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Complete genome sequence of polycaprolactone-degrading *Janibacter terrae* strain COS04-44, isolated from tide flat polluted with crude oil

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원유 오염 갯벌 토양에서 분리한 *Janibacter terrae* COS04-44 균주의 유전체 염기서열

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Janibacter terrae strain COS04-44, a bacterium that degrades polycaprolactone (PCL), was isolated from crude oil-contaminated tidal flat in Taean, Republic of Korea. *Janibacter terrae* strain COS04-44 has a genome that is 98.85% identical to that of *J. terrae* NBRC 107853^T and consists of one circular chromosome with 3,394,906 bp. *J. terrae* COS04-44 has 3,299 protein-coding genes and 58 non-coding RNAs. The G + C content of the genome is 71.9%. These findings provide information on various biodegradable polymer-degrading enzymes and compare differences among the complete genome of the current members of the *Janibacter* genus.

Keywords: *Janibacter terrae*, PCL-degrading bacterium, whole genome sequence

Janibacter terrae, isolated from soil surrounding wastewater treatment plants in Republic of Korea, was first reported by Yoon *et al.* (2000) as a novel species. *Janibacter terrae* degrades trichlorethylene (Imamura *et al.*, 2000; Lang *et al.*, 2003). *Janibacter terrae* strain COS04-44 was isolated using R2A agar medium under aerobic conditions at 28°C from a sea sand sample from the coast of Taean, Republic of Korea, where an oil spill occurred in 2007. Strain identification by 16S rRNA gene amplification and sequencing was carried out as in previously described (Mignard and Flandrois, 2006). The strain was classified as a member of the genus *Janibacter* by phylogenetic comparison of the 16S rRNA gene using MEGA 11 (Tamura *et al.*, 2021). The 16S rRNA gene sequence of COS04-44 was shown to be 98.85% identical to that of *J. terrae* NBRC 107853^T. COS04-44 cell color was light yellow, and it showed a maximum OD_{600} within 24 h of growth in R2A medium. Strain COS04-44 can decompose polycaprolactone (PCL). Growth was observed in minimal medium containing 0.1% PCL as the sole carbon source. In addition, a clear zone, with an area of 2.6 ± 0.3 cm^2, was formed around colonies grown in minimal agar medium containing PCL after 20 days.

Genomic DNA of COS04-44 was extracted by the DNeasy UltraClean microbial kit (QIAGEN) and sequenced using the PacBio Sequel System and Illumina HiSeq platform at Macrogen Inc. PacBio Sequel sequencing results were assembled *de novo* using SMRT Link version 8.0 (Du *et al.*, 2021). Pilon version 1.21 was used to rectify any faults in the constructed sequence. Subread searches with the NCBI database using BLAST

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Table 1. Genome features of *Janibacter terrae* COS04-44

Genome feature	Chromosome
Genome size (bp)	3,394,906
G + C content (%)	71.9
Total genes	3,347
tRNAs	51
rRNAs (5S, 16S, 23S)	6 (1, 1, 4)
Pseudogenes	141
GenBank accession No.	CP104874

version 2.7.1 enabled pre-assembled read quality checks. After the genome was assembled, gene predictions and functional annotations were performed by the NCBI Prokaryotic Genomes Annotation Pipeline and Rapid Annotation Subsystem Technology (Tatusova *et al.*, 2016).

The total number of bases in the filtered data was 4,090,971,860, with 27,101,004 reads. There were 8,508 bases in the mean subread and 11,105 bases in the N50 read. The genome comprised a single chromosome of 3,394,906 bp, with an average reference coverage of 201.1×. The entire genome contained 3,357 genes discovered, of which 3,299 were predicted to contain coding sequences (CDS), 51 tRNA, 5 rRNAs, and 141 pseudogenes. The G + C content is 71.9% (Table 1). Strain COS04-44 shared 98.85% nucleotide sequence identity with *J. terrae* NBRC 107853^T, according to the Orthologous Average Nucleotide Index (OrthoANI, OAT v0.93).

