

# UC Davis

## UC Davis Previously Published Works

### Title

Draft Genome Sequence of Bacillus vietnamensis Strain UCD-SED5 (Phylum Firmicutes)

### Permalink

<https://escholarship.org/uc/item/1q77b8n4>

### Journal

Microbiology Resource Announcements, 3(6)

### ISSN

2576-098X

### Authors

Lee, Ruth D  
Jospin, Guillaume  
Lang, Jenna M  
et al.

### Publication Date

2015-12-31

### DOI

10.1128/genomea.01376-15

Peer reviewed

# Draft Genome Sequence of *Bacillus vietnamensis* Strain UCD-SED5 (Phylum *Firmicutes*)

Ruth D. Lee,<sup>a</sup> Guillaume Jospin,<sup>a</sup> Jenna M. Lang,<sup>a</sup> Jonathan A. Eisen,<sup>a,b</sup> David A. Coil<sup>a</sup>

University of California Davis Genome Center, Davis, California, USA<sup>a</sup>; University of California Davis, Department of Evolution and Ecology, Department of Medical Microbiology and Immunology, Davis, California, USA<sup>b</sup>

Here, we present the draft genome sequence of *Bacillus vietnamensis* UCD-SED5 (phylum *Firmicutes*). This strain was isolated from sediment surrounding *Zostera marina* roots near the UC Davis Bodega Marine Laboratory (Bodega Bay, California) and represents the second genome of this species. The assembly consists of 4,325,707 bp, in 108 contigs.

Received 1 October 2015 Accepted 5 October 2015 Published 19 November 2015

Citation Lee RD, Jospin G, Lang JM, Eisen JA, Coil DA. 2015. Draft genome sequence of *Bacillus vietnamensis* strain UCD-SED5 (phylum *Firmicutes*). *Genome Announcements* 3(6):e01376-15. doi:10.1128/genomeA.01376-15.

Copyright © 2015 Lee 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/3.0/).

Address correspondence to Jonathan A. Eisen, [jaeisen@ucdavis.edu](mailto:jaeisen@ucdavis.edu).

*Bacillus vietnamensis* UCD-SED5 was isolated from sediment surrounding common eelgrass (*Zostera marina*) roots near the UC, Davis Bodega Marine Laboratory (Bodega Bay, California, USA). The sampling site was located north of Westshore Park, California (38°19'10.0"N, 123°03'13.8"W).

*B. vietnamensis* was originally isolated from fermented fish consumables, a common food used in Asian cuisine, and was shown to be halotolerant (1). Previous studies have also claimed that the genus *Bacillus* plays a large and necessary role in the fermentation of fish products (1).

Dilutions of sediment in lysogeny broth (LB) of 1:100 and 1:1000 were made and spread on LB plates, grown at room temperature for 24 h, and individual colonies were double dilution struck. A Wizard Genomic DNA purification kit (Promega) was used to extract DNA from a fresh 5-mL overnight culture. Sanger sequencing was performed on the amplified 16S rRNA PCR products (27F: AGAGTTTGATCMTGGCTCAG and 1391R: GACGG GCGGTGTGTRCA). Examination of BLAST search results and phylogenetic analyses (2) suggested identity to either *Bacillus vietnamensis* or *Bacillus aquimaris*. BLAST results were both >99% identical and the 16S phylogeny was ambiguous. Because *B. vietnamensis* can grow well outside the pH range of *B. aquimaris* (1, 3), we tested media at various pH, and this suggested the identification as *B. vietnamensis*. Hopefully, the addition of more genome sequences from both species will allow better phylogenetic resolution between the two groups, if such a division even exists.

A Nextera DNA sample prep kit (Illumina) was used to make a paired-end library (Illumina). Libraries were sequenced on an Illumina MiSeq, at a read length of 300 bp. A total of 883,585 high-quality paired-end reads was processed by the A5 assembly pipeline (4). This pipeline automates data cleaning, error correction, contig assembly, quality control, and scaffolding. The resulting assembly consisted of 108 contigs (longest: 618,024 bp;  $N_{50}$ : 287,494) that were submitted to GenBank. This final assembly had 4,325,707 bp with a G+C content of 43.5% and an overall coverage estimate of ~102×. Genome completeness was assessed using the PhyloSift software (5), which searches for a list of 37 highly

conserved, single-copy marker genes (6), of which all 37 were found in this assembly.

The RAST server was used to perform an automated annotation (7–9). *B. vietnamensis* UCD-SED5 contains 4,470 predicted protein-coding sequences and 145 predicted noncoding RNAs.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LIXZ00000000. The version described in this paper is version LIXZ01000000.

## ACKNOWLEDGMENTS

Illumina sequencing was performed at the DNA Technologies Core facility in the Genome Center at UC Davis, Davis, California.

This work was funded by a grant from the Gordon and Betty Moore Foundation (GBMF333) “Investigating the co-evolutionary relationships between seagrasses and their microbial symbionts.”

We thank Qingyi “John” Zhang for his help with the Illumina library preparation.

## REFERENCES

- Noguchi H, Uchino M, Shida O, Takano K, Nakamura LK, Komagata K. 2004. *Bacillus vietnamensis* sp. nov., a moderately halotolerant, aerobic, endospore-forming bacterium isolated from Vietnamese fish sauce. *Int J Syst Evol Microbiol* 54:2117–2120. <http://dx.doi.org/10.1099/ijs.0.02895-0>.
- Dunitz MI, Lang JM, Jospin G, Darling AE, Eisen JA, Coil DA. 2015. Swabs to genomes: A comprehensive workflow. *PeerJ* 3:e453v452. <http://dx.doi.org/10.7717/peerj.960>.
- Yoon J-H, Kim I-G, Kang KH, Oh T-K, Park Y-H. 2003. *Bacillus marisflavi* sp. nov. and *Bacillus aquimaris* sp. nov., isolated from seawater of a tidal flat of the Yellow Sea in Korea. *Int J Syst Evol Microbiol* 53:1297–1303. <http://dx.doi.org/10.1099/ijs.0.02365-0>.
- Tritt A, Eisen JA, Facciotti MT, Darling AE. 2012. An integrated pipeline for *de novo* assembly of microbial genomes. *PLoS One* 7:e42304. <http://dx.doi.org/10.1371/journal.pone.0042304>.
- Darling AE, Jospin G, Lowe E, Matsen IV FA, Bik HM, Eisen JA. 2014. PhyloSift: phylogenetic analysis of genomes and metagenomes. *PeerJ* 2:e243.
- Wu D, Jospin G, Eisen J. 2013. Systematic identification of gene families for use as “markers” for phylogenetic and phylogeny-driven ecological studies of bacteria and archaea and their major subgroups. *PLoS One* 8:e77033.

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. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
8. Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomason JA, Stevens R, Vonstein V, Wattam AR, Xia F. 2015. RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep* 5:8365. <http://dx.doi.org/10.1038/srep08365>.
9. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42: D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.