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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Pyrene-Degrading Bacterium *Cycloclasticus* sp. Strain P1

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***Cycloclasticus* sp. strain P1 was isolated from deep-sea sediments of the Pacific Ocean and characterized as a unique bacterium in the degradation of pyrene, a four-ring polycyclic aromatic hydrocarbon (PAH). Here we report the complete genome of P1 and genes associated with PAH degradation.**

Cycloclasticus sp. strain P1 (= MCCC 1A01040) was isolated from deep-sea sediments of the Pacific Ocean enriched by pyrene (7). In addition to pyrene, strain P1 can use naphthalene, 2-methylnaphthalene, 2,6-dimethylnaphthalene, biphenyl, fluorene, acenaphthene, dibenzofuran, dibenzothiophene, phenanthrene, or anthracene as the only carbon source for growth. As of now, there are 24 strains of this genus that can be retrieved in NCBI that have been reported to have polycyclic aromatic hydrocarbon (PAH) degradation ability. Strain P1 was the only one that could use pyrene as the only carbon source for growth. Prior to this study, only one gene cluster of naphthalene dioxygenase was found in strain P1 as the key enzyme in PAH degradation (7), the same cluster as that found in *Cycloclasticus* sp. A5 (2), which had been confirmed as having a function in naphthalene degradation. No genes related to pyrene degradation in *Cycloclasticus* spp. have been reported.

The complete genome sequence of *Cycloclasticus* sp. P1 was first determined by the Chinese National Human Genome Center at Shanghai (CNHGC, Shanghai, China) using 454 technology (6) and then was corrected by the transcription data determined by BGI (Shenzhen, China) using Solexa paired-end sequencing technology. In the case of 454 pyrosequencing, a total of 74,420,589 high-quality base pairs (196,120 high-quality reads, with an average read length of 379 bp), giving 31.5-fold coverage of the genome, were assembled into 23 contigs (defined as >500 bp) using Newbler software of the 454 suite package (454 Life Sciences). Gaps between contigs were closed by custom primer walks or by PCR amplification followed by DNA sequencing at CNHGC. A total of 26,478,508 reads (using a 500-bp library) were generated to reach a 1,000-fold depth of coverage with an Illumina/Solexa Genome Analyzer IIx (Illumina, San Diego, CA) and mapped to the complete genome using the Burrows-Wheeler alignment (BWA) tool (4). Both groups of sequencing data were combined, and the genome sequence was analyzed by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (SMBBC, Shanghai, China). Together, 118 indels and 30 single-nucleotide polymorphisms (SNP) were corrected for the complete genome sequence of strain P1.

The genome of *Cycloclasticus* sp. P1 consists of a single circular chromosome of 2,363,215 bp in size and has an average G+C content of 42.0%. There are a total of 2,249 putative open reading frames (with an average size of 958 bp) predicted by Glimmer (1), giving a coding intensity of 91.2%. Together, 35 tRNA genes for all 20 amino acids and one 16S-23S-5S rRNA operon were identified by tRNAscan-SE (5) and RNAmmer (3), respectively.

There are 18 PAH-degrading dioxygenase alpha (or large) subunits found in the genome of *Cycloclasticus* sp. P1, including the previously confirmed naphthalene-degrading gene cluster in *Cycloclasticus* sp. A5 (2). However, which dioxygenase is related to pyrane degradation in strain P1 is still unknown and needs further experimentation. The P1 genome sequence and its curated annotation are important assets to better understand the physiology and metabolic potential of *Cycloclasticus* sp. and will open up new opportunities in the functional genomics of this species.

Nucleotide sequence accession number. The nucleotide sequence comprising the *Cycloclasticus* sp. P1 genome was deposited in the GenBank database with the accession number CP003230 (chromosome).

ACKNOWLEDGMENTS

We acknowledge Huajun Zheng and his colleagues for genome sequencing performed at the Chinese National Human Genome Center at Shanghai. We acknowledge Qiang Li and his colleagues for genome sequencing and analysis at Shanghai Majorbio Bio-pharm Technology Co., Ltd.

This work was financially supported by the National Natural Science Foundation of China (41076105), the COMRA program (no. DY125-15-R-01), and the Public Welfare Project of SOA (201005032).

REFERENCES

1. **Delcher AL, Bratke KA, Powers EC, Salzberg SL.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23**: 673–679.
2. **Kasai Y, Shindo K, Harayama S, Misawa N.** 2003. Molecular characterization and substrate preference of a polycyclic aromatic hydrocarbon dioxygenase from Cycloclasticus sp. strain A5. Appl. Environ. Microbiol. **69**: 6688–6697.
3. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
4. **Li H, Durbin R.** 2010. Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics **26**:589–595.
5. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**: 955–964.
6. **Margulies M, et al.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437**:376–380.
7. **Wang B, Lai Q, Cui Z, Tan T, Shao Z.** 2008. A pyrene-degrading consortium from deep-sea sediment of the West Pacific and its key member Cycloclasticus sp. P1. Environ. Microbiol. **10**:1948–1963.

Received 25 September 2012 **Accepted** 28 September 2012

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doi:10.1128/JB.01837-12