JOURNAL OF BACTERIOLOGY, Nov. 2011, p. 6404–6405 Vol. 193, No. 22
0021-9193/11/$12.00 doi:10.1128/JB.06050-11

Genome Sequence of *Sphingobium yanoikuyae* XLDN2-5, an Efficient Carbazole-Degrading Strain

Zhonghui Gai,‡ Xiaoyu Wang,‡ Hongzhi Tang, Cui Tai, Fei Tao, Geng Wu, and Ping Xu*

State Key Laboratory of Microbial Metabolism and School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai, People's Republic of China

Received 23 August 2011/Accepted 2 September 2011

***Sphingobium yanoikuyae* XLDN2-5 is an efficient carbazole-degrading strain. Carbazole-degrading genes are accompanied on both sides by two copies of IS*6100* elements. Here, we describe the draft genome sequence of strain XLDN2-5, which may provide important clues as to how it recruited exogenous genes to establish pathways to degrade the xenobiotics.**

The *Sphingomonas* genus was proposed by Yabuuchi et al. in 1990 and is characterized by an outer membrane that contains glycosphingolipids instead of lipopolysaccharide (13). By 2001, the *Sphingomonas* genus has been subdivided into four genera: *Sphingomonas*, *Sphingobium*, *Novosphingobium*, and *Sphingopyxis* (10). These genera are commonly referred to collectively as sphingomonads. Recently, sphingomonads have received increasing attention due to their biodegradative and biosynthetic capabilities and have been utilized for a wide range of biotechnological applications, from bioremediation of contaminants to production of extracellular polymers.

Sphingobium yanoikuyae XLDN2-5, a member of the sphingomonads, was isolated from petroleum-contaminated soils (3, 11) and is able to degrade carbazole efficiently. Moreover, this strain could also cometabolically catabolize dibenzofuran, dibenzothiophene, and benzothiophene (3, 4), which are among the most potent environmental pollutants (12). Carbazole is converted by carbazole 1,9a-dioxygenase, *meta*-cleavage enzyme, and hydrolase to anthranilate and 2-hydroxypenta-2,4-dienoate. Two gene clusters involved in the carbazole degradation by strain XLDN2-5 were identified and sequenced (5). The *car* gene cluster (*carRAaBaBbCAc*) and *fdr* gene are accompanied on both sides by two copies of IS*6100* elements and organized as IS*6100*::ISSspI-*ORF1-carRAaBaBbCAc-ORF8*-IS*6100-fdr*-IS*6100*. The *ant* gene cluster (*antRAcAdAbAa*), which is involved in the conversion of anthranilate to catechol, is also sandwiched between two IS*6100* elements as IS*6100-antRAcAdAbAa*-IS*6100*. Together the structure genes and IS*6100* elements make up two catabolic transposons, responsible for carbazole degradation, indicating that the insertion sequence (IS*6100*) played an important role in the evolution of the carbazole-degrading pathway. Here, we describe the draft genome of *Sphingobium yanoikuyae* XLDN2-5.

The genome of this strain was sequenced using the 454 Life Sciences GS FLX system. The reads were assembled using the Newbler assembler, version 2.3. The contig N50 was approximately 73.7 kb, and the largest contig assembled was approximately 251.4 kb. This assembly generated 159 large contigs (>500 bp). The draft genome was 5,353,044 bases in length, with a mean GC content of 64.3%. The genome was annotated using the RAST annotation server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (7). A total of 5,057 coding sequences and 52 structural RNAs were predicted.

As expected, strain XLDN2-5 encodes a diverse array of proteins with predicted roles in aromatic compound metabolism. We also identified mobile genetic elements, including insertion sequences, transposons, and plasmids, suggesting that the genome of strain XLDN2-5 has been extensively shaped by horizontal gene transfers. Strain XLDN2-5 contains at least one megaplasmid. The megaplasmid contains *car* and *ant* clusters, which are involved in carbazole degradation (5). In addition, we identified a gene cluster from strain XLDN2-5 responsible for the aerobic catechol degradation via a *meta*-cleavage pathway. The order of the genes in the *meta*-pathway of strain XLDN2-5 is *carLM-catS-carJK-catR-carDEFGHIYX* and remarkably different from that of plasmid-borne *xyl* (9), *dmp* (8), *nah* (6), and *bph* (2) pathways. Further genomic analyses may provide important clues about the functional capability of strain XLDN2-5.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AFXE00000000. The version described in this paper is the first version, AFXE01000000.

