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Genome Announcements

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

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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.

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

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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 v3.02[8] 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 software[12] and tRNA genes were detected using tRNAscane-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 cinnamea* 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. cinnamea* strain P4, respectively. Similarly, AlkB like hydroxylase was 83% and 82% identity to from *Dietzia* sp. strain UCD-THP and *D. cinnamea* 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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REFERENCES

1. von der Weid, Marques JM, Cunha CD, et al. Identification and biodegradation potential of a novel strain of *Dietzia cinnamea* isolated from a petroleum-contaminated tropical soil. *System Appl Microbiol*. 2007;30:331–339.
2. Wang XB, Chi CQ, Nie Y, et al. Degradation of petroleum hydrocarbons (C6-C40) and crude oil by a novel *Dietzia* strain. *Bioresour Technol*. 2011;102:7755–7761.
3. Nie Y, Chi CQ, Fang H, et al. Diverse alkane hydroxylase genes in microorganisms and environments. *Sci Rep*. 2014;4:4968.
4. Procópio L, Alvarez VM, Jurelevicius DA, et al. Insight from the draft genome of *Dietzia cinnamea* P4 reveals mechanisms of survival in complex tropical soil habitats and biotechnology potential. *Antonie Van Leeuwenhoek*. 2012;101:289–302.
5. Kim J, Roh SW, Bae JW. Draft genome sequence of *Dietzia alimentaria* 72T, belonging to the family *Dietziaceae*, isolated from a traditional Korean food. *J Bacteriol*. 2011;193:6791.
6. Diep AL, Lang JM, Darling AE, et al. Draft genome sequence of *Dietzia* sp. strain UCD-THP (Phylum Actinobacteria). *Genome Announc*. 2013;1:e00197–e213.
7. Li R, Li Y, Kristiansen K, et al. SOAP: short oligonucleotide alignment program. *Bioinformatics*. 2008;24:713–714.
8. Delcher AL, Bratke KA, Powers EC, et al. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics*. 2007;23:673–679.
9. Tatusov RL, Fedorova ND, Jackson JD, et al. The COG database: an updated version includes eukaryotes. *BMC Bioinforma*. 2003;4:41.
10. Ashburner M, Ball CA, Blake JA, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat Genet*. 2000;25:25–29.
11. Kanehisa M, Goto S, Kawashima S, et al. The KEGG resource for deciphering the genome. *Nucl Acids Res*. 2004;32:D277–D280.
12. Lagesen K, Hallin P, Rodland EA, et al. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucl Acids Res*. 2007;35:3100–3108.
13. Lowe TM, Eddy SR. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucl Acids Res*. 1997;25:955–964.