



HAL
open science

Draft Genome Sequence of *Campylobacter coli* Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease

Alexis Criscuolo, Arnaud de La Blanchardière, Solène Coeuret, Virginie Passet, Virginie Saguet-Rysanek, Michel Vergnaud, Renaud Verdon, Alexandre Leclercq, Marc Lecuit, Sylvain Brisse

► To cite this version:

Alexis Criscuolo, Arnaud de La Blanchardière, Solène Coeuret, Virginie Passet, Virginie Saguet-Rysanek, et al.. Draft Genome Sequence of *Campylobacter coli* Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease. *Genome Announcements*, 2014, 2 (2), pp.e00079-14. 10.1128/genomeA.00079-14. pasteur-02869569

HAL Id: pasteur-02869569

<https://pasteur.hal.science/pasteur-02869569v1>

Submitted on 16 Jun 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.



Distributed under a Creative Commons Attribution 4.0 International License

Draft Genome Sequence of *Campylobacter coli* Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease

Alexis Criscuolo,^{a,b} Arnaud de la Blanchardière,^c Solène Coeuret,^c Virginie Passet,^{a,b} Virginie Saguet-Rysanek,^d Michel Vergnaud,^e Renaud Verdon,^c Alexandre Leclercq,^{f,g,h} Marc Lecuit,^{f,g,h} Sylvain Brisse^{a,b}

Institut Pasteur, Evolutionary Microbial Genomics Unit, Paris, France^a; CNRS, UMR 3525, Paris, France^b; Infectious Diseases Unit, University of Caen, Caen, France^c; Department of Pathology, University of Caen, Caen, France^d; Department of Microbiology, University Hospital of Caen, Caen, France^e; Institut Pasteur, Biology of Infection Unit, Paris, France^f; Institut National de la Santé et de la Recherche Médicale U1117, Paris, France^g; Paris Descartes University, Sorbonne Paris Cité, Department of Infectious Diseases and Tropical Medicine, Necker-Pasteur Centre for Infectious Diseases, Necker-Enfants Malades University Hospital, Institut Imagine, APHP, Paris, France^h

The genome sequence and annotation of *Campylobacter coli* strain IPSID-1 are reported here. This bacterial isolate is the first to be cultured from a patient with immunoproliferative small intestinal disease (IPSID). The draft genome sequence is 1.683 Mb long, comprises 64 contigs, and has 31.26% G+C content.

Received 23 January 2014 Accepted 13 February 2014 Published 13 March 2014

Citation Criscuolo A, de la Blanchardière A, Coeuret S, Passet V, Saguet-Rysanek V, Vergnaud M, Verdon R, Leclercq A, Lecuit M, Brisse S. 2014. Draft genome sequence of *Campylobacter coli* strain IPSID-1 isolated from a patient with immunoproliferative small intestinal disease. *Genome Announc.* 2(2):e00079-14. doi:10.1128/genomeA.00079-14.

Copyright © 2014 Criscuolo et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Marc Lecuit, marc.lecuit@pasteur.fr, or Sylvain Brisse, sylvain.brisse@pasteur.fr.

Gram-negative bacteria of the genus *Campylobacter* are often implicated in human and animal diseases, including enteritis, abortion, and septicemia. *Campylobacter jejuni* and *Campylobacter coli* are the medicinally most important species of the genus (1). Based on 16S rRNA gene sequencing, *in situ* hybridization, and immunohistochemistry, *Campylobacter* spp. have also been associated with immunoproliferative small intestinal disease (IPSID), a rare variant of B-cell mucosa-associated lymphoid tissue (MALT) lymphoma of the small intestine, characterized by the synthesis of a monotypic truncated immunoglobulin alpha heavy chain lacking an associated light chain (2, 3, 4). Recently, *C. coli* was isolated from the stool of a patient with ileocecal IPSID (5). Here, we report the draft genome sequence of this IPSID-associated *C. coli* strain, IPSID-1.

Whole-genome shotgun sequencing was performed using an Illumina HiSeq 2000 sequencer. Libraries were constructed using Nextera technology and sequenced using a 2 × 100 nucleotide paired-end strategy, leading to ~10,585,000 paired-read sequences. All reads were preprocessed to remove low-quality or artifactual bases. Library adapters, as well as base pairs occurring at 5' and 3' ends and supported by a Phred quality score <20, were trimmed off using AlienTrimmer (6). Reads of length <95 bp after the above cleaning steps were discarded, as well as those containing >20% bp with a Phred score of <20. Finally, the program fqduplicate (<ftp://ftp.pasteur.fr/pub/gensoft/projects/fqtools>) was used to discard every duplicate paired-end read. The remaining reads (~6,682,000 paired-end and ~2,176,000 single-end) were assembled using clc_assembler (version 4.10.86742) from the CLC Genomics Workbench analysis package (<http://www.clcbio.com/products/clc-genomics-workbench/>), with contig sequences of <500 nucleotides being discarded and with a de Bruijn graph *k*-mer parameter value of 57, which maximized the N₅₀, N₇₅, and N₉₀ values (i.e., 302,476, 162,145, and 45,795 bp, respectively).

