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Data Article

# Draft genome sequence and morphological data of *Planifilum fimeticola* PLACP1, a thermophilic chloramphenicol-resistant bacterium isolated from thermophilic sludge

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A R T I C L E I N F O

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A B S T R A C T

*Planifilum* is a thermophilic aerobic Actinomyces often found in compost that is suggested to play a primary role in the degradation of organic matter and is a potential antibiotic-resistance gene (ARG)-hosting bacterium during the composting process. *Planifilum fimeticola* PLACP1 was isolated from thermophilic sludge on a Columbia plate supplemented with chloramphenicol. PLACP1 was Gram-stain-positive with cells longer than 20 $\mu$m that branched and intertwined with each other. A draft genome sequence of *P. fimeticola* PLACP1 was generated using the Illumina NovaSeq system and deposited in the National Center for Biotechnology Information database under the BioProject accession numbers PRJDB17484 and SAMD00736731. The genome sequence comprised 3,395,140 bp, with 57.97 % GC content and 3,368 genes, including 3,267 protein-coding, 6 rRNA, and 56 tRNA genes. Based on the Comprehensive Antibiotic Resistance Database, 237 predicted gene products were related to ARGs, including 44 macrolide antibiotic-related genes (19 %) as the largest group. This dataset will be beneficial for the morphological identification, comparative genomic analyses, and ARG research in the genus *Planifilum*.

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Specifications Table

| | |
|---|---|
| Subject | Biological Sciences |
| Specific subject area | Microbiology, Genomics |
| Data format | Raw and Analysed Data |
| Type of data | Draft genome sequence data<br>Figure<br>Table |
| Data collection | *Planifilum Fimeticola* PLACP1 was isolated from thermophilic sludge via the pour plate method using a Columbia plate supplemented with chloramphenicol. Whole-genome sequencing libraries were constructed using a VAHTS Universal DNA Library Prep Kit and the Illumina NovaSeq 6000 system. Software used for genome assemblies included Velvet, SSPACE, and GapFiller. The draft genome assemblies were further analysed using the DDBJ Fast Annotation and Submission Tool, Comprehensive Antibiotic Resistance Database, and Type (Strain) Genome Server for a phylogenomic analysis. The genome map was generated using Proksee. |
| Data source location | Institution: Tokyo University of Agriculture<br>City/Town/Region: Setagaya-ku, Tokyo<br>Country: Japan |
| Data accessibility | The draft genome sequence data for P. fimeticola PLACP1 were deposited in the National Center for Biotechnology Information (NCBI) GenBank database<br>Accession number: BAABOJ010000000<br>Direct URL: https://www.ncbi.nlm.nih.gov/nuccore/BAABOJ010000000<br>BioProject: PRJDB17484<br>Direct URL: https://www.ncbi.nlm.nih.gov/bioproject/PRJDB17484<br>BioSample: SAMD00736731<br>Direct URL: https://www.ncbi.nlm.nih.gov/biosample/SAMD00736731<br>Sequence Read Archive (SRA): DRR530440<br>Direct URL: https://trace.ncbi.nlm.nih.gov/Traces?run=DRR530440 |

## 1. Value of the Data

- These data on *P. fimeticola* PLACP1 provide essential information on the genes and morphological characteristics of *Planifilum* isolated from thermophilic sludge.
- The prediction of the ARG of *P. fimeticola* PLACP1 is summarised, providing a basis for understanding the ARG composition of *Planifilum* during composting.
- These data will be beneficial to researchers focusing on microbial genomics, especially thermophilic composting processes and ARGs.
- The data presented here can be used for the morphological identification and comparative genomic analyses of *Planifilum*.

## 2. Background

*Planifilum* is a thermophilic aerobic Actinomyces often found in compost and has been suggested to play a primary role in the degradation of organic matter during the late composting or maturation period [1–3]. During composting using manure, *Planifilum* was reported to potentially host antibiotic-resistance genes (ARGs) [4]. Recently, many ARGs in livestock manure have been shown to pose a serious safety risk to ecosystems, which has drawn great attention to their control [3]. Although genomic data are available for *Planifilum fimeticola* DSM 44946

(PVNE00000000) *and P. fulgidum* DSM 44945 (FOOK00000000), knowledge of the genomic characteristics and ARG features of *Planifilum* remains insufficient. This study aimed to provide morphological observations, draft genome sequence data, and ARG predictions for *P. fimeticola* for the benefit of researchers working on microbial genomics and ARG.

