


# Genome sequence of *Microbacterium* sp. STF-2 isolated from expanded polystyrene in landfill

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## 쓰레기 매립지의 스티로폼 조각에서 분리한 *Microbacterium* sp. STF-2균주의 유전체 서열

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In this study, we report the genomic information of the microorganism, belonging to the genus *Microbacterium*, isolated from expanded polystyrene in an unsanitary landfill in South Korea. The draft genome of strain STF-2 is composed of 3.9 Mb (68.4% G + C), including 3,839 protein-coding genes, 5 rRNA genes, and 48 tRNAs. Genes involved in detoxification of heavy metals and degradation of aromatic compound were identified. It might support the potential of strain STF-2 to resist the effects of a variety of contaminated substances in landfill.

**Keywords:** *Microbacterium*, landfill, mercury

As the importance of municipal solid waste (MSM) disposal and management increases, landfill-related research has conducted in various fields including study of microbial communities (Meyer-Dombard *et al.*, 2020). To understand the microbial communities in landfill, culture-dependent and culture-independent studies have been conducted (Meyer-Dombard *et al.*, 2020). However, most studies focused on landfill leachate (Meyer-Dombard *et al.*, 2020; Zhao *et al.*, 2021; Gu *et al.*, 2022). In this study, genomic analysis

performed of a bacterium isolated from coring sample of landfill during the study to analyze the microbial diversity of landfill.

Sample was carried out using core drilling from landfill. A piece of expanded polystyrene was obtained from a depth of 16 m. The portion of the fragment was moved to a new conical tube and suspended in phosphate saline solution. Serially diluted solutions were spread on R2A plate and a yellow colony among several colonies was selected for further study. To identify the yellow colony, named as STF-2, a genomic DNA was extracted by DNeasy blood & tissue kit (Qiagen). 16S rRNA gene was amplified and sequenced using 27F and 1492R (Lane, 1991). Finally, strain STF-2 was classified to genus *Microbacterium* belonging to *Actinomycetota* using Ezbiocloud (Yoon *et al.*, 2017). The production of DNA library (TruSeq Nano DNA kit) and sequencing of strain STF-2 by Illumina HiSeqX were performed at Macrogen Inc. The obtained raw reads were qualified by FastQC and assembled by SPAdes (v. 3.15) (Bankevich *et al.*, 2012), with 145 × coverage. The assembled genome was annotated with Prokaryote Genomes Automatic Annotation Pipeline (PGAAP) (Tatusova *et al.*, 2016). Signal peptides and transmembrane structures were predicted using SignalP (Almagro Armenteros *et al.*, 2019) and

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**Table 1.** General genomic features of *Microbacterium* sp. STF-2.

Features	STF-2
Length	3,935,905 bp
G + C	68.4
Number of scaffolds	5
Total genes	3,839
Total coding genes	3,773
rRNAs (5S, 16S, 23S)	3*,1,1
tRNAs	48
Accession number	JARKMW000000000

\*Two partial rRNAs were included.

TMHMM (Krogh *et al.*, 2001), respectively.

The genome of strain STF-2 composes 5 scaffold with a length of 3,935,905 bp (G + C content, 68.4%), including 3,773 coding genes, 5 rRNAs and 48 tRNAs (Table 1). Comparison of 16S rRNA gene with the closet related strain showed 100% similarity with *Microbacterium oxydans* DSM 20578<sup>T</sup> but the average nucleotide identity was 86%. It showed that strain STF-2 could be a new species in the genus *Microbacterium*, according to new species criteria (Jain *et al.*, 2018).

An extracellular type of intradiol ring-cleavage dioxygenase (MicroSTF\_17290) was found in this genome, which catalyzes the decyclization reaction of aromatic ring structures (Kumar *et al.*, 2018). Also, the genome of strain STF-2 encoded Poly (3-hydroxybutyrate) (PHB) depolymerase family esterase (MicroSTF\_02155). PHB depolymerase is known as the enzyme that hydrolyzes PHB, which is one of the biodegradable plastics. The availability of plastic degradation of strain STF-2 need to check in further study because the gene encoded PHB depolymerase was intracellular type.

Since MSM includes industrial wastes, consumer electronics and household products that contain mercury, mercury can affect the microbial ecosystem in landfills (Lee *et al.*, 2016). This genome contained organomercurial lyase (MerB, MicroSTF\_111570) and mercuric reductase (MerA, MicroSTF\_111575), that can detoxify methylmercury and inorganic mercury to gaseous elemental mercury. In addition, genes related to heavy metal resistance were observed in the genome such as chromate resistance protein ChrB (MicroSTF\_11405) and arsenate reductase ArsC (MicroSTF\_05220). The detoxification mechanisms of heavy metals of strain STF-2 might enhance the survival ability in landfill.

## Nucleotide sequence accession number

Strain STF-2 has been deposited at Korean Collection for Type Cultures as KCTC 49960 and the genome sequence has been deposited at GenBank under the accession number JARKMW000000000.

## 적 요

본 연구는 대한민국의 비위생 매립지에서 채취한 스티로폼 시료로부터 분리한 *Microbacterium* 속에 속하는 미생물의 계통 정보를 보고한다. STF-2 균주의 게놈 초안은 3,839개의 단백질 코딩 유전자, 5개의 rRNA 유전자 및 48개의 tRNA를 포함하여 3.9 Mb (68.4% G + C)로 구성된다. 중금속 해독 및 방향족 화합물 분해에 관여하는 유전자가 확인되었다. 이는 다양한 오염 물질의 영향에 저항하는 STF-2 균주의 잠재력을 뒷받침할 수 있다.

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## Conflict of Interest

So-Jeong Kim is Editor of KJM. Dr. Kim was not involved in the review process of this article. Also, authors have no conflicts of interest to report.

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