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Permalink
https://escholarship.org/uc/item/3b2981w9

Journal
Microbiology resource announcements, 10(14)

ISSN
2576-098X

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Publication Date
2021-04-08

DOI
10.1128/mra.01035-19

Peer reviewed
Draft Genome Sequence of *Bordetella* sp. Strain FB-8, Isolated from a Former Uranium Mining Area in Germany

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**ABSTRACT**

Here, we present the draft genome sequence of *Bordetella* sp. strain FB-8, a mixotrophic iron-oxidizing bacterium isolated from creek sediment in the former uranium-mining district of Ronneburg, Germany. To date, iron oxidation has not been reported in *Bordetella* species, indicating that FB-8 may be an environmentally important *Bordetella* sp.

The Gessen Creek, in the former uranium-mining district of Ronneburg (Thuringia, Germany), is contaminated with heavy metals and acid mine drainage (AMD) due to legacy acid leaching of low-grade black shale (1–3). However, heavy metals are naturally attenuated via coupled microbial iron cycling and metal precipitation (4, 5). To better understand the role of iron-oxidizing bacteria at the site, we isolated *Bordetella* sp. strain FB-8 from iron-rich, slightly acidic (pH 6.3) Gessen Creek sediments (site R3 [4]). Strain FB-8 was isolated as a microaerophilic, autotrophic iron oxidizer on FeCO₃ plates and screened for metabolic properties (Table 1) in medium described by Akob et al. (6).

For genome sequencing, FB-8 was grown to high cell density in lysogeny broth (LB) under oxic conditions. Biomass was harvested by centrifugation, frozen at −20°C, and shipped to the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ; Braunschweig, Germany) for DNA extraction. DNA was extracted using the U.S. Department of Energy’s (DOE) Joint Genome Institute (JGI) cetyltrimethylammonium bromide (CTAB) procedure for isolating high-molecular-weight genomic DNA (gDNA) (http://my.jgi.doe.gov/index.html). gDNA was assessed for quality control using agarose gel electrophoresis to evaluate the quality and quantity, including molecular weight, of the extract according to the JGI protocol “Genomic DNA QC Using Standard Gel Electrophoresis” (http://my.jgi.doe.gov/index.html).

DNA extracts were sent to the JGI for genome sequencing using Illumina technology. An Illumina standard shotgun library and long-insert mate pair library were constructed and sequenced using the Illumina HiSeq 2000 platform, which yielded 19,057,432 and 55,056,510 sequence reads, respectively. Raw sequence data were passed through DUK (7), which removes known Illumina sequencing and library preparation artifacts. Default Illumina reads were assembled using AllpathsLG version R37654 (PrepareAllpathsInputs: PHRED 64=1 PLOIDY=1 FRAG COVERAGE=125 JUMP COVERAGE=25; RunAllpathsLG: THREADS=8 RUN=std pairs TARGETS=standard VAPI WARN ONLY=True OVERWRITE=True) (8). The final assembly was based on 2,858.2 Mb of Illumina standard paired-end (PE) and 4,789.5 Mb of Illumina Cre-LoxP inverse PCR (CLIP) PE postfiltered data, which provided an average of

Citation Harris CR, Akob DM, Fabisch M, Beulig F, Woyke T, Shapiro N, Lapidus A, Klenk H-P, Küsel K. 2021. Draft genome sequence of *Bordetella* sp. strain FB-8, isolated from a former uranium mining area in Germany. Microbiol Resour Announc 10:e01035-19. https://doi.org/10.1128/MRA.01035-19.

Editor J. Cameron Thrash, University of Southern California

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Received 22 August 2019
Accepted 12 March 2021
Published 8 April 2021
The Bordetella sp. strain FB-8 genome contains 6 contigs (N₅₀, 2.4 Mbp) in 2 scaffolds (N₅₀, 4.1 Mbp) and constitutes a total of 4,079,718 bp with 63.35% G+C content. The FB-8 genome was annotated in the Integrated Microbial Genomes (IMG) database (10). One round of manual curation was performed using GenePRIMP (11). The genome of Bordetella sp. strain FB-8 contained 3,906 genes and 3,835 protein-coding genes. Functional annotation identified 3 copies of the 16S rRNA gene, 9 total rRNAs, 50 tRNAs, 12 other RNAs, and 138 pseudogenes.

The genus Bordetella contains mainly pathogens that infect different host organisms. Bordetella sp. strain FB-8 is unique because it is an environmental species that was isolated as an iron oxidizer. The genome of Bordetella sp. strain FB-8 may enable further analysis of the biomineralization in contaminated sites.

Data availability. Bordetella sp. strain FB-8 is available from the DSMZ under accession number DSM 24873. The genome sequence of strain FB-8 is available from IMG under the genome ID 2522125081 and the NCBI database under accession numbers PRJNA187096 (BioProject) and SRP053466 (Sequence Read Archive).

Acknowledgments
We thank Lynne Goodwin and Linda Meincke (JGI) for project management and Beatrice Trümper (DSMZ) for performing DNA extractions.

The work conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, is supported by the Office of Science of the U.S. Department of Energy under contract number DE-AC02-05CH11231. A.L. was partially supported by the Russian Science Foundation (number 19-16-00049). Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. government.

We declare no competing financial interest.

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