A total of 64 contigs organized into 38 scaffolds were obtained, with a total length of 1,683,384 bp. An average coverage depth of ~920× was obtained. The G+C content of the genome sequence is 31.26%. The sequences were submitted to the RAST server (7) for gene prediction and annotation, which led to 1,766 protein-coding sequences, 40 detected tRNA genes, and 3 rRNA regions. Extraction of gene sequences corresponding to the *Campylobacter* multilocus sequence typing scheme (8) showed that IPSID-1 belongs to sequence type 4956 (ST-4956), which is associated with clonal complex 828. The genome comprises genes homologous to the *cdtABC* cluster, coding for cytolethal distending toxin (9, 10).

The availability of the draft genome sequence of *C. coli* IPSID-1, the first *Campylobacter* isolate from a case of IPSID, will contribute to a better understanding of the pathophysiological mechanisms of this disease.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [CBXC000000000](https://www.ncbi.nlm.nih.gov/nuccore/CBXC000000000). The version described in this paper is the first version, [CBXC010000000](https://www.ncbi.nlm.nih.gov/nuccore/CBXC010000000).

ACKNOWLEDGMENTS

A.C. was supported financially by a grant from Region Île-de-France.

This work was supported by the French Government's Investissement d'avenir program, Laboratoire d'Excellence "Integrative Biology of Emerging Infectious Diseases" (grant ANR-10-LABX-62-IBEID).

REFERENCES

- Silva J, Leite D, Fernandes M, Mena C, Gibbs PA, Teixeira P. 2011. *Campylobacter* spp. as a foodborne pathogen: a review. *Front. Microbiol.* 2:200. <http://dx.doi.org/10.3389/fmicb.2011.00200>.
- Lecuit M, Abachin E, Martin A, Poyart C, Pochart P, Suarez F, Bengoufa D, Feuillard J, Lavergne A, Gordon JI, Berche P, Guillevin L, Lortholary O. 2004. Immunoproliferative small intestinal disease associated with *Campylobacter jejuni*. *N. Engl. J. Med.* 350:239–248. <http://dx.doi.org/10.1056/NEJMoa031887>.
- Mesnard B, De Vroey B, Maunoury V, Lecuit M. 2012. Immunoprolif-

- erative small intestinal disease associated with *Campylobacter jejuni*. *Dig. Liver Dis.* 44:799–800. <http://dx.doi.org/10.1016/j.dld.2012.03.020>.
4. Suarez F, Lortholary O, Hermine O, Lecuit M. 2006. Infection-associated lymphomas derived from marginal zone B cells: a model of antigen-driven lymphoproliferation. *Blood* 107:3034–3044. <http://dx.doi.org/10.1182/blood-2005-09-3679>.
 5. Coeuret S, de La Blanchardière A, Saguet-Rysanek V, Chèze S, Tavernier M, Arsène D, Criscuolo A, Brisse S, Vergnaud M, Verdon R, Lecuit M. 2014. *Campylobacter coli* cultured from the stools of a patient with immunoproliferative small intestinal disease. *Clin. Microbiol. Infect.* <http://dx.doi.org/10.1111/1469-0691.12545>.
 6. Criscuolo A, Brisse S. 2013. AlienTrimmer: a tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. *Genomics* 102:500–6. <http://dx.doi.org/10.1016/j.ygeno.2013.07.011>.
 7. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
 8. Dingle KE, Colles FM, Wareing DR, Ure R, Fox AJ, Bolton FE, Bootsma HJ, Willems RJ, Urwin R, Maiden MC. 2001. Multilocus sequence typing system for *Campylobacter jejuni*. *J. Clin. Microbiol.* 39:14–23. <http://dx.doi.org/10.1128/JCM.39.1.14-23.2001>.
 9. Lara-Tejero M, Galán JE. 2001. CDTA, CdtB, and CdtC form a tripartite complex that is required for cytolethal distending toxin activity. *Infect. Immun.* 69:4358–4365. <http://dx.doi.org/10.1128/IAI.69.7.4358-4365.2001>.
 10. Mortensen NP, Schiellerup P, Boisen N, Klein BM, Loch H, Abuoun M, Newell D, Krogfelt KA. 2011. The role of *Campylobacter jejuni* cytolethal distending toxin in gastroenteritis: toxin detection, antibody production, and clinical outcome. *APMIS* 119:626–634. <http://dx.doi.org/10.1111/j.1600-0463.2011.02781.x>.