This work was supported in part by grants from the Chinese National Natural Science Foundation (grant numbers 20977061 and 30821005) and from the Ministry of Science and Technology of China (National Basic Research Program of China, grant number 2009CB118906). We also acknowledge the financial support of the Key Basic Research Program of Shanghai (grant number 09JC1407700).

REFERENCES

1. **Aziz, R. K., et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9:**75.
2. **Carrington, B., A. Lowe, L. E. Shaw, and P. A. Williams.** 1994. The lower pathway operon for benzoate catabolism in biphenyl-utilizing *Pseudomonas* sp. strain IC and the nucleotide sequence of the *bphE* gene for catechol 2,3-dioxygenase. Microbiology **140:**499–508.
3. **Gai, Z. H., et al.** 2007. Cometabolic degradation of dibenzofuran and dibenzothiophene by a newly isolated carbazole-degrading *Sphingomonas* sp. strain. Appl. Environ. Microbiol. **73:**2832–2838.

* Corresponding author. Mailing address: School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai 200240, People's Republic of China. Phone: 86 21 34206647. Fax: 86 21 34206723. E-mail: pingxu@sjtu.edu.cn.

‡ These authors contributed equally to this work.

4. **Gai, Z., B. Yu, X. Wang, Z. Deng, and P. Xu.** 2008. Microbial transformation of benzothiophenes, with carbazole as the auxiliary substrate, by *Sphingomonas* sp. strain XLDN2-5. Microbiology **154:**3804–3812.
5. **Gai, Z. H., et al.** 2010. The genes coding for the conversion of carbazole to catechol are flanked by IS*6100* elements in *Sphingomonas* sp. strain XLDN2-5. PLoS One **5:**e10018.
6. **Greated, A., L. Lambertsen, P. A. Williams, and C. M. Thomas.** 2002. Complete sequence of the IncP-9 TOL plasmid pWW0 from *Pseudomonas putida*. Environ. Microbiol. **4:**856–871.
7. **Pruitt, K. D., T. Tatusova, W. Klimke, and D. R. Maglott.** 2009. NCBI reference sequences: current status, policy and new initiatives. Nucleic Acids Res. **37:**D32–D36.
8. **Shingler, V., J. Powlowski, and U. Marklund.** 1992. Nucleotide sequence and functional analysis of the complete phenol/3,4-dimethylphenol catabolic pathway of *Pseudomonas* sp. strain CF600. J. Bacteriol. **174:**711–724.
9. **Sota, M., et al.** 2006. Genomic and functional analysis of the IncP-9 naphthalene-catabolic plasmid NAH7 and its transposon Tn*4655* suggests catabolic gene spread by a tyrosine recombinase. J. Bacteriol. **188:**4057–4067.
10. **Takeuchi, M., K. Hamana, and A. Hiraishi.** 2001. Proposal of the genus *Sphingomonas sensu stricto* and three new genera, *Sphingobium*, *Novosphingobium* and *Sphingopyxis*, on the basis of phylogenetic and chemotaxonomic analyses. Int. J. Syst. Evol. Microbiol. **51:**1405–1417.
11. **Wang, X., et al.** 2007. Degradation of carbazole by microbial cells immobilized in magnetic gellan gum gel beads. Appl. Environ. Microbiol. **73:**6421–6428.
12. **Xu, P., et al.** 2006. Microbial degradation of sulfur, nitrogen and oxygen heterocycles. Trends Microbiol. **14:**398–405.
13. **Yabuuchi, E., et al.** 1990. Proposals of *Sphingomonas paucimobilis* gen. nov. and comb. nov., *Sphingomonas parapaucimobilis* sp. nov., *Sphingomonas yanoikuyae* sp. nov., *Sphingomonas adhaesiva* sp. nov., *Sphingomonas capsulata* comb. nov., and two genospecies of the genus *Sphingomonas.* Microbiol. Immunol. **34:**99–119.