

Draft Genome Sequence of *Hafnia paralvei* Strain GTA-HAF03

Melissa E. Kohlman,^a Catherine D. Carrillo,^b Alex Wong^a

Department of Biology, Carleton University, Ottawa, Ontario, Canada^a; Canadian Food Inspection Agency, Government of Canada, Ottawa, Ontario, Canada^b

***Hafnia paralvei* is a Gram-negative member of the *Enterobacteriaceae* family, closely related to the opportunistic pathogen *Hafnia alvei*. We report here the first draft genome sequence of *H. paralvei*, from the beef trim isolate GTA-HAF03, consisting of a 5.0-Mbp assembly encoding 4,382 proteins and 90 predicted RNAs.**

Received 5 January 2015 Accepted 8 January 2015 Published 19 February 2015

Citation Kohlman ME, Carrillo CD, Wong A. 2015. Draft genome sequence of *Hafnia paralvei* strain GTA-HAF03. *Genome Announc* 3(1):e01592-14. doi:10.1128/genomeA.01592-14.

Copyright © 2015 Kohlman 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 Catherine D. Carrillo, catherine.carrillo@inspection.gc.ca, or Alex Wong, Alex.Wong@Carleton.ca.

Hafnia paralvei is a potential pathogen of both animals and humans (1). Originally considered a subtype of *Hafnia alvei*, differences in the sequences of the *ampC* and 16S rRNA genes led to their taxonomic split (2). There is some uncertainty regarding *H. paralvei*'s pathogenicity. While *H. alvei* is often found in the bowels of healthy humans (3), it has been associated with diarrhea in children (3) and with a range of infections in patients with other underlying conditions (4). *H. paralvei* may similarly be an opportunistic pathogen and has been implicated in a case of bacteremia, cultured concomitantly with *Enterococcus faecalis* (5). Some studies have suggested that *H. paralvei* is less pathogenic than *H. alvei*, due to the absence of Shiga-like cytolytic toxins (3). Moreover, it was recently suggested that strains previously identified as pathogenic *H. alvei* were isolates of the much more pathogenic bacterium *Escherichia albertii* (1), and this misidentification may also apply to some *H. paralvei* strains. Given the association of this organism with food, farm animals and agricultural settings, evaluation of the potential pathogenicity of *H. paralvei* is important in determining the risk of this bacterium to human and animal health.

H. paralvei GTA-HAF03 was recovered from beef trim, and genomic DNA was isolated from cultures grown overnight on nutrient agar (Difco, Becton, Dickinson & Co., Sparks, MD, USA) using the Maxwell 16 Cell DNA purification kit (Promega, Madison, WI, USA). Sequencing libraries were constructed using the Nextera XT DNA sample preparation kit (Illumina, Inc., San Diego, CA, USA) and paired-end sequencing was performed on the Illumina MiSeq platform (Illumina Inc.), using a 500-cycle MiSeq version 2 reagent kit. Sequencing errors were corrected using Quake version 0.3 with a *k*-mer size of 15 (6), and reads were then assembled *de novo* using SPAdes version 3.1.1 (7). The total length of the draft genome sequence was 4,998,224 bp, in 47 contigs, with an N_{50} of 161,556. Contigs were annotated with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (8), resulting in the prediction of 4,579 genes, including 4,382 coding sequences (CDSs), and 78 tRNA and 9 rRNA sequences. Phylogenetic analysis based on 16S rRNA sequences clustered this genome with published *H. paralvei* sequences (data not shown), supporting its identification as *H. paralvei* rather than its close relative *H. alvei*.

While the *H. paralvei* GTA-HAF03 genome lacks the proposed *H. alvei* virulence factors *eaeA*, *fepA*, and cytolytic toxins (1, 9), a number of genes associated with virulence were detected. For example, the adhesion gene *gidE* found in pathogenic strains of *Escherichia coli* (10), genes encoding a β -lactamase, and an operon with similarity to a *Mycobacterium* virulence operon were identified. The absence of some of the key virulence factors encoded in *H. alvei* strains associated with disease may indicate that *H. paralvei* GTA-HAF03 poses little risk to human and animal health; however, further *in vitro* and *in vivo* studies are required to characterize virulence potential of this organism.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number **JWGWZ00000000**. The version described in this paper is the first version, JWGWZ01000000.

ACKNOWLEDGMENTS

This work was supported by Canadian Safety and Security Program (CSSP) funding to C.D.C. (CSSP-2013-TI-1145) and a Natural Sciences and Engineering Research (NSERC) Discovery grant to A.W.

We especially thank Robyn Kenwell for assistance with sequencing, Dr. Adam Koziol for assistance with bioinformatic analyses, and George Huszinski's group for isolation and biochemical characterization of the strains.

REFERENCES

- Janda JM, Abbott SL. 2006. The genus *Hafnia*: from soup to nuts. *Clin Microbiol Rev* 19:12–18. <http://dx.doi.org/10.1128/CMR.19.1.12-28.2006>.
- Abbott SL, Moler S, Green N, Tran RK, Wainwright K, Janda JM. 2011. Clinical and laboratory diagnostic characteristics and cytotoxicogenic potential of *Hafnia alvei* and *Hafnia paralvei* strains. *J Clin Microbiol* 49: 3122–3126. <http://dx.doi.org/10.1128/JCM.00866-11>.
- Albert MJ, Alam K, Islam M, Montanaro J, Rahaman AS, Haider K, Hossain MA, Kibriya AK, Tzipori S. 1991. *Hafnia alvei*, a probable cause of diarrhea in humans. *Infect Immun* 59:1507–1513.
- Günthard H, Pennekamp A. 1996. Clinical significance of extraintestinal *Hafnia alvei* isolates from 61 patients and review of the literature. *Clin Infect Dis* 22:1040–1045. <http://dx.doi.org/10.1093/clinids/22.6.1040>.
- Osuka H, Hitomi S, Koganemaru H, Kaneko T. 2011. A case of bacteremia caused by *Hafnia paralvei*. *J Infect Chemother* 17:855–857. <http://dx.doi.org/10.1007/s10156-011-0255-9>.
- Kelley DR, Schatz MC, Salzberg SL. 2010. Quake: quality-aware detection and correction of sequencing errors. *Genome Biol* 11:R116. <http://dx.doi.org/10.1186/gb-2010-11-11-r116>.

7. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.
8. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Ciufu S, Li W. 2013. Prokaryotic genome annotation pipeline. *In* The NCBI handbook, 2nd ed. National Center for Biotechnology Information, Bethesda, MD. <http://www.ncbi.nlm.nih.gov/books/NBK174280>. Accessed 30 December 2014.
9. Seral C, Castillo FJ, Llorente MT, Varea M, Clavel A, Rubio MC, Gómez-Lus R. 2001. The *eaeA* gene is not found in *Hafnia alvei* from patients with diarrhea in Aragón, Spain. *Int Microbiol* 4:81–82.
10. Torres AG, Jeter C, Langley W, Matthyse AG. 2005. Differential binding of *Escherichia coli* O157:H7 to alfalfa, human epithelial cells, and plastic is mediated by a variety of surface structures. *Appl Environ Microbiol* 71:8008–8015. <http://dx.doi.org/10.1128/AEM.71.12.8008-8015.2005>.