarate oxidoreductase (OOR)

subunits was mutated at position 187, resulting in an Ile63Thr mutation located within the second (4Fe-4S) cluster. This may affect the structure and therefore the activity of OOR. In *Helicobacter pylori*, OOR catalyzes the formation of succinyl-coenzyme A (CoA), an intermediate of the tricarboxylic acid (TCA) cycle (10, 11), and it seems to provide NADPH with a respiratory donor electron (11). In *H. pylori*, the oxygen-labile OOR enzyme contributes to the microaerophilic phenotype (11). *C. jejuni* has a TCA cycle similar to that of *H. pylori*, and the same *oorDABC* operon is observed. Therefore, a mutation in the *C. jejuni* Bf *oorD* gene may result in an altered phenotype regarding the oxygen metabolism in this strain, although an increased sensitivity to oxygen would be expected. To conclude, the aerotolerance of *C. jejuni* Bf could not clearly be attributed to gene acquisition or mutation accumulation. Modifications at the transcriptional, posttranscriptional, translational, or posttranslational level might therefore be hypothesized to explain the atypical phenotype of this strain.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in ENA under the accession numbers [FCEZ01000001](https://www.ebi.ac.uk/ena/record/FCEZ01000001) to [FCEZ01000095](https://www.ebi.ac.uk/ena/record/FCEZ01000095). The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

This work was supported by the MICA division of the French National Institute for Agricultural Research (Ph.D. grant to V.B.), by UMR1014 Secalim, and by Pays de la Loire region. We acknowledge LABGeM (CEA/IG/Genoscope & CNRS UMR8030) and the France Génomique National infrastructure (funded as part of Investissement d'Avenir program managed by Agence Nationale pour la Recherche, contract ANR-10-INBS-09) for support within the MicroScope annotation platform.

REFERENCES

- EFSA. 2015. The European Union summary report on trends and sources of zoonoses, zoonotic agents and foodborne outbreaks in 2013. *EFSA J* 13:3391.
- Park SF. 2005. *Campylobacter jejuni* stress responses during survival in the food chain and colonization, p 311–330. In Ketley JM, Konkel ME (ed),

- Campylobacter* molecular cellular biology. Horizon Scientific Press, Wymondham, Norfolk, United Kingdom.
3. Moen B, Oust A, Langsrud Ø, Dorrell N, Marsden GL, Hinds J, Kohler A, Wren BW, Rudi K. 2005. Explorative multifactor approach for investigating global survival mechanisms of *Campylobacter jejuni* under environmental conditions. *Appl Environ Microbiol* 71:2086–2094. <http://dx.doi.org/10.1128/AEM.71.4.2086-2094.2005>.
 4. Murphy C, Carroll C, Jordan KN. 2006. Environmental survival mechanisms of the foodborne pathogen *Campylobacter jejuni*. *J Appl Microbiol* 100:623–632. <http://dx.doi.org/10.1111/j.1365-2672.2006.02903.x>.
 5. Rodrigues RC, Pocheron AL, Hernould M, Haddad N, Tresse O, Cappelletti JM. 2015. Description of *Campylobacter jejuni* Bf, an atypical aero-tolerant strain. *Gut Pathog* 7:30. <http://dx.doi.org/10.1186/s13099-015-0077-x>.
 6. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
 7. Parkhill J, Wren BW, Mungall K, Ketley JM, Churcher C, Basham D, Chillingworth T, Davies RM, Feltwell T, Holroyd S, Jagels K, Karlyshev AV, Moule S, Pallen MJ, Penn CW, Quail MA, Rajandream MA, Rutherford KM, van Vliet AH, Whitehead S, Barrell BG. 2000. The genome sequence of the foodborne pathogen *Campylobacter jejuni* reveals hypervariable sequences. *Nature* 403:665–668. <http://dx.doi.org/10.1038/35001088>.
 8. Gundogdu O, Bentley SD, Holden MT, Parkhill J, Dorrell N, Wren BW. 2007. Re-annotation and re-analysis of the *Campylobacter jejuni* NCTC11168 genome sequence. *BMC Genomics* 8:162. <http://dx.doi.org/10.1186/1471-2164-8-162>.
 9. Vallenet D, Belda E, Calteau A, Cruveiller S, Engelen S, Lajus A, Le Fèvre F, Longin C, Mornico D, Roche D, Rouy Z, Salvignol G, Scarpelli C, Thil Smith AA, Weiman M, Médigue C. 2013. MicroScope—an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. *Nucleic Acids Res* 41:D636–D647. <http://dx.doi.org/10.1093/nar/gks1194>.
 10. Gilbreath JJ, West AL, Pich OQ, Carpenter BM, Michel S, Merrell DS. 2012. Fur activates expression of the 2-oxoglutarate oxidoreductase genes (*oorDABC*) in *Helicobacter pylori*. *J Bacteriol* 194:6490–6497. <http://dx.doi.org/10.1128/JB.01226-12>.
 11. Hughes NJ, Clayton CL, Chalk PA, Kelly DJ. 1998. *Helicobacter pylori* *porCDAB* and *oorDABC* genes encode distinct pyruvate: flavodoxin and 2-oxoglutarate: acceptor oxidoreductases which mediate electron transport to NADP. *J Bacteriol* 180:1119–1128.