JOURNAL OF BACTERIOLOGY, June 2011, p. 2894–2895 Vol. 193, No. 11
0021-9193/11/$12.00 doi:10.1128/JB.00333-11

Complete Genome Sequence of *Polymorphum gilvum* SL003B-26A1^T, a Crude Oil-Degrading Bacterium from Oil-Polluted Saline Soil$^\nabla$

Shu-Guang Li,† Yue-Qin Tang,† Yong Nie,† Man Cai, and Xiao-Lei Wu*

Department of Energy and Resources Engineering, College of Engineering, Peking University, Beijing 100871, People's Republic of China

Received 9 March 2011/Accepted 25 March 2011

***Polymorphum gilvum* SL003B-26A1^T is a type strain of a newly published novel species in the novel genus *Polymorphum*. It was isolated from a crude oil-polluted saline soil in Shengli Oilfield, China, and was able to use the crude oil as the sole carbon source. Here we report the complete genome of SL003B-26A1^T and the genes likely to be involved in oil degradation and ecological adaption.**

Oil pollution has become a global issue because of its severe ecological impact and destruction. Bioremediation has proved to be an effective process to restore oil-polluted environments. As one of the novel bacterial species isolated from the crude oil-polluted saline soil in Shengli Oilfield, China (2, 6, 11–13), *Polymorphum gilvum* SL003B-26A1^T (= LMG 25793^T = CGMCC 1.9160^T) represents a novel species and a novel genus (2a) which could use the crude oil as the sole carbon source.

The complete genome sequencing of *Polymorphum gilvum* SL003B-26A1^T was performed with a combined strategy of 454 sequencing (9) and Solexa paired-end sequencing (1) technologies. Genomic libraries containing 8-kb inserts were constructed. A total of 248,467 paired-end reads were generated using the GS FLX system (454 Life Sciences Corporation, Branford, CT), giving a 64.0-fold coverage of the genome. And 96.4% of the reads were assembled into two large scaffolds by using the 454 Newbler assembler, including 139 nonredundant contigs. A total of 3,487,313 reads (3-kb library) were generated with an Illumina Solexa IIx genome analyzer (Illumina, San Diego, CA) to reach a depth of 151.5-fold coverage and mapped to the scaffolds using the Burrows-Wheeler alignment (BWA) tool (8). The gaps between the scaffolds were filled by sequencing PCR products using an ABI 3730 capillary sequencer. Protein-encoding genes were predicted by the Glimmer 3.0 software program (3). The analysis of the genome was performed as described previously (4). Genomic islands (GIs) were analyzed by using the IslandViewer software tool (http://www.pathogenomics.sfu.ca/islandviewer) (7).

The complete genome of *Polymorphum gilvum* SL003B-26A1^T consists of a circular 4,649,365-bp chromosome and a 69,598-bp plasmid with G+C contents of 67.22% and 61.55%, respectively. The chromosome contains 4,334 predicted protein-encoding genes with an average size of 951 bp, giving a coding intensity of 88.68%. The plasmid contains 71 predicted protein-encoding genes with an average size of 869 bp, giving a coding intensity of 88.63%. Fifty tRNA- and 2 rRNA-encoding operons are identified in the chromosome.

The well-known integral-membrane alkane monooxygenase (AlkB) and cytochrome P450 enzymes are not found in the genome. However, a *ladA* gene (SL003B_1417) for long-chain-length *n*-alkane hydroxylation has been found in the genome sequence. Distinct from the AlkB and P450 enzymes, which can oxidize the C_5 to C_{16} *n*-alkanes (10), LadA is an extracellular enzyme and can act on long-chain alkanes ranging from C_{15} to C_{36} (5), suggesting that the LadA enzyme might play important roles in the alkane hydroxylation in this strain. The presence of GI is often an evidence of horizon gene transfer (HGT) in genome shaping. The location of the *ladA* gene in one of the 17 predicted GIs suggests that the *ladA* gene might come from HGT. Furthermore, SL003B-26A1^T has 34, 15, and 312 genes, respectively, encoding histidine kinases, two-component transcriptional regulators involved in signal transduction, and ATP-binding cassette (ABC) superfamily proteins for producing antimicrobial metabolites and taking up substrates.

Nucleotide sequence accession numbers. The nucleotide sequence of *Polymorphum gilvum* SL003B-26A1 has been deposited in the GenBank database under accession numbers CP002568 (chromosome) and CP002569 (plasmid).

This study was supported by the National Natural Science Foundation of China (30870086, 31070107, and 40821140541) and the National High Technology Research and Development Program of China (2007AA021303).

REFERENCES

1. **Bentley, D. R., et al.** 2008. Accurate whole human genome sequencing using reversible terminator chemistry. Nature **456:**53–59.
2. **Cai, M., et al.** *Salinarimonas ramus* sp. nov. and *Tessaracoccus oleiagri* sp. nov., isolated from a crude oil contaminated saline soil. Int. J. Syst. Evol. Microbiol., in press.
2a. **Cai, M., et al.** *Rubrimonas shengliensis* sp. nov. and *Polymorphum gilvum* gen. nov., sp. nov., novel members of *Alphaproteobacteria* from crude oil contaminated saline soil. Syst. Appl. Microbiol., in press.
3. **Delcher, A. L., et al.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23:**673–679.
4. **Feng, L., et al.** 2008. A recalibrated molecular clock and independent origins for the cholera pandemic clones. PLoS One **3:**e4053.
5. **Feng, L., et al.** 2007. Genome and proteome of long-chain alkane degrading Geobacillus thermodenitrificans NG80-2 isolated from a deep-subsurface oil reservoir. Proc. Natl. Acad. Sci. U. S. A. **104:**5602–5607.

* Corresponding author. Mailing address: Department of Energy and Resources Engineering, College of Engineering, Peking University, Beijing 100871, PR China. Phone and fax: 86-10-62759047. E-mail: xiaolei_wu@pku.edu.cn.
† Contributed equally to the work.
$^\nabla$ Published ahead of print on 1 April 2011.

6. **Gu, J., et al.** 2007. *Marinobacter gudaonensis* sp. nov., isolated from an oil-polluted saline soil in a Chinese oilfield. Int. J. Syst. Evol. Microbiol. **57:**250–254.
7. **Langille, M. G. I., and F. S. L. Brinkman.** 2009. IslandViewer: an integrated interface for computational identification and visualization of genomic islands. Bioinformatics **25:**664–665.
8. **Li, H., and R. Durbin.** 2010. Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics **26:**589–595.
9. **Margulies, M., et al.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437:**376–380.
10. **van Beilen, J. B., and E. G. Funhoff.** 2007. Alkane hydroxylases involved in microbial alkane degradation. Appl. Microbiol. Biotechnol. **74:**13–21.
11. **Wang, Y. N., et al.** 2007. *Halomonas shengliensis* sp. nov., a moderately halophilic, denitrifying, crude-oil-utilizing bacterium. Int. J. Syst. Evol. Microbiol. **57:**1222–1226.
12. **Wang, Y. N., et al.** 2007. *Halomonas gudaonensis* sp. nov., isolated from a saline soil contaminated by crude oil. Int. J. Syst. Evol. Microbiol. **57:**911–915.
13. **Wu, X. L., et al.** 2009. *Filomicrobium insigne* sp. nov., isolated from an oil-polluted saline soil. Int. J. Syst. Evol. Microbiol. **59:**300–305.