JOURNAL OF BACTERIOLOGY, Aug. 2011, p. 4266–4267 Vol. 193, No. 16
0021-9193/11/$12.00 doi:10.1128/JB.05356-11

Genome Sequence of the 17β-Estradiol-Utilizing Bacterium *Sphingomonas* Strain KC8▽

Anyi Hu,[1] Jibing He,[1,2] Kung-Hui Chu,[3] and Chang-Ping Yu[1]*

Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, China[1]; College of Earth and Environment, Anhui University of Science and Technology, Huainan 232001, China[2]; and Zachry Department of Civil Engineering, Texas A&M University, College Station, Texas 77843[3]

Received 23 May 2011/Accepted 6 June 2011

***Sphingomonas* strain KC8 is known for its ability to utilize 17β-estradiol, a natural estrogen and an environmental endocrine-disrupting compound, as the sole carbon and energy source. Here, we report the draft genome sequence of the strain KC8 (4,074,265 bp, with a GC content of 63.7%) and major findings from its annotation.**

Estrogens are one of the most worrisome environmental endocrine-disrupting compounds because exposure to estrogens or estrogen-like chemicals is known to cause adverse health effects on wildlife (11, 13). As biodegradation is considered the major removal mechanism in human-made and natural environments, a better understanding of microbial transformation of estrogens is warranted (3). Among known estrogen-degrading isolates, *Sphingomonas* strain KC8 is of particular interest because strain KC8 can degrade 17β-estradiol into nonestrogenic end products (14). However, the degrading mechanism remains largely unclear. Here, we present the draft genome sequence of strain KC8. To our knowledge, this is the first genome report of estrogen-degrading bacteria.

The genome of KC8 was sequenced by a whole-genome shotgun strategy using Roche 454 GS-FLX Titanium pyrosequencing technology. A total of 217,810 reads and 85,408,792 bp of sequence were produced, providing about 21-fold coverage of the genome. Genome sequences were assembled *in silico* using Newbler Assembler 2.3 (Roche), resulting in 70 contigs (>1,000 bp in size) with an N_{50} length of 142,404 bp. The protein-coding genes were predicted using Glimmer 3.02 (4), while tRNAscan-SE (9) and RNAmmer (8) were used to identify tRNA and rRNA, respectively. The genome sequence was also uploaded into Rapid Annotation using Subsystem Technology (RAST) (1) to check the annotated sequences. The functions of predicted protein-coding genes were then annotated through comparisons with the databases of NCBI-NR (2), COG (12), and KEGG (6).

The KC8 draft genome sequence has a total of 4,074,265 bp with an average GC content of 63.7%. It contains 3,950 predicted coding sequences (CDSs), one 16S-23S-5S operon, and 46 tRNAs. Using COG functional assignment, the majority of predicted proteins (89.4%) could be classified into 22 COG categories. According to subsystem-based annotation generated by RAST, strain KC8 has 369 subsystems. The four most abundant of the subsystems are related to amino acids and derivatives (number of CDSs = 328), carbohydrates (n = 264), protein metabolism (n = 213), and fatty acids, lipids, and isoprenoids (n = 199). In addition, a large number of the CDSs are found to be related to resistance to antibiotics and toxic compounds (n = 101), stress response (n = 125), and motility and chemotaxis (n = 128). These findings suggest that strain KC8 has a very diverse catabolic ability and a unique ability to adapt and/or survive in different environments.

According to the proposed estrogen and testosterone degradation pathways (5, 7, 10), several genes encoding the enzymes putatively involved in estrogen degradation, such as hydroxysteroid dehydrogenase, 3-ketosteroid-delta1-dehydrogenase, Rieske dioxygenase, and catechol 2,3-dioxygenase, were also observed in the genome of KC8. Further studies are needed to clone these genes to confirm their functions. In addition, a more detailed analysis of this genome and comparative genome analysis with other polycyclic aromatic hydrocarbon-degrading *Sphingomonas* members will reveal the unique biochemical and molecular characteristics of this strain.

Nucleotide sequence accession number. The draft genome sequence of *Sphingomonas* strain KC8 has been deposited at GenBank under accession number AFMP01000000.

We thank the members of the Chinese National Human Genome Center at Shanghai for their support in sequencing and assembling the genome.

This work was supported by the Hundred Talents Program of the Chinese Academy of Sciences, Special Program for Key Basic Research of the Ministry of Science and Technology, China (2010CB434802); the Science and Technology Planning Project of Xiamen, China (3502Z20102017); and the CAS/SAFEA International Partnership Program for Creative Research Teams (KZCX2-YW-T08).

REFERENCES

1. **Aziz, R. K., et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9:**75.
2. **Benson, D. A., I. Karsch-Mizrachi, D. J. Lipman, J. Ostell, and D. L. Wheeler.** 2008. GenBank. Nucleic Acids Res. **36:**D25–D30.
3. **Combalbert, S., and G. Hernandez-Raquet.** 2010. Occurrence, fate, and biodegradation of estrogens in sewage and manure. Appl. Microbiol. Biotechnol. **86:**1671–1692.
4. **Delcher, A. L., K. A. Bratke, E. C. Powers, and S. L. Salzberg.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23:**673–679.

* Corresponding author. Mailing address: Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, People's Republic of China. Phone: 86-592-6190768. Fax: 86-592-6190977. E-mail: cpyu@iue.ac.cn.

▽ Published ahead of print on 17 June 2011.

5. **Horinouchi, M., T. Hayashi, and T. Kudo.** 2004. The genes encoding the hydroxylase of 3-hydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione in steroid degradation in *Comamonas testosteroni* TA441. J. Steroid Biochem. **92:**143–154.
6. **Kanehisa, M., et al.** 2008. KEGG for linking genomes to life and the environment. Nucleic Acids Res. **36:**D480–D484.
7. **Kurisu, F., M. Ogura, S. Saitoh, A. Yamazoe, and O. Yagi.** 2010. Degradation of natural estrogen and identification of the metabolites produced by soil isolates of *Rhodococcus* sp and *Sphingomonas* sp. J. Biosci. Bioeng. **109:**576–582.
8. **Lagesen, K., et al.** 2007. RNAmmer: consistent and rapid annotation of rRNA genes. Nucleic Acids Res. **35:**3100–3108.
9. **Lowe, T. M., and S. R. Eddy.** 1997. tRNAscan-SE: a program for improved detection of tRNA genes in genomic sequence. Nucleic Acids Res. **25:**955–964.
10. **Ren, H. Y., S. L. Ji, N. U. D. Ahmad, W. Dao, and C. W. Cui.** 2007. Degradation characteristics and metabolic pathway of 17α-ethynylestradiol by *Sphingobacterium* sp JCR5. Chemosphere **66:**340–346.
11. **Sumpter, J. P., and A. C. Johnson.** 2008. 10th anniversary perspective: reflections on endocrine disruption in the aquatic environment: from known knowns to unknown unknowns (and many things in between). J. Environ. Monit. **10:**1476–1485.
12. **Tatusov, R. L., E. V. Koonin, and D. J. Lipman.** 1997. A genomic perspective on protein families. Science **278:**631.
13. **Tyler, C. R., S. Jobling, and J. P. Sumpter.** 1998. Endocrine disruption in wildlife: a critical review of the evidence. Crit. Rev. Toxicol. **28:**319–361.
14. **Yu, C. P., H. Roh, and K. H. Chu.** 2007. 17β-Estradiol-degrading bacteria isolated from activated sludge. Environ. Sci. Technol. **41:**486–492.