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GENOME ANNOUNCEMENT

Genome Sequence of Benzo(a)pyrene-Degrading Bacterium *Novosphingobium pentaromativorans* US6-1

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Novosphingobium pentaromativorans **US6-1 showed a good ability to degrade high-molecular-weight polycyclic aromatic hydrocarbons. We report the draft genome sequence of strain US6-1, which contains a main chromosome (5,096,413 bp, G+C content of 63.1%) and two plasmids (188,476 and 60,085 bp). The majority of the aromatic-hydrocarbon-degrading genes are encoded in the larger plasmid.**

Polycyclic aromatic hydrocarbons (PAHs) are widely distributed in the environment generated by natural combustion processes and human activities. Benzo(a)pyrene is of environmental concern due to its high carcinogenic and bioaccumulation potential. *Novosphingobium pentaromativorans* US6-1 can utilize high-molecular-weight PAHs as a sole carbon and energy source. Strain US6-1 especially showed a good ability to degrade benzo(a)pyrene (8). Here we report the whole genome of *Novosphingobium pentaromativorans* US6-1, which, based on our knowledge, is the first bacterial genome that can degrade benzo(a)pyrene.

The genome sequence of strain US6-1 was obtained by using the 454 GS FLX Titanium from two libraries, a shotgun library and a 3-kb paired-end library. A total of 541,457 reads were generated from the shotgun library, reaching about 31-fold coverage of the genome. Genome sequences were assembled using the GS De Novo Assembler (v 2.5.3), resulting in 122 contigs with an N_{50} size of 117,882 bp. The annotation was done by merging the results obtained from the Rapid Annotation using Subsystem Technology (RAST) server (1), the Glimmer 3.02 modeling software package (3), tRNAscan-SE 1.21 (5), and RNAmmer 1.2 (4).

The US6-1 genome is comprised of a draft chromosomal genome of 5,096,941 bp (G+C content of 63.1%) and two plasmids, designated pLA1 (188,476 bp, G+C content of 62.6%) and pLA2 (60,085 bp, G+C content of 60.2%). The chromosome of strain US6-1 contains 4,948 predicted protein-coding sequences, 1 rRNA operon, 51 tRNAs, and 1 integrated phage, whereas 199 and 87 coding genes were found in plasmids pLA1 and pLA2, respectively. The presence of 38 transposases and 13 phage integrases over the genome demonstrated that genetic rearrangement is widely occurring. Eight copies of transposases and 3 copies of phage integrases are present in pLA1, and 2 transposases are present in pLA2. Strain US6-1 contains 19 total copies of polysaccharide biosynthesis or export-related genes, which explains the sticky nature of the culture broth.

The genome of *N. pentaromativorans* US6-1 showed a high level of homology to the genome of *Novosphingobium aromaticivorans* DSM12444 (GenBank accession no. CP000248), which is able to degrade mono- and biaromatic hydrocarbons (7). Plasmid pLA1 is similar to pCAR3 from *Sphingomonas* sp. strain KA1 and pNL1 from *N. aromaticivorans* DSM12444 in the conjugative region. The PAH catabolic region responsible for PAH degradation was found to be located in plasmid pLA1. Several genes involved in PAH catabolism were also scattered in the chromosomal genome. Interestingly, 3 sets of aromatic-ring-hydroxylating dioxygenase genes commonly exist in aromatic-compound-degrading sphingomonads, *bphA1a*, *bphA2a*, *bphA1b*, *bphA2b*, *bphA1e*, and *bphA2e* in *Sphingobium yanoikuyae* strain B1 (2), the genes carried by pNL1 in *N. aromaticivorans* DSM12444 (7), and *ahdA1a*, *ahdA2a*, *ahdA1b*, *ahdA2b*, *ahdA1e*, and *ahdA2e* in *Sphingomonas* sp. P2 (6); however, only *ahdA1e* and *ahdA2e* were found to be localized in strain US6-1. Since this is the first whole genome of a 5-ring-PAH-degrading bacterium, we assume that strain US6-1 may possess some unknown mechanism in PAH degradation. Further study of degradation metabolism will be carried out with high-molecular-weight PAHs.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AGFM00000000. The version described in this paper is the first version, accession number AGFM01000000.

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