## 3. Data Description

After 72 h of cultivation at 60°C on a Columbia plate, the colony of *P. fimeticola* PLACP1 was approximately 1 mm in size, cream-yellow coloured, and had a slightly matte surface with irregular shape and undulate margin (Fig. 1A). Cells of *P. fimeticola* PLACP1 were Gram-stain-positive with a size longer than 20 $\mu$m which branched and intertwined with each other (Fig. 1B). The draft genome sequence of *P. fimeticola* PLACP1 (accession number BAABOJ010000000) is available in the National Center for Biotechnology Information database under the BioProject number PRJDB17484 and BioSample number SAMD00736731 (Table 1). Raw reads (19,194,214 total reads) were deposited in the NCBI Sequence Read Archive (SRA) database (DRR530440). The

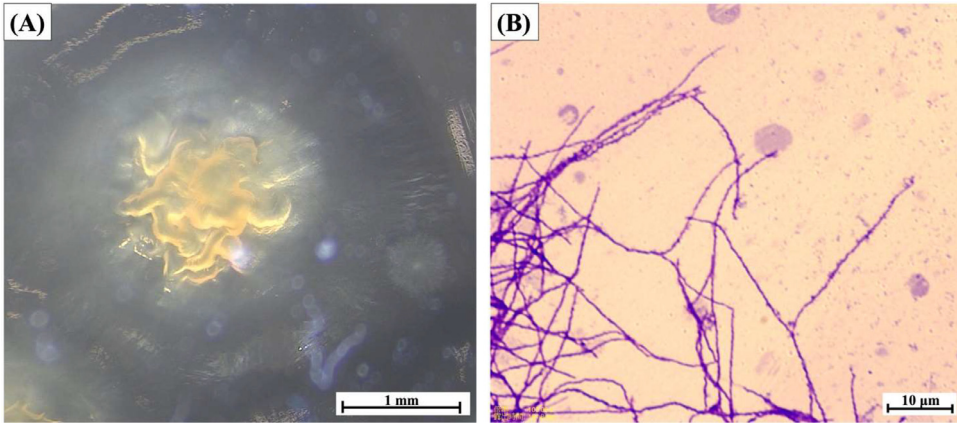


**Fig. 1.** *P. fimeticola* PLACP1 after 3 d of incubation on Columbia medium at 60°C. (A) Colony image observed under the binocular wide-field dissecting microscope SMZ-161. (B) Cell morphologies observed via light microscopy using Nikon Eclipse Ni after Gram staining.

**Table 1**
Genomic features of *P. fimeticola* PLACP1.

| Features | *P. fimeticola* PLACP1 |
|---|---|
| Assembly size (bp) | 3,395,140 |
| GC content (%) | 57.97 |
| Number of Contigs | 20 |
| N50 | 333,497 |
| Total number of genes | 3,368 |
| Protein | 3,267 |
| rRNA | 6 |
| tRNA | 56 |
| Other RNA | 39 |
| BioProject | PRJDB17484 |
| BioSample | SAMD00736731 |
| Sequence read archive | DRR530440 |
| GenBank accession | BAABOJ010000000 |

