



Genome Announcements

Draft genome analysis of *Dietzia* sp. 111N12-1, isolated from the South China Sea with bioremediation activity

Shanjun Yang¹, Mingjia Yu^{*,1}, Jianming Chen

State Oceanic Administration, Third Institute of Oceanography, Engineering Research Center of Marine Biological Resource Comprehensive Utilization, Xiamen, Fujian Province, People's Republic of China

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ABSTRACT

Dietzia sp. 111N12-1, isolated from the seawater of South China Sea, shows strong petroleum hydrocarbons degradation activity. Here, we report the draft sequence of approximately 3.7-Mbp genome of this strain. To the best of our knowledge, this is the first genome sequence of *Dietzia* strain isolated from the sea. The genome sequence may provide fundamental molecular information on elucidating the metabolic pathway of hydrocarbons degradation in this strain.

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Genome Announcement

Dietzia sp. is a Gram-positive bacteria belonging to the order actinomycetales. Owing to their ability to degrade petroleum hydrocarbons and crude oil, members of the genus *Dietzia* have gained considerable economic importance and research focus.^{1,2} Although species from nearly 65 genera have the ability to degrade hydrocarbons and are widely distributed in nature, few are known to utilize a wide range of *n*-alkanes. Recently few of the *Dietzia* strains have been reported to act on a wide range of saturated hydrocarbons,^{1,2} and also possess the unique ability to degrade aromatic compounds including naphthalene, phenanthrene, benzoate and

fluoranthene, amongst others.² The ability to degrade *n*-alkanes has been attributed to the presence of two key genes in the genome of hydrocarbon degrading bacteria,³ the integral-membrane alkane monooxygenase (AlkB)-like hydroxylases and cytochrome P450 enzyme CYP153.³ Although several strains of *Dietzia* sp. have been sequenced before,^{4–6} yet a high quality genome of a marine *Dietzia* strain from the South China Sea is entirely lacking. Here, we report the complete genome sequence of *Dietzia* sp. 111N12-1, isolated from the seawater of South China Sea.

Dietzia sp. 111N12-1 was cultured in 2216E medium and incubated at 25 °C, 200 rpm for 48 h. The genomic DNA was isolated using commercially available DNA extraction kit from

* Corresponding author at: Engineering Research Center of Marine Biological Resource Comprehensive Utilization, Third Institute of Oceanography, State Oceanic Administration, Xiamen 361005, China.

E-mail: yumingjia@tio.org.cn (M. Yu).

¹ These authors contributed equally to this work.

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TIANGEN Biotech (Beijing), China. The genome sequence of *Dietzia* sp. 111N12-1 was obtained by paired-end sequencing on Illumina MiSeq platform at MajorBio, Shanghai. Reads were assembled using SOAPdenovo software v2.04.⁷ Protein-coding sequences were predicted by Glimmer software v3.02⁸ and annotated using BLAST searches of non-redundant (nr) protein sequences from the NCBI, COG,⁹ Gene Ontology (GO)¹⁰ and KEGG database.¹¹ rRNA genes were detected using RNAmmer software¹² and tRNA genes were detected using tRNAscan-SE.¹³ To scan for the presence of hydrocarbon degrading genes, the sequence of AlkB like hydroxylase and CYP153 from various available *Dietzia* strains were blasted (tblastx, NCBI) against the draft genome of *Dietzia* sp. 111N12-1. The gene sequences were aligned using the software ClustalW2.

The draft genome of *Dietzia* sp. 111N12-1 comprises 114 scaffolds, with an N50 125,068 bp, approximately 3.7-Mbp with 70.24% GC content. The size of the genome is larger than that of previously sequenced *Dietzia cinnamomea* strain P4 (3.5-Mbp) and *Dietzia alimentaria* 72^T (3.3-Mbp), but was smaller than *Dietzia* sp. strain UCD-THP (3.9-Mbp), with GC content more or less similar to the three sequenced strains.^{4–6} The genome of *Dietzia* sp. 111N12-1 encodes 3570 proteins, and the total length of genes was 3,321,267 bp, which makes up for 87.9% of the genome. The genome also encodes 49 tRNAs and 2 rRNAs. The gene encoding putative CYP153 protein was identified which contains 446 predicted amino acids. It shared a 99% and 99% amino acid similarity with CYP153 proteins from *Dietzia* sp. strain UCD-THP and *D. cinnamomea* strain P4, respectively. Similarly, AlkB like hydroxylase was 83% and 82% identity to from *Dietzia* sp. strain UCD-THP and *D. cinnamomea* strain P4, respectively. This study provided an excellent platform to study the genetics and physiology of a potent bioremediation tool from the South China Sea.

Nucleotide sequence accession number

This Whole Genome Sequencing project has been deposited at DDBJ/EMBL/GenBank under the accession LSSV00000000.

Conflicts of interest

The authors declare no conflicts of interest.

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