

Draft Genome Sequence of Oil-Degrading Bacterium *Gallaecimonas pentaromativorans* Strain YA_1 from the Southwest Indian Ocean

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Gallaecimonas pentaromativorans has been previously reported to be capable of degrading crude oil and diesel oil. *G. pentaromativorans* strain YA_1 was isolated from the southwest Indian Ocean and can degrade crude oil. This study reports the draft genome sequence of *G. pentaromativorans*, which can provide insights into the mechanisms of microbial oil biodegradation.

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As reported previously, the genus *Gallaecimonas* is composed of only two species, *Gallaecimonas pentaromativorans* and *Gallaecimonas xiamenensis* (1). *G. pentaromativorans* was previously isolated from the Corcubi6n Ria in northwestern Spain, which was a coastal system that was heavily polluted by the Prestige oil spill in 2002 (2). It has been reported that *G. pentaromativorans* can grow vigorously with crude oil and slightly with diesel oil (3). Also, it was revealed that *G. pentaromativorans* can produce biosurfactants through experiments using the hemolytic test, drop collapse, and oil-spreading test, which can promote the oil degradation process by dispersing oil molecules (4). These research results demonstrated that *G. pentaromativorans* has the potential to treat oil pollution. The shotgun sequencing of the *Gallaecimonas pentaromativorans* genome sequence will facilitate the application of *Gallaecimonas* strains in the treatment of oil pollution.

Gallaecimonas pentaromativorans strain YA_1 was isolated from the deep sea of the southwest Indian Ocean at the depth of 2,168 m (49°44'E, 37°37'S). Strain YA_1 has been deposited in Marine Culture Collection of China (accession no. MCCC A11635). The genomic DNA of strain YA_1 was extracted using the bacterial genomic DNA extraction kit (BioTeke, Beijing, China), according to the instructions. The whole-genome shotgun project was performed on an Illumina MiSeq 2000 platform using paired-end (300 bp to ~500 bp) sequencing. First, the raw data were filtered to remove the unqualified data and then assembled using SOAPdenovo version 2.04 (5). GapCloser version 1.12 (6) was used for local gap closure and base correction. The prediction of rRNA and tRNA was performed by Barrnap 0.4.2 (7) and tRNAscan-SE version 1.3.1 (8), respectively. Glimmer 3.02 (9) was used to predict the genes. The genes were annotated by a BLAST search against several databases, including NCBI-NR (nonredundant), string (version 9.05), Gene Ontology (GO), and Kyoto Encyclopedia of Genes and Genomes (KEGG) (10).

The draft genome of *G. pentaromativorans* strain YA_1 is composed of 86 scaffolds, with a total length of 4,325,653 bp and a

G+C content of 58.25%; the largest contig length is 617,526 bp, and the contig N_{50} length is 206,153 bp. According to the Glimmer server, 3,917 genes of 3,821,355-bp total length were predicted. The average gene length is 975 bp, and the G+C content in the gene region is 59.5%. In total, there are 14 predicted enzymes that may be involved in the pathways related to oil degradation, including one *cis*-muconate cycloisomerase (EC 5.5.1.2), three acetyl-coenzyme A (CoA) acyltransferases (EC 2.3.1.16), one 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157), two acetyl-CoA C-acetyltransferases (EC 2.3.1.9), two alcohol dehydrogenases (EC 1.1.1.1), one amidase (EC 3.5.1.4), one homogentisate 1,2-dioxygenase (EC 1.13.11.5), one maleylacetoacetate isomerase (EC 5.2.1.2), one fumarylacetoacetate (FAA) hydrolase (EC 3.7.1.2), and one glutaconate CoA-transferase (EC 2.8.3.12). Clusters of Orthologous Groups of proteins (COG) function classification revealed that there are 156 genes with unknown functions. They account for >9% of 1,724 sequences in total, which means *G. pentaromativorans* strain YA_1 deserves more exploration.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [LFWC00000000](https://www.ncbi.nlm.nih.gov/nuclink/LFWC00000000). The version described in this paper is version LFWC01000000.

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