Genome Sequence of the Solvent-Producing Bacterium
Clostridium carboxidivorans Strain P7T

Debarati Paul,1 Frank W. Austin,1 Tony Arick,4 Susan M. Bridges,2,3 Shane C. Burgess,1,3,4 Yoginder S. Dandass;2 and Mark L. Lawrence1,3,*

College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi;1 Department of Computer Sciences and Engineering, Mississippi State University, Mississippi State, Mississippi2; Institute for Digital Biology, Mississippi State University, Mississippi State, Mississippi3; and Life Sciences and Biotechnology Institute, Mississippi State University, Mississippi State, Mississippi4

Received 26 July 2010/Accepted 6 August 2010

Clostridium carboxidivorans strain P7T is a strictly anaerobic acetogenic bacterium that produces acetate, ethanol, butanol, and butyrate. The C. carboxidivorans genome contains all the genes for the carboxyl branch of the Wood-Ljungdahl pathway for CO2 fixation, and it encodes enzymes for conversion of acetyl coenzyme A into butanol and butyrate.

C. carboxidivorans strain P7T (equivalent to ATCC BAA-624T and DSM 15243T) is an obligate anaerobe that can grow autotrophically with H2 and CO2 or CO (fixing carbon via the Wood-Ljungdahl pathway, or it can grow chemolithoautotrophically with simple sugars (1). Acetate, ethanol, butanol, and butyrate are end products of metabolism.

For slow-growing strict anaerobes such as Clostridium carboxidivorans, genome sequencing provides a rapid theoretical characterization of its metabolism compared to traditional methods. We isolated and amplified genomic C. carboxidivorans DNA using the Wizard genomic DNA purification kit (Promega, Madison, WI) and the REPLI-g kit (Qiagen). The sequence was deposited in GenBank under accession number ADEK00000000.

The sequence was annotated using Annotation Engine (J. Craig Venter Institute) and manually curated using Manatee (http://manatee.sourceforge.net). The genome has 29.7% G+C content and contains 4,174 protein-coding sequences, 3 rRNA operons, 1 tRNA (dual tRNA-like and mRNA-like nature), 6 noncoding RNAs (ncRNAs), and 48 tRNA genes. Comparison of 16S RNA genes showed that C. carboxidivorans is closely related to Clostridium scatologenes ATCC 25775T (97% sequence identity) and Clostridium drakei type strain SL1T (99% sequence identity). C. carboxidivorans shares 94% 16S rRNA sequence identity with Clostridium ljungdahlii (4.6 Mb), another solventogenic species.

Pathway analyses indicated that C. carboxidivorans is similar to other anaerobic acetogens, such as Moorella thermoacetica (8), in having an incomplete reductive tricarboxylic acid (TCA) cycle where fumarate reductase is absent. Like other acetogenic clostridia, C. carboxidivorans uses the Wood-Ljungdahl pathway for fixing carbon dioxide to organic carbon via acetyl coenzyme A (acetyl-CoA) (5). Two of these genes encode carbon monoxide dehydrogenase (CODH) and acetyl-CoA synthase (ACS), which form a complex to catalyze the carboxyl branch of the pathway for carbon fixation and acetyl-CoA production. C. carboxidivorans has genes that encode phospho-transacetylase and acetate kinase for converting acetyl-CoA into acetate, yielding ATP (2).

C. carboxidivorans is unique among other known acetogenic clostridia because it can fix carbon via the Wood-Ljungdahl pathway and convert acetyl-CoA into butanol, which is more energy dense than ethanol. Both C. carboxidivorans and Clostridium acetobutylicum encode NADPH-dependent butanol dehydrogenase (74% identity) to convert acetyl-CoA into butanol (3, 4), but C. acetobutylicum cannot fix CO2 or CO into acetyl-CoA. Conversely, C. ljungdahlii can fix CO and CO2, but it lacks butanol dehydrogenase and cannot convert acetyl-CoA into butanol. Therefore, P7 includes beneficial properties of both these industrially important strains. The genome sequence of C. carboxidivorans P7 could potentially accelerate research allowing its industrial application for biofuel production or to enable some of its pathways to be used directly in synthetic biology for biofuel production.

Nucleotide sequence accession number. The genome sequence was deposited in GenBank under accession number ADEK00000000.

* Corresponding author. Mailing address: Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS 39762. Phone: (662) 325-1195. Fax: (662) 325-1031. E-mail: lawrence@cvm.msstate.edu.

1 Published ahead of print on 20 August 2010.
This research was supported by the U.S. Department of Energy under Award Number DE-FG3606GO86025.
We thank Todd French for technical advice, and we thank Michelle Banes, Elise McKinley, and Larry Ballard for technical assistance. We are grateful to the Mississippi State University Life Sciences and Biotechnology Institute for hosting Manatee.

REFERENCES


