




First Draft Genome Sequence of Thermophilic *Laceyella tengchongensis* BKK01, Isolated from Municipal Solid Waste in Thailand

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ABSTRACT *Laceyella tengchongensis* BKK01 is a thermophilic bacterium isolated from municipal solid waste. The genome of *L. tengchongensis* BKK01 includes a gene putatively encoding gramicidin S synthase. Gramicidin S has antibiotic activity against some bacteria and fungi. The newly sequenced 3.44-Mb draft genome of *L. tengchongensis* BKK01 will shed some light on the biosynthesis of gramicidin S.

Laceyella tengchongensis is a Gram-positive and thermophilic bacterium (1). *L. tengchongensis* produces white to yellow-white mycelia in substrate and endospores on sporophores (1, 2). The optimal growth temperature of *L. tengchongensis* is 55°C (2).

Bacterial strain BKK01 was isolated from municipal solid waste in Bangkok, Thailand. Ten grams of the sample was heated with a hot-air oven at 120°C for 1 h. Then, the heated sample was suspended in phosphate-buffered saline (PBS), and a 10-fold serial dilution was performed with PBS. Each dilution was spread onto tryptic soy agar and incubated at 45°C for 2 days. Afterward, a single colony was selected for cultivation in tryptic soy broth with 200 rpm shaking at 45°C for 2 days, and genomic DNA (gDNA) of the strain BKK01 was extracted by the phenol-chloroform method described by Sambrook and Russel (3). A NanoDrop spectrophotometer (Thermo Fisher Scientific, USA) was used to determine the quality and quantity of the gDNA. A sequencing library was prepared using the Ion PI Hi-Q OT2 template and Ion Plus fragment library kits. The library was placed on an Ion PI chip, and sequencing was performed using an Ion Proton sequencer (Thermo Fisher Scientific). There were 5,058,644 raw reads (207× depth of coverage), of which the average read length was 135 bp, generated from the sequencing run.

The quality of the raw reads was determined using After QC version 0.9.6 with default parameters (4), and *de novo* genome assembly was subsequently performed with the raw reads and SPAdes 3.13.1 in the careful mode (5). The genome assembly

Citation Wachiralurpan S, Ruangsuj P, Yamprayooswat W, Sopha P, Jumpathong W, Sittihan S, Kanjanavas P, Areekit S, Chansiri K, Chauyrod K, Yasawong M. 2020. First draft genome sequence of thermophilic *Laceyella tengchongensis* BKK01, isolated from municipal solid waste in Thailand. *Microbiol Resour Announc* 9:e00798-20. <https://doi.org/10.1128/MRA.00798-20>.

Editor Frank J. Stewart, Georgia Institute of Technology

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Received 10 July 2020

Accepted 3 August 2020

Published 10 September 2020

metric was determined using QCAST version 5.0.2 with default parameters (6). The draft genome sequence of strain BKK01 comprises 3,439,142 bp in 234 contigs with an N_{50} value of 27,994 bp and GC content of 48.87%.

The draft genome sequence of strain BKK01 was identified using the Type Strain Genome Server (TYGS) (7). This bacterial strain was affiliated with *Laceyella tengchongensis* with a 94.8% supported value of the digital DNA-DNA hybridization (dDDH), and the GC content difference between strain BKK01 and the type strain of *Laceyella tengchongensis* (DSM 45262) was 0.18%. Gene prediction was performed using Prokka version 1.13.7 with default parameters (8). The annotated genome sequence of *L. tengchongensis* BKK01 contains 3,651 total genes, 3,502 protein-coding sequences, 80 tRNAs, 5 rRNAs, 1 transfer-messenger RNA (tmRNA) gene, and 12 CRISPR regions.

One annotated locus in the *L. tengchongensis* BKK01 genome was the *grsB* gene, putatively encoding a gramicidin S-synthesizing enzyme. Gramicidin S is a naturally occurring cyclic decapeptide widely applied in the pharmaceutical industry due to its antimicrobial and membrane-penetrating activities (9). The draft genome sequence of the bacterial strain BKK01 contributes to the understanding of the biosynthesis of gramicidin S and pathway regulation in *L. tengchongensis*.

Data availability. The whole-genome shotgun sequence of *L. tengchongensis* BKK01 has been deposited at DDBJ/ENA/GenBank under the accession number [WJFE00000000](https://www.ncbi.nlm.nih.gov/nuccore/WJFE00000000) and SRA accession number [SRR10357966](https://www.ncbi.nlm.nih.gov/sra/SRR10357966).

ACKNOWLEDGMENTS

This work was financially supported by Chulabhorn Graduate Institute (CGI), Chulabhorn Royal Academy and the Center of Excellence in Biosensors (COE) and Welding Evaluation and Learning Laboratory (WELLab), Maintenance Technology Center, Institute for Scientific and Technological Research and Services, King Mongkut's University of Technology Thonburi.

Bacterial culture and genomic extraction were performed at the Department of Microbiology, Faculty of Science, King Mongkut's University of Technology Thonburi.

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