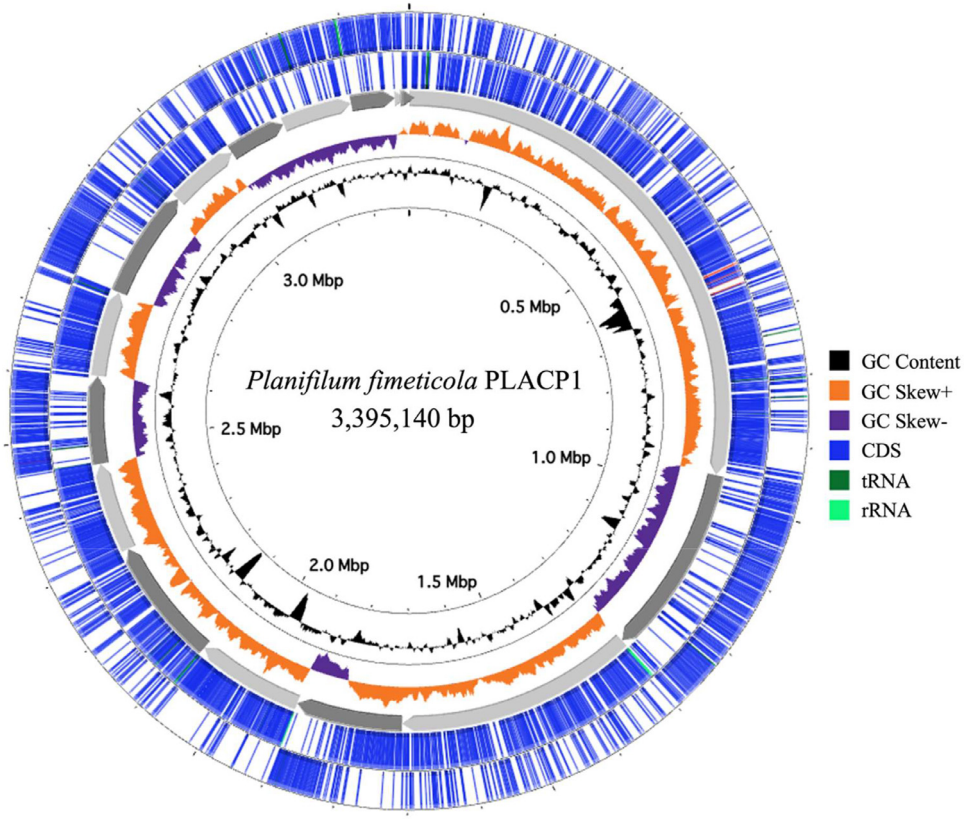


**Fig. 2.** Genome map of *P. fimeticola* PLACP1. Inner to outer tracks indicate the GC content (black), GC skew (orange and purple), contigs (gray), CDS (blue), tRNA (dark green) and rRNA (light green). This genome map was constructed using Proksee.

draft genome of the strain PLACP1 had a total length of 3,395,140 bp, with a GC content of 57.97 %. It contained 3,368 genes, including 3,267 protein-coding, 6 rRNA, and 56 tRNA genes (Table 1). Fig. 2 presents a circular genome map of *P. fimeticola* PLACP1 along with information on its genomic features. The phylogenomic tree (Fig. 3) showed that *P. fimeticola* PLACP1 was most closely related to *P. fimeticola* DSM 44946 (PVNE00000000) and *P. fulgidum* DSM 44945 (FOOK00000000), which belonged to the same clade as a monophyletic group. Comprehensive Antibiotic Resistance Database (CARD) analysis of the *P. fimeticola* PLACP1 genomic data identified 237 ARGs, including 44 macrolide antibiotic-related genes (19 %) as the largest group. ARGs were further classified into six classes based on their mechanism of resistance (Fig. 4): antibiotic efflux (130 genes, 54 %), antibiotic target alteration (85 genes, 35 %), antibiotic target protection (12 genes, 5 %), antibiotic inactivation (11 genes, 4 %), reduced permeability to antibiotics (2 genes, 1 %), and antibiotic target replacement (2 genes, 1 %). We have also provided detailed information on the genes identified in CARD as supplementary data (Supplementary Material S1).

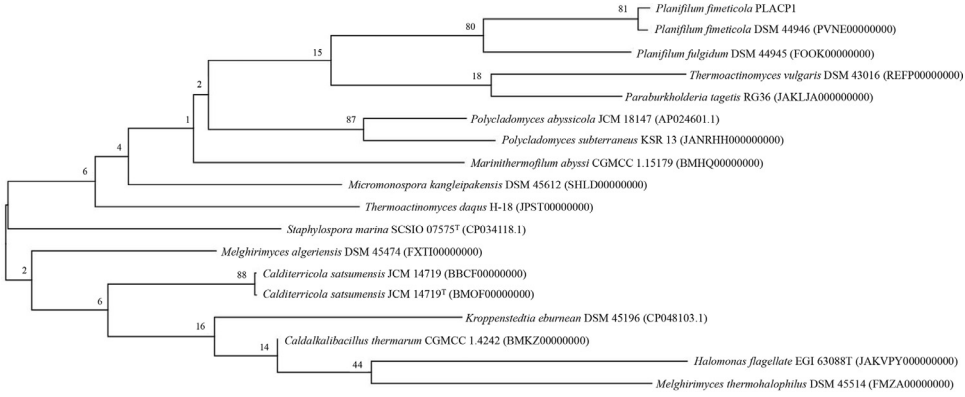


**Fig. 3.** Phylogenomic tree of *P. fimeticola* PLACP1 and its closely related genome generated using the Type (Strain) Genome Server.

