

Draft Genome Sequence of *Novosphingobium* sp. Strain MBES04, Isolated from Sunken Wood from Suruga Bay, Japan

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This report describes the draft genome sequence of *Novosphingobium* sp. strain MBES04, isolated from sunken wood from Suruga Bay, Japan, which is capable of degrading a wide range of lignin-related aromatic monomers. The draft genome sequence contains 5,361,448 bp, with a G+C content of 65.4%.

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The genus *Novosphingobium* is an important group involved in the biodegradation of a wide range of mono- and polycyclic aromatic compounds (1–3). These compounds are widely known as components of fossil fuel and share structural features with lignin, which is produced in terrestrial plants and is the most abundant aromatic biomass on Earth (4). The evolution of microbial pathways for using a wide variety of aromatic molecules as carbon sources was likely triggered by naturally produced aromatic compounds during lignin decomposition by some microorganisms (5). We recently isolated a marine *Novosphingobium* strain, isolated from sunken wood recovered from a depth of 260 m in Suruga Bay, off the Pacific coast of Shizuoka Prefecture, central Japan (6). The strain was found to metabolize a wide range of lignin-related aromatic monomers. To gain deeper insight into the genetic mechanism and evolution in the utilization of terrestrial plant-derived compounds developed in marine bacteria, we sequenced the draft genomic sequence of *Novosphingobium* sp. strain MBES04.

The draft genome of strain MBES04 was sequenced using both 454 GS FLX (454 Life Sciences) and Ion Torrent PGM (Life Technologies). The 454 GS FLX sequencing revealed 142,389 mate-pair reads and 62,888,162 nucleotide bases, with an average read length of 442 bp, whereas the Ion Torrent PGM sequencing revealed 2,652,670 reads and 873,653,659 nucleotide bases, with an average read length of 329 bp. Assembly using Newbler version 2.6 (454 Life Sciences) generated 124 contigs contained in 33 scaffolds (maximum, 3,129,454 bp; minimum, 553 bp). The draft genome consists of 5,361,448 nucleotides with a G+C content of 65.4%. Based on the genomic data, 4,728 coding sequences (CDSs) were predicted by GeneMark (7) and annotated by a BLAST tools search against the GenBank nonredundant protein database (NR) and Kyoto Encyclopedia of Genes and Genomes (KEGG). In addition, 50 tRNAs and 3 rRNAs were identified with the tRNAscan-SE 1.23 (8) and RNAmmer 1.2 (9) servers, respectively.

The draft genome of strain MBES04 showed the presence of a benzoate-degrading gene cluster with the presence of benzoate transporter proteins, 2-chlorobenzoate 1,2-dioxygenase, and genes for the catechol branch of the β -ketoacid pathway (10).

Additionally, genes known to be involved in aromatic compound degradation, including *p*-hydroxybenzoate 3-monooxygenase and vanillate monooxygenase, were also found in the scattered position of the genome. Interestingly, this strain had three copies of the protocatechuate 4,5-dioxygenase α and β subunits for the meta-cleavage pathway of protocatechuate, which is a key compound in lignin-related aromatic compound-degrading pathways (11). Furthermore, the multiple hemicellulose-degrading enzymes, such as xylan 1,4- β -xylosidase, α -*N*-arabinofuranosidase, and the other glucoside hydrolases were classified into glycoside hydrolase families 2, 16, and 43 (see <http://www.cazy.org/Glycoside-Hydrolases.html>).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [BBNP0000000](https://www.ncbi.nlm.nih.gov/nuccore/BBNP0000000). The 124 contigs have been deposited under the accession numbers BBNP01000001 to BBNP01000124.

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