The Scope of Its Metabolic Capabilities

A particulate butane monooxygenase (pBMO) to grow on C2 to C6 alkanes. The pBMO monooxygenase represents a deeply branched third lineage in the groups of ammonia monooxygenases (AMO) (from the ammonia-oxidizing bacteria), and the particulate methane monooxygenases (pMMO) (from the methane-oxidizing bacteria) (4).

The genome of Nocardioides sp. strain CF8 was sequenced using paired-end sequencing on an Illumina genome analyzer IIx (Illumina, Inc., CA) at the Center for Genome Research and Biocomputing at Oregon State University. The sequence reads (average length of 80 bp) were de novo assembled using Velvet version 0.7.55 (5) into 165 contigs that were >200 bp in length. A high-quality draft genome sequence was derived by reordering and coalescing the contigs into 21 scaffolds using the mauveAligner program (6) and the Nocardioides SJ614 genome (ac-cession no. NC_008699.1) as a reference. The size of the CF8 genome was estimated to be 4,204,777 bases in length, with approximately 32× coverage. There are a total of 4,003 coding genes (coding sequence features without a pseudoqualifier) that represent 3,759,514 bases (G+C content, 69.9%) for a density of 0.952 genes per kilobase (1,050 bases per gene). Several transposase- and mutator-type coding sequences could not be ordered correctly and were simply reported at the end of the genome sequence. Annotation was based on the xBASE bacterial genome annotation service (http://www.xbase.ac.uk/annotation/) and a secondary automatic genome annotation performed by the Center for Genome Research and Biocomputing at Oregon State University (ETA xbase pipeline). The manual analysis of the genome composition was performed using Artemis Sanger Institute software (7).

In addition to previously characterized genes and enzyme activities for hydrocarbon utilization (e.g., pBMO and a binuclear-iron-containing AlkB-type alkane monooxygenase), the genome contains genes that potentially encode a second AlkB-type monoxygenase and four aromatic-ring (hydroxylytating and cleavaging) dioxygenases. Preliminary analyses of the draft genome sequence of Nocardioides sp. strain CF8 reveal its potential for applications in bioremediation. The sequence is useful for genome-enabled approaches to study the full scope of substrates that this organism is capable of using (6).

Nocardioides sp. strain CF8 was isolated from a soil sample collected at the Hanford Department of Energy site, Richland, WA. The strain was identified in microcosms based on its ability to grow on butane and has been characterized for its potential applications in the biodegradation of halogenated hydrocarbons. Here, the draft genome sequence is reported.
REFERENCES

1. Hamamura N, Arp DJ. 2000. Isolation and characterization of alkane-utilizing *Nocardioides* sp. strain CF8. FEMS Microbiol. Lett. 186: 21–26.

2. Hamamura N, Page C, Long T, Semprini L, Arp DJ. 1997. Chloroform cometabolism by butane-grown CF8, *Pseudomonas butanovora*, and *Mycobacterium vaccae* JO85 and methane-grown *Methylosinus trichosporium* OB3b. Appl. Environ. Microbiol. 63:3607–3613.

3. Halsey KH, Sayavedra-Soto LA, Bottomley PJ, Arp DJ. 2005. Trichloroethylene degradation by butane-oxidizing bacteria causes a spectrum of toxic effects. Appl. Microbiol. Biotechnol. 68:794–801.

4. Sayavedra-Soto LA, Hamamura N, Liu C-H, Kimbrel JA, Chang JH, Arp DJ. 2011. The membrane-associated monooxygenase in the butane-oxidizing Gram-positive bacterium *Nocardioides* sp. strain CF8 is a novel member of the AMO/PMO family. Environ. Microbiol. Rep. 3:390–396.

5. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18:821–829.

6. Rissman AI, Mau B, Biehl BS, Darling AE, Glasner JD, Perna NT. 2009. Reordering contigs of draft genomes using the mauveAligner. Bioinformatics 25:2071–2073.

7. Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B. 2000. Artemis: sequence visualization and annotation. Bioinformatics 16:944–945.