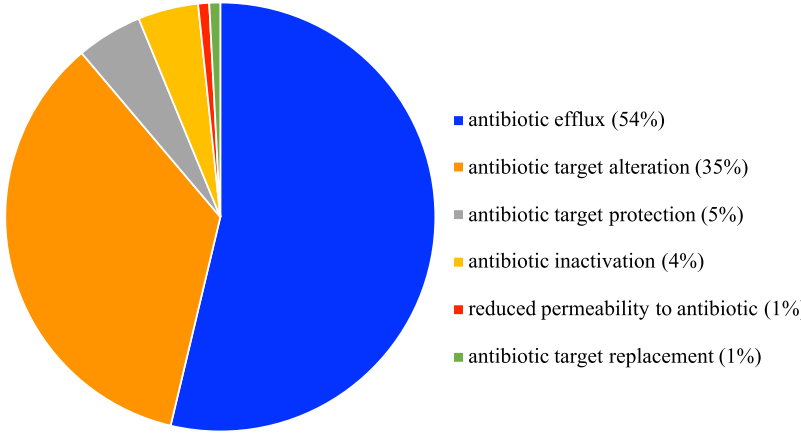


**Fig. 4.** Classification of ARGs based on the mechanism of resistance.

## 4. Experimental Design, Materials And Methods

### *4.1. Bacterial isolation and maintenance*

*P. fimeticola* PLACP1 was isolated from thermophilic sludge, which was treated after decomposition of polylactic acid for over 3 months [5]. Isolation was conducted at 55 °C for 7 d using Columbia broth (Difco, BD, Franklin Lakes, NJ, USA) supplemented with 25 mg/L chloramphenicol for the pour plate method [6]. A single colony of each possible microbial strain was selected and streaked onto a fresh Columbia broth or Luria-Bertani (LB) broth (Kanto Chemical, Japan) plate (solidified with 1 % Gellan Gum). This process was repeated twice or thrice to obtain a pure culture. The culture was maintained using Columbia or LB plate under aerobic conditions at 55∼60°C for further experiments.

### 4.2. Morphological observation and gram staining method

Morphological analysis of a single colony on the Columbia plate at 60°C after 3 days of incubation was performed under the binocular wide-field dissecting microscope SMZ-161 (Shimadzu, Kyoto, Japan) with a Digital Slight 1000 camera (Nikon, Tokyo, Japan) for image capturing**.** The vegetative cells were observed under a Nikon Eclipse Ni light microscope (Nikon, Tokyo, Japan) after Gram staining [7].

### 4.3. Genomic DNA preparation and whole-genome sequencing and assembly

Chromosomal DNA was extracted from PLACP1 using a DNeasy PowerSoil Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. Whole-genome sequencing libraries were constructed using a VAHTS Universal DNA Library Prep Kit (Vazyme Biotech, Nanjing, China) and loaded onto an Illumina NovaSeq 6000 Sequencing System (Illumina, San Diego, CA, USA), according to the manufacturer's instructions, using a 2 × 150 paired-end configuration to obtain raw sequencing data. The quality scores (Q20 and Q30) of the sequencing data were checked based on the Phred Q scores, [8] and the reads were trimmed using Cutadapt (v1.9.1) [9]. Sequencing data were assembled using Velvet (version 1.2.10) [10] and gap-filled with SSPACE (version 3.0) [11] and GapFiller (version 1–10) [12] to construct the draft genome.

### 4.4. Phylogenomic analysis, genome annotation, and gene prediction

The whole-genome sequence was analysed using the Type (Strain) Genome Server for phylogenomic analysis of other related bacterial genomes [13]. The draft genome assemblies were functionally annotated and predicted using the DDBJ Fast Annotation and Submission Tool prokaryotic genome annotation pipeline to obtain the GC content (%), total number of predicted genes, coding sequences (CDS), and proteins [14]. Gene products related to antibiotic resistance were investigated using CARD with the default settings [15]. A genome map for *P. fimeticola* PLACP1 was constructed using Proksee [16].

## Limitations

None.

## Ethics Statement

This study did not involve human participants, animal experiments, or data collection from social media platforms.

## Data Availability

Planifilum fimeticola strain PLACP1, whole genome shotgun sequencing project (Original data) (National Center for Biotechnology Information).

## CRediT Author Statement

**Hou-Chia Tseng:** Conceptualization, Investigation, Writing – original draft, Visualization; **Minenosuke Matsutani:** Methodology, Software; **Naoshi Fujimoto:** Project administration; **Akihiro Ohnishi:** Supervision.

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## Declaration of Competing Interest

The authors declare that they have no competing financial interests or personal relationships that may have influenced the work reported in this study.

## Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2024.110447.

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