Esterase, cutinase, and lipase are enzymes involved in the degradation of PCL (Zhu *et al.*, 2022). Strain COS04-44 genome encodes esterases and lipases, which are thought to play a role in cleaving PCL. Lipase 1 extracted from *Pelosinus fermentans* showed degradation activity against the poly (1,4-butylene adipate-co-terephthalate) polyester (Almeida *et al.*, 2019). Based on this findings, we speculated that lipase 1 of strain COS04-44 is also important in the degradation of PCL (Urbanek *et al.*, 2020). Information on enzymes involved in polyester degradation of strain COS04-44 is expected to contribute to degradation studies of various polyesters such as PCL. Research on the decomposition of various polyesters as well as PCL is anticipated. The genetic resources of strain COS04-44 obtained through genome sequencing can be used to engineer microorganisms that will efficiently degrade PCL, which will help hasten international efforts to reduce plastic-related pollution and degrade plastics.

Nucleotide sequence accession number

Janibacter terrae COS04-44 has been deposited in the Korean Agricultural Culture Collection with the accession number KACC 81218BP. GenBank accession number CP104874 have been assigned to this whole-genome study.

적 요

폴리카프로락톤(PCL) 분해균인 *Janibacter terrae* COS04-44 균주는 대한민국 태안의 원유로 오염된 갯벌에서 분리되었다. COS04-44 균주의 유전체는 *J. terrae* NBRC 107853^{T}와 유사도가 98.85%이었으며 3,394,906 bp의 하나의 원형 염색체로 구성된다. COS04-44 균주는 3,299개의 단백질 암호화 유전자와 58개의 비암호화 RNA를 가지고 있으며 유전체 G + C 함량은 71.9%이다. 본 연구는 다양한 생분해성 고분자 분해효소에 대한 정보를 제공할 뿐만 아니라 완전한 유전체정보를 제공하여 현재의 *Janibacter* 속과의 차이점을 비교할 수 있는 데이터를 제공한다.

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Conflict of Interest

The authors have no conflict of interest to report.

References

Almeida BC, Figueiredo P, and Carvalho AT. 2019. Polycaprolactone enzymatic hydrolysis: a mechanistic study. *ACS Omega* **4**, 6769–6774.

Du Z, Sun L, Lin Y, Yang F, and Cai Y. 2021. The use of PacBio SMRT technology to explore the microbial network and fermentation characteristics of woody silage prepared with exogenous carbohydrate additives. *J. Appl. Microbiol.* **131**, 2193–2211.

Imamura Y, Ikeda M, Yoshida S, and Kuraishi H. 2000. *Janibacter*

brevis sp. nov., a new trichloroethylene-degrading bacterium isolated from polluted environments. *Int. J. Syst. Evol. Microbiol.* **50**, 1899–1903.

Lang E, Kroppenstedt RM, Swiderski J, Schumann P, Ludwig W, Schmid A, and Weiss N. 2003. Emended description of *Janibacter terrae*, including ten dibenzofuran-degrading strains and *Janibacter brevis* as its later heterotypic synonym. *Int. J. Syst. Evol. Microbiol.* **53**, 1999–2005.

Mignard S and Flandrois JP. 2006. 16S rRNA sequencing in routine bacterial identification: a 30-month experiment. *J. Microbiol. Methods* **67**, 574–581.

Tamura K, Stecher G, and Kumar S. 2021. MEGA11: molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* **38**, 3022–3027.

Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, and Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res.* **44**, 6614–6624.

Urbanek AK, Mirończuk AM, García-Martín A, Saborido A, de la Mata I, and Arroyo M. 2020. Biochemical properties and biotechnological applications of microbial enzymes involved in the degradation of polyester-type plastics. *Biochim. Biophys. Acta Proteins Proteom.* **1868**, 140315.

Yoon JH, Lee KC, Kang SS, Kho YH, Kang KH, and Park YH. 2000. *Janibacter terrae* sp. nov., a bacterium isolated from soil around a wastewater treatment plant. *Int. J. Syst. Evol. Microbiol.* **50**, 1821–1827.

Zhu B, Wang D, and Wei N. 2022. Enzyme discovery and engineering for sustainable plastic recycling. *Trends Biotechnol.* **40**, 22–37.