Genome Sequence of *Oceanibaculum indicum* Type Strain P24

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***Oceanibaculum indicum* type strain P24 was isolated from a polycyclic-aromatic-hydrocarbon-degrading consortium enriched from a deep-seawater sample collected from the Indian Ocean. Here we present the draft genome of strain P24^T, which contains 3,952,792 bp with a G+C content of 65.5% and contains 3,755 protein-coding genes and 45 tRNAs.**

Oceanibaculum indicum P24^T (= CCTCC AB 208226^T = LMG 24626^T = MCCC 1A02083^T) was isolated from a polycyclic-aromatic-hydrocarbon (PAH)-degrading consortium enriched from a deep-seawater sample collected from the Indian Ocean. By now, 14 strains of this species from marine environments have been isolated in our lab (<http://www.mccc.org.cn>) (with 100% 16S rRNA gene sequence similarity) and only six uncultured bacterial clone 16S sequences (with 99% 16S rRNA gene sequence similarity) can be retrieved from NCBI. The genus *Oceanibaculum* was first proposed by Lai et al. in 2009 and contains only two type strains of *Oceanibaculum pacificum* and *O. indicum* (1, 2).

The genome sequence of *O. indicum* P24^T was determined by the Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), by Solexa paired-end sequencing technology. A total of 6,476,755 paired-end reads (500-bp library) were generated to reach a 265-fold depth of coverage with Illumina/Solexa Genome Analyzer IIx (Illumina, San Diego, CA), and the gaps between scaffolds were closed by custom primer walks or by PCR amplification followed by DNA sequencing. The genome of *O. indicum* P24^T consists of 71 contigs (>200 bp, 32 N₉₀ contigs) of 3,952,792 bp and had an average G+C content of 65.5%. Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which was followed by manual editing. The genome contains 3,755 candidate protein-encoding genes (with an average size of 955 bp), giving a coding intensity of 90.8%. A total of 2,882 proteins could be assigned to cluster of orthologous groups (COG) families (3). Forty-five tRNA genes for all 20 amino acids were identified. The proteins associated with amino acid transport and metabolism (COG initial, E) were the most abundant COG group (415 open reading frames [ORFs], 14.4%), followed by the ones associated with inorganic ion transport and metabolism (P; 244 ORFs, 8.5%) and transcription (K; 216 ORFs, 7.4%).

Strain P24^T cannot use all of the PAHs tested, including naph-

thalene, phenanthrene, and pyrene, as sole carbon sources for growth, though it was isolated from a PAH-degrading consortium. Genome sequence analysis revealed a gene encoding a ring-hydroxylating dioxygenase that awaits further characterization. The genome sequence of strain P24^T and its curated annotation are important assets to better understand the physiology and metabolic potential of *O. indicum* and will open up new opportunities for the analysis of the function of this species in PAH consortia.

Nucleotide sequence accession number. The draft genome sequence of *O. indicum* P24^T has been deposited at GenBank under accession number [AMRL00000000](#) (chromosome).

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