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Mark W. J. van Passel
Wageningen University

Ravi Kant
University of Helsinki

Airi Palva
University of Helsinki

Susan Lucas
DOE Joint Genome Institute

Alex Copeland
DOE Joint Genome Institute

See next page for additional authors

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Genome Sequence of *Victivallis vadensis* ATCC BAA-548, an Anaerobic Bacterium from the Phylum *Lentisphaerae*, Isolated from the Human Gastrointestinal Tract▽

Mark W. J. van Passel,[1] Ravi Kant,[2] Airi Palva,[2] Susan Lucas,[3,4] Alex Copeland,[3,5] Alla Lapidus,[3,5]† Tijana Glavina del Rio,[3,5] Eileen Dalin,[3,5]‡ Hope Tice,[3,5] David Bruce,[6] Lynne Goodwin,[6] Sam Pitluck,[3,5] Karen Walston Davenport,[6] David Sims,[7] Thomas S. Brettin,[8] John C. Detter,[6] Shunsheng Han,[6] Frank W. Larimer,[8] Miriam L. Land,[8] Loren Hauser,[8] Nikolaos Kyrpides,[3,5] Galina Ovchinnikova,[3,5] P. Paul Richardson,[3,5] Willem M. de Vos,[1,2] Hauke Smidt,[1] and Erwin G. Zoetendal[1]*

Laboratory of Microbiology, Wageningen University, Wageningen, Netherlands[1]; Department of Veterinary Biosciences, Faculty of Veterinary Medicine, FIN-00014 University of Helsinki, Finland[2]; DOE Joint Genome Institute, Walnut Creek, California 94598[3]; Lawrence Livermore National Laboratory, Livermore, California 94550[4]; Lawrence Berkeley National Laboratory, Berkeley, California 94720[5]; Los Alamos National Laboratory, Los Alamos, New Mexico 87545[6]; HudsonAlpha Genome Sequencing Center, Huntsville, Alabama 35806[7]; Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831[8]

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***Victivallis vadensis* ATCC BAA-548 represents the first cultured representative from the novel phylum *Lentisphaerae*, a deep-branching bacterial lineage. Few cultured bacteria from this phylum are known, and *V. vadensis* therefore represents an important organism for evolutionary studies. *V. vadensis* is a strictly anaerobic sugar-fermenting isolate from the human gastrointestinal tract.**

The gastrointestinal (GI) tract is inhabited by a complex mixture of bacteria, which perform various functions that are beneficial to the host (13). Although numerous bacteria in the GI tract have yet to be cultivated, metagenomic analyses have unraveled much of the microbiome's genetic complexity (9). Still, validation of the actual capacities of microbes requires pure strains and, if possible, their genome sequences. Here, we represent the genome sequence of *Victivallis vadensis* ATCC BAA-548.

V. vadensis is a Gram-negative, nonmotile, strictly anaerobic coccus-shaped bacterium isolated from human feces (12). It is only capable of growth on a range of sugars in basal media, either as broth or semisolid (0.75%) agar, and does not grow on regular agar plates. *V. vadensis* was the first isolate from the phylum *Lentisphaerae*. Currently, this phylum holds only two orders, the *Victivallales* and the *Lentisphaerales*, with the latter order represented by the Gram-negative aerobic marine bacterium *Lentisphaera araneosa* (2, 10). Both *V. vadensis* and *L. araneosa* produce extracellular slime.

The phylum *Lentisphaerae* is most closely related to the deep-branching *Planctomycetes-Verrucomicrobia-Chlamydia* (PVC) superphylum. The *V. vadensis* genome is only the second from the *Lentisphaerae*, which may help to illustrate the lack of known diversity within this phylum.

The genome of *Victivallis vadensis* was sequenced using a combination of Sanger (2.5-kb pUC, 8-kb pMCL, and fosmids) and 454 sequencing (GS FLX). All general aspects of library construction and sequencing can be found at the JGI website (http://www.jgi.doe.gov/). Pyrosequencing reads were assembled using the Newbler assembler, version 1.1.02.15 (Roche). Large Newbler contigs were broken into 5,854 overlapping fragments of 1,000 bp and entered into assembly as pseudoreads. Quality scores were assigned based on Newbler consensus q-scores with modifications to account for overlap redundancy and adjust inflated q-scores. A hybrid 454/Sanger assembly was made using the Phrap assembler. Possible misassemblies were corrected and gaps between contigs were closed by editing in Consed or by custom primer walks from subclones or PCR products.

Genes were identified using Prodigal (4) as part of the Oak Ridge National Laboratory genome annotation pipeline, followed by a round of manual curation with the GenePRIMP pipeline (8). Noncoding genes and other miscellaneous features were predicted using tRNAscan-SE (7), RNAMMer (6), Rfam (3), TMHMM (5), and signalP (1).

The unclosed draft genome has 4,577,257 bases comprising 3,541 predicted protein-coding sequences (CDS) and a GC content of 59.5%. There are three predicted copies of the 5S but only one each of the 16S and 23S rRNA genes. A total of 48 predicted tRNAs were identified. A putative function could be predicted for 2,031 CDS (57.4%). Similar to other representatives from the PVC superphylum, including the human gut isolate *Akkermansia muciniphila* (11), a relatively large

* Corresponding author. Mailing address: Laboratory of Microbiology, University of Wageningen, Dreijenplein 10, 6703 HB Wageningen, Netherlands. Phone: 31 317 483111. Fax: 31 317 483829. E-mail: Erwin.Zoetendal@wur.nl.
† Present address: Fox Chase Cancer Center, Philadelphia, PA.
‡ Present address: Synthetic Genomics, La Jolla, CA 92037.
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number of genes containing signal peptides were found (877 CDS, 24.8%).

Nucleotide sequence accession number. The draft genome sequence of *V. vadensis* is available in GenBank under accession numbers ABDE02000001 to ABDE02000027.

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