

Whole-genome sequence accessions for the *Alcanivorax* sp. strain 97CO-6 isolated from a crude oil-consuming bacterial consortium, enriched from Yellow Sea sediments from China in April of 2007.

Website: <https://www.bco-dmo.org/dataset/771936>

Data Type: Other Field Results

Version: 1

Version Date: 2019-06-26

Project

» [Collaborative Research: Oxygenation of Hydrocarbons in the Ocean](#) (Oxygenation of Hydrocarbons)

Contributors	Affiliation	Role
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Abstract

Whole-genome sequence accessions for the *Alcanivorax* sp. strain 97CO-6 isolated from a crude oil-consuming bacterial consortium, enriched from Yellow Sea sediments from China in April of 2007.

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Coverage

Spatial Extent: Lat:36.67 Lon:121.99

Temporal Extent: 2017-04-19

Dataset Description

Whole-genome sequence accessions for the *Alcanivorax* sp. strain 97CO-6 isolated from a crude oil-consuming bacterial consortium, enriched from Yellow Sea sediments from China in April of 2007. The genetic accessions can be found at The National Center for Biotechnology Information (NCBI) under master accession number PIXQ01000000 (<https://www.ncbi.nlm.nih.gov/nucore/PIXQ01000000>). These results were published in Yin et al. (2018).

Methods & Sampling

Project accession number
PIXQ01000000

Species name
Alcanivorax sp. 97CO-6

Description of types of sequences:
The draft genome of strain 97CO-6, which contains 3,253,423 bp, with a G+C content of 54.53%, as well as 2,931 protein-coding genes and 42 tRNAs.

Locations where species were collected

Alcanivorax sp. Strain 97CO-6 was isolated from a crude oil-consuming bacterial consortium, enriched from Yellow Sea sediments from China

Sequencing and analysis methods

Whole-genome shotgun sequencing of the Alcanivorax sp. 97CO-6 genome was done using Solexa paired-end sequencing technology by Shanghai Majorbio Bio-Pharm Technology Co., Ltd (Shanghai, China). A total of 13,445,638 paired-end reads (180-bp and 800-bp libraries) were generated to reach a 398-fold depth of coverage using the Illumina HiSeq 2000 platform (Illumina, Inc., San Diego, CA, USA). The reads were assembled using SOAPdenovo version 1.05. The resulting genome sequence of Alcanivorax sp. 97CO-6 comprises 43 contigs (N90 = 78,739), with 3,253,423 bp and an average G+C content of 54.53%. Gene annotation was carried out using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (<https://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which was followed by manual editing. The annotation of the genome includes 2,931 candidate protein-encoding genes (with an average size of 960 bp), yielding a coding intensity of 86.50%. A total of 2,118 proteins could be assigned to clusters of orthologous (COG) groups; 42 tRNAs for all 20 amino acids and one 16S-23S-5S rRNA operon were identified using tRNAscan version 1.23 (8) and rRNAmmer version 1.2 (9), respectively.

All of the above information is from the published article "Genome Sequence of a Marine Alkane Degrader, Alcanivorax sp. Strain 97CO-6." Xiafei Yin, Xiao Luan, Angela Xu, Qian Li, Zhisong Cui, and David L. Valentine, Genome Announcements 2018 6 (8): e00087-18 doi: 10.1128/genomeA.00087-18

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Related Publications

Yin, X., Luan, X., Xu, A., Li, Q., Cui, Z., & Valentine, D. L. (2018). Genome Sequence of a Marine Alkane Degrader, Alcanivorax sp. Strain 97CO-6. Genome Announcements, 6(8). doi:10.1128/genomeA.00087-18
<https://doi.org/10.1128/genomeA.00087-18>
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Parameters

Parameters for this dataset have not yet been identified

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Project Information

Collaborative Research: Oxygenation of Hydrocarbons in the Ocean (Oxygenation of Hydrocarbons)

Coverage: Gulf of Mexico between Mississippi Slope, Gould Basin, and Castillo Basin (27 N 91 W)

NSF abstract:

More than 400,000 tons of petroleum hydrocarbons are released annually into the ocean, where they are subject to physical, chemical and biological processes, known as weathering, that are known to remove select hydrocarbons from the ocean. However, little attention has been given to the residues left by the weathering of oil, and studies indicate that oxygenation of these hydrocarbons can play a part in the formation of recalcitrant tar and toxic compounds. To address this gap, researchers from Woods Hole Oceanographic Institution, University of Mary Washington, and University of California Santa Barbara will conduct research to lay a scientific foundation for understanding 1) which processes control the formation of oxygenated hydrocarbons, 2) the rates of these processes, 3) the identity of the major products, 4) the rates at which they are formed and destroyed, and 5) for distinguishing photochemical oxygenation from biological oxygenation. The results from these experiments will contribute to a better understanding of the petroleum oxygenation processes and the environmental fate of understudied oxygenation products.

Broader Impacts: This study will provide for several undergraduates and two postdoctoral scholars to be trained in innovative analytical and experimental techniques. The results of this effort will help regulatory agencies to define new analytical methods and target compounds for oil spill research, and will add to our understanding regarding the fate and impacts of hydrocarbons released into the ocean.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1333162

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