Genome Sequence of *Gallaecimonas xiamenensis* Type Strain 3-C-1

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Gallaecimonas xiamenensis 3-C-1^T was isolated from a crude-oil-degrading consortium enriched from the surface seawater around Xiamen Island. Here, we present the draft genome of strain 3-C-1^T, which contains 4,062,282 bp with a G+C content of 60.58% and contains 3,798 protein-coding genes and 65 tRNAs.

Gallaecimonas xiamenensis 3-C-1^T (= CCTCC AB 209060^T = LMG 25226^T = MCCC 1A01354^T) was isolated from a crude-oil-degrading consortium enriched from the surface seawater around the Xiamen Island, Taiwan Strait (3, 4). The genus *Gallaecimonas* was first proposed by Rodriguez-Blanco et al. (1) and contained two species at the time of writing. By now, 6 strains of the genus *Gallaecimonas* have been isolated from marine environments in our lab (<http://www.mccc.org.cn>), two of which are close to *G. xiamenensis* 3-C-1^T, and four of which are close to *G. pentaromativorans* CEE_131^T (with 100% similarity of 16S rRNA genes).

The genome sequence of *G. xiamenensis* 3-C-1^T was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using Solexa paired-end sequencing technology. A total of 7,434,109 paired-end reads (500-bp library) were generated to reach a 267-fold depth of coverage with an Illumina/Solexa genome analyzer IIx (Illumina, San Diego, CA), and the gaps among scaffolds were closed by specific PCR and Sanger sequencing, using the ABI 3730 system (Applied Biosystems). The genome of *G. xiamenensis* 3-C-1^T consists of 66 contigs ($N_{90} = 32$) of 4,062,282 bp and had an average G+C content of 60.58%. Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which was followed by manual editing. The genome contains 3,798 candidate protein-encoding genes (with an average size of 970 bp), giving a coding intensity of 90.7%. A total of 2,738 proteins could be assigned to cluster of orthologous groups (COG) families (2). Sixty-five tRNA genes for 18 amino acids (lacking Glu and Ile) were identified.

G. pentaromativorans CEE_131^T was able to degrade polycyclic aromatic hydrocarbons (PAHs) of high molecular mass. However, *G. xiamenensis* 3-C-1^T cannot degrade the tested PAHs, and no PAH-degrading related dioxygenase was found in the genome sequence, nor was there any AlkB-like monooxygenase. The ge-

nome sequence of strain 3-C-1^T and its curated annotation are important assets to better understand the physiology and metabolic potential of *Gallaecimonas xiamenensis* and will open up new opportunities in the functional genomics of this species.

Nucleotide sequence accession number. The draft genome sequence of *G. xiamenensis* 3-C-1^T has been deposited in GenBank under accession no. [AMRI000000000](https://www.ncbi.nlm.nih.gov/nuccore/AMRI000000000) (chromosome).

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