UC Davis
UC Davis Previously Published Works

Title
Draft Genome Sequence of Tenacibaculum soleae UCD-KL19

Permalink
https://escholarship.org/uc/item/2br406px

Journal
Microbiology Resource Announcements, 4(5)

ISSN
2576-098X

Authors
Lujan, Karley M
Eisen, Jonathan A
Coil, David A

Publication Date
2016-10-27

DOI
10.1128/genomea.01120-16

Peer reviewed

Draft Genome Sequence of *Tenacibaculum soleae* UCD-KL19

Karley M. Lujan,ᵃ Jonathan A. Eisen,ᵃ,ᵇ David A. Coilᵃ

Davis Genome Center, University of California Davis, Davis, California, USAᵃ; Department of Evolution and Ecology and Department of Medical Microbiology and Immunology, University of California Davis, Davis, California, USAᵇ

Here, we present the draft genome sequence of *Tenacibaculum soleae* strain UCD-KL19. The assembly contains 3,012,701 bp in 46 contigs. This strain was isolated from a seagrass leaf (*Zostera marina*) collected from Bodega Bay, CA, as a part of an undergraduate student research project on isolating bacteria from seagrass.

Address correspondence to Jonathan A. Eisen, jaeisen@ucdavis.edu.

Some species within the genus *Tenacibaculum* are known fish pathogens that cause tenacibaculosis, an infectious disease that impacts farmed marine finfish all across the world (1). *Tenacibaculum soleae* is a Gram-negative rod-shaped bacterium with gliding motility, belonging to the family *Flavobacteriaceae* (2).

T. soleae UCD-KL19 was isolated from a phosphate-buffered saline (PBS) rinse of a seagrass leaf as a part of the Seagrass Microbiome Project (https://seagrassmicrobiome.org/), with a focus on culturing bacterial isolates. The PBS rinse of the seagrass leaf was cultured on a Difco marine broth agar plate at 25°C for two days. A single colony was selected for two rounds of dilution streaking, and one of the resulting colonies was used to make an overnight culture in liquid Difco marine broth at 25°C. Genomic DNA was extracted using a Promega Wizard genomic DNA purification kit. After the extraction, PCR amplification of the 16S rRNA gene was undertaken using the 27F and 1391R primers. This PCR product was Sanger sequenced, and the resulting consensus sequence was analyzed using BLAST (3). Using the Ribosomal Database Project (RDP) (4), an alignment of this isolate and other *Tenacibaculum* isolates was created (4). This alignment was used to infer a maximum-likelihood phylogenetic tree, which was created in Fast-Tree (5) and viewed in Dendroscope (5, 6). This isolate was found within a well-supported monophyletic clade that contained several other *T. soleae* strains that did not occur elsewhere in the tree. In order to complete the whole-genome sequencing, a paired-end library was created using a Nextera XT library preparation kit (Illumina). Using a PippinPrep (Sage Science), we selected 600- to 900-bp fragments. The size-selected library was sequenced on a paired-end 300-bp run of an Illumina MiSeq. Following the completion of quality trimming and error correction by the A5-miseq assembly pipeline (7, 8), 1,066,673 quality reads assembled into 26 scaffolds, with an estimated 87× coverage and a G+C content of 30.3% (8, 9). PhyloSift (7) was used to estimate genome completeness by searching for a list of 37 highly conserved single-copy marker genes, and a single copy of each one was present in this assembly.

Annotation was completed using RAST (10). The annotated *T. soleae* strain UCD-KL19 genome contains 2,812 coding sequences and 54 noncoding RNAs. The full-length 16S sequence (1,515 bp) from RAST was used in a BLAST search, which revealed 100% identity to a *T. soleae* strain. This same 16S sequence was then used to build a second phylogenetic tree using the methods described above (https://dx.doi.org/10.6084/m9.figshare.3469766.v1). As described above, *T. soleae* strain UCD-KL19 was located in a monophyletic clade of *T. soleae* strains.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. MAKX00000000. The version described in this paper is version MAKX01000000.

REFERENCES

1. **López JR, Piñeiro-Vidal M, García-Lamas N, de la Herran R, Navas JI, Hachero-Cruzado I, Santos Y**. 2010. First isolation of *Tenacibaculum soleae* from diseased cultured wedge sole, *Dicologoglossa cuneata* (Moreau), and brill, *Scophthalmus rhombus* (L.). J Fish Dis **33**:273–278. http://dx.doi.org/10.1111/j.1365-2761.2009.01105.x.
2. **Piñeiro-Vidal M, Carballas CG, Gómez-Barreiro O, Riaza A, Santos Y**. 2008. *Tenacibaculum soleae* sp. nov., isolated from diseased sole (*Solea senegalensis* Kaup). Int J Syst Evol Microbiol **58**:881–885. http://dx.doi.org/10.1099/ijs.0.65539-0.
3. **Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ**. 1990. Basic Local Alignment Search Tool. J Mol Biol **215**:403–410. http://dx.doi.org/10.1016/S0022-2836(05)80360-2.
4. **Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, Brown CT, Porras-Alfaro A, Kuske CR, Tiedje JM**. 2014. Ribosomal Database project: data and tools for high throughput rRNA analysis. Nucleic Acids Res **42**:D633–D642. http://dx.doi.org/10.1093/nar/gkt1244.
5. **Price MN, Dehal PS, Arkin AP**. 2010. FastTree 2—approximately maximum-likelihood trees for large alignments. PLoS One **5**:e9490. http://dx.doi.org/10.1371/journal.pone.0009490.
6. **Huson DH, Scornavacca C**. 2012. Dendroscope 3: an interactive tool for rooted phylogenetic trees and networks. Syst Biol **61**:1061–1067. http://dx.doi.org/10.1093/sysbio/sys062.
7. **Darling AE, Jospin G, Lowe E, Matsen F, Bik HM, Eisen JA**. 2014. PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ **2**:e243. http://dx.doi.org/10.7717/peerj.243.

8. **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.

9. **Coil D, Jospin G, Darling AE**. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics **31**:587–589. http://dx.doi.org/10.1093/bioinformatics/btu661.

10. **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.