



Genome Announcements

Draft genome of *Nocardia farcinica* TRH1, a linear and polycyclic aromatic hydrocarbon-degrading bacterium isolated from the coast of Trindade Island, Brazil

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ABSTRACT

Here, we report the draft genome sequence and annotation of *Nocardia farcinica* TRH1, a petroleum hydrocarbons degrading Actinobacteria isolated from the coastal water of Trindade Island, Brazil.

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Several species of the genus *Nocardia* are known to degrade hydrocarbons.¹ The strain *Nocardia farcinica* TRH1 was isolated from the coastal water of Trindade Island, a pristine oceanic island in Brazil.² It is capable of growing using several petroleum hydrocarbons as the sole source of carbon and energy, such as phenanthrene, pyrene, anthracene, eicosane, pentacontane, triacontane, tetracosane, naphthalene, hexadecane, octane, toluene and xylene.²

Genome sequencing of *N. farcinica* TRH1 was performed using the Ion Torrent PGM platform (ThermoFisher Scientific). Briefly, the genomic DNA was fragmented using the Bioruptor UCD-200. The template library was prepared with the Ion Plus fragment library kit and clonally amplified in the One Touch System with the Ion PGM template OT2 400 kit. The amplified library was sequenced using the Ion PGM sequencing 400 kit within the 318 v2 microchip. A total of

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2531733 reads were obtained with sizes ranging from 25 to 492 bp in length. The reads were filtered for length (minimum, 100 bp) and quality (minimum score, Q20) and used for *de novo* assembling using CLC Genomics Workbench version 6.5.1 (CLC bio). From assembling, we obtained 321 contigs, corresponding to 5230013 bp, with an average size (N_{50}) of 9853 bp, longest contig size of 122221 bp, G+C content of 68.0% and genome coverage of 52.53X. Genes from the contigs were predicted using GeneMarkS,³ which revealed 4946 coding sequence set (CDS). The protein sets were functionally annotated using BLAST (<http://blast.ncbi.nlm.nih.gov/>), and approximately 68.6% of the proteins were assigned to Clusters of Orthologous Groups (COG) families.⁴

Genome annotation was performed using BlastKOALA⁵ and revealed 1869 protein-coding-sequences, including 106 related with xenobiotics biodegradation and metabolism, and 309 unclassified. The KEGG Automatic Annotation Server (KASS)⁶ was used for pathways analysis, which identified 516 genes related to metabolic pathways, including 21 genes related to biodegradation of aromatic compounds.

KASS also identified the presence of *catA* and *dmpC*, which are among the genes of the catabolic pathways of ortho and meta-cleavage of catechol, respectively. Catechol is a toxic intermediate generated during the biodegradation of polycyclic aromatic hydrocarbons.⁷ Furthermore, several genes were identified as being related to biodegradation of aliphatic hydrocarbons as the *alkB* gene. We also found *aldH*, *paaF*, *fadB* and *fadJ* genes related to biodegradation of the nylon precursor caprolactam, as well as the *atzD* gene, related to the degradation of the pesticide atrazine, showing another possibility for biotechnological applications of this strain.

The abundance of genes involved in biodegradation pathways in the genome of *N. farcinica* TRH1 implies in high metabolic plasticity of this strain, what is consistent with the results obtained during the screening of bacteria for hydrocarbon biodegradation.² The genome sequencing data from this study will support a better understanding of the metabolism and the potential applications of *N. farcinica* TRH1 in biotechnological processes, as hydrocarbons and xenobiotics bioremediation.

Nucleotide sequence accession numbers: This WGS Bio-Project has been deposited at DDBJ/EMBL/GenBank under the accession number PRJNA322144 and the sequences under the accession number LYCQ00000000. The versions described in this paper are the first versions.

Conflicts of interest

The authors declare no conflicts of interest.

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