Genome Sequence of *Nitratireductor indicus* Type Strain C115

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***Nitratireductor indicus* strain C115^T was isolated from a crude-oil-degrading consortium enriched from deep seawater of the Indian Ocean. Here, we present the draft genome of strain C115^T, which contains 4,992,479 bp with a G+C content of 60.8% and contains 4,825 protein-coding genes and 45 tRNA genes.**

Nitratireductor indicus strain C115^T (CCTCC AB 209298^T, LMG 25540^T, MCCC 1A01260^T) was isolated from a crude-oil-degrading consortium enriched from deep seawater of the Indian Ocean (2). The genus *Nitratireductor* was first proposed by Labbé (1), and it currently comprises seven species (3). Up to now, only one strain of this species was isolated from a marine environment (<http://www.mccc.org.cn>), and 49 strains of the genus *Nitratireductor* were collected in MCCC (Marine Culture Collection of China), though most of them belong to the species of *Nitratireductor aquibiodomus* (38 strains).

The genome sequence of *N. indicus* C115^T was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using Solexa paired-end sequencing technology. A total of 6,553,341 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 among scaffolds were closed by custom primer walks or by PCR amplification followed by DNA sequencing. The genome of *N. indicus* C115^T consists of 75 contigs (>200 bp; $N_{90} = 20$) of 4,992,479 bp and had an average G+C content of 60.8%. 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>), followed by manual editing. The genome contains 4,825 candidate protein-encoding genes (with an average size of 925 bp), giving a coding intensity of 89.5%. A total of 3,560 proteins were assigned to cluster of orthologous groups (COG) families (4). Forty-five tRNA genes for all 20 amino acids were identified.

Strain C115^T cannot use *n*-alkanes or polycyclic aromatic hydrocarbons (PAHs) as the sole carbon source for growth, though it was isolated from a crude-oil-degrading consortium. The genome sequence analysis failed to reveal any alkane-degrading monooxygenase or PAH-degrading dioxygenase. The genome sequence of

strain C115^T and its curated annotation are important assets to better understand the physiology and metabolic potential of *Nitratireductor indicus* and will open up new opportunities in the function analysis of this species in an oil-degrading consortium.

Nucleotide sequence accession number. The draft genome sequence of *Nitratireductor indicus* C115^T has been deposited in GenBank under accession number [AMSI000000000](https://www.ncbi.nlm.nih.gov/nuccore/AMSI000000000) (chromosome).

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