



# Complete genome sequence of phenol biodegrading bacterium, *Microbacterium* sp. ABRD28, isolated from petroleum-contaminated stream sediment

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## 석유로 오염된 수변 침전물로부터 분리한 페놀 분해 미생물 *Microbacterium* sp. ABRD28의 전장 유전체 서열

정상은 · 강혜경 · 조복연 · 류병곤 · 이미화 · 진현미\* 

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The *Microbacterium* sp. ABRD28, capable of degrading phenol, was isolated from contaminated petroleum-contaminated stream sediment. Here, we investigate the whole genome sequence of *Microbacterium* sp. ABRD28. Its whole genome only contains a circular single chromosome without plasmid and consist of total 3,266,665 bp length with 69.7 % G + C contents. A total of 3,170 genes were predicted, comprising 3,118 coding DNA sequences (CDSs), 46 tRNAs, 3 rRNAs, and 3 noncoding RNAs (ncRNAs). The genome of strain ABRD28 has putative genes encoding the phenol oxidation protein such as phenol hydroxylase, peroxidase and polyphenol oxidase.

**Keywords:** *Microbacterium*, bioremediation, phenol degradation

The genus *Microbacterium* was first proposed by Orla-Jensen (1919) as a novel species more than 129 species have been published so far (<https://lpsn.dsmz.de/genus/microbacterium>). The member of genus *Microbacterium* have been generally isolated from a wide range of sources, such as soil, plants, water, animals including oil-contaminated sediment (Fidalgo *et al.*, 2016) and these strains which often produce yellow colonies after growth on nutrient-rich media are Gram positive,

non-spore-forming rods. The average genome size of reported strains, belonging to genus *Microbacterium*, is approximately 3.46 Mb encoding 3246 genes and the GC contents range between 63 and 75 % (median value 69.6 %, NCBI database, <https://www.ncbi.nlm.nih.gov/genome/14190>). Here, we suggest the complete genome sequence of newly isolated bacterium, *Microbacterium* sp. ABRD28, which containing putative genes related with phenol degradation.

A new phenol degradation bacterium, *Microbacterium* sp. ABRD28, was isolated from petroleum-contaminated sediment by enrichment cultivation with phenol as sole carbon source and a time-course experiment showed that strain is able to utilize phenol for biomass production (data not shown). The gDNA was purified by Wizard Genomic DNA Purification kit (Promega) from the colonies grown on R2A agar during 3 days. The purified genomic DNA was completely sequenced by PacBio RSII system with a error correction by Illumina Hiseq 4000 sequencing. Briefly, the sequencing library (total 20-kb) was constructed using a PacBio DNA Template Prep Kit 1.0 and analyzed by single-molecule real-time (SMRTbell™) sequencing at Macrogen. *De novo* assembly of the sequencing reads was performed through the hierarchical genome assembly

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**Table 1.** General genomic features of the *Microbacterium* sp. ABRD28

Feature	Chromosome
GenBank accession	CP031015
Genome size (bp)	3,266,665
G + C content (%)	69.7
No. of contig	1
Total no. of genes (including pseudo genes)	3,170
No of coding sequence (CDS)	3,118
No of pseudo gene sequence	29
No of rRNA (5S, 16S, 23S)	3
No of tRNA	46
No of ncRNA (3S)	3

process (HGAP 2, version 2.3.0), and paired-end reads (101 bp) obtained from the Illumina sequencing were mapped on assembled contig for error corrections (pilon, v1.22). The genome was annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Tatusova *et al.*, 2016).

Total of 1,054,930,370 bp consisting 107,489 sequencing reads (N50, 13,840 bp) was yielded from PacBio platform. After *de novo* assembly and error correction, we verified that the genome of strain ABRD28 was complete, with a circular form of 3,266,665 bp and a GC content of 69.7%. Sequencing depth is about 270.0 times. The whole genome of strain ABRD28 consisting of a circular single chromosome without plasmid have been deposited in GenBank with the accession numbers of CP031015. After genomic annotation, a total of 3,170 genes were predicted, comprising 3,118 coding DNA sequences (CDSs), 52 tRNAs, 3 rRNAs, and 3 noncoding RNAs (ncRNAs) and these genome feature of strain ABRD28 are presented in Table 1.

Phenols are toxic pollutants that can be detected in effluent environments from coal conversion processes, petrochemical plants, and oil refining. In microbial biodegradation of phenol under aerobic condition, the first step include oxygenation of this monoaromatic hydrocarbon by hydroxylation enzyme such as hydroxylase, peroxidase, laccase and polyphenol oxidase (Sridevi *et al.*, 2012). The genome of strain ABRD28 contains more than 11 oxygenase genes related with catalyzing oxidation of various organic compounds such as aromatic hydrocarbon. In particular, genes annotated as peroxidase (DT073\_RS07045 and DT073\_RS07990) probably degrading of phenol are identified.

## Nucleotide sequence accession number

The whole-genome sequence was deposited in GenBank under accession number CP031015.

## 적 요

페놀 분해능력을 보유한 미생물인 *Microbacterium* sp. ABRD28 균주는 석유로 오염된 수변 침전물로부터 분리되었다. 이 보고문에서는 ABRD28 균주의 전장 유전체에 대해 서술한다. 해당 균주는 플라스미드가 없는 원형으로 완성된 하나의 염색체를 갖고 있으며, 전체 3,266,665 bp 크기와 69.7%의 GC 함량을 나타낸다. 유전체로부터 분석된 3,170개의 유전자는 3,118개의 CDS, 46개의 tRNA, 3개의 rRNA 및 3개의 noncoding RNA 유전자로 구성되어 있다. ABRD28 균주는 peroxidase와 같은 잠재적 페놀분해유전자를 함유하고 있다.

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## Conflict of Interest

The authors have no conflict of interest to report.

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