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Complete Genome Sequence of the Soil-Isolated *Psychrobacillus* sp. Strain AK 1817, Capable of Biotransforming the Ergostane Triterpenoid Antcin K

Luis B. Gómez-Luciano,[a] Yu-Wei Wu,[b] Chien-Min Chiang,[c] Te-Sheng Chang,[d] Jiumn-Yih Wu,[e] Tzi-Yuan Wang[f]

[a]Office of the VP for Research and Graduate Studies, Universidad Católica del Cibao, La Vega, Dominican Republic
[b]Graduate Institute of Biomedical Informatics, College of Medical Science and Technology, Taipei Medical University, Taipei, Taiwan
[c]Department of Biotechnology, Chia Nan University of Pharmacy and Science, Jen-Te District, Tainan, Taiwan
[d]Department of Biological Sciences and Technology, National University of Tainan, Tainan, Taiwan
[e]Department of Food Science, National Quemoy University, Jin-Ning Township, Kinmen County, Taiwan
[f]Biodiversity Research Center, Academia Sinica, Taipei, Taiwan

Author order was determined on the basis of seniority.

ABSTRACT The soil bacterium *Psychrobacillus* sp. strain AK 1817 was isolated from a tropical soil sample collected in Taiwan. Strain AK 1817 biotransforms the ergostane triterpenoid antcin K from the fungus *Antrodia cinnamomea*. The genome was sequenced using the PacBio RS II platform and consists of one chromosome of 4,096,020 bp, comprising 3,907 protein-coding genes, 75 tRNAs, 30 rRNAs, 5 noncoding RNAs (ncRNAs), and 100 pseudogenes.

Psychrobacillus sp. strain AK 1817 is a Gram-positive, motile, endospore-forming, rod-shaped bacterium; of 4,311 soil bacteria isolated using the plating method, only *Psychrobacillus* sp. strain AK1817 was able to biotransform the triterpenoid antcin K into antcamphin E and antcamphin F (1). It was classified into a genus of bacteria in the phylum *Firmicutes*, from the family *Bacillaceae* (1); however, its function/character in the ecosystem remain unknown. This organism's triterpenoid biotransformation makes it interesting for potential industrial applications.

AK 1817 was isolated from a soil sample collected in southern Taiwan (global position system coordinates 1.345771°N, 103.6801°E) using the Spin Air sampler (IUL, Spain). The colonies were isolated by culturing them on LB agar at 25°C and in LB + 0.2% glucose broth overnight at 25°C prior to DNA extraction. Genomic DNA was purified using the ZR soil microbe DNA kit (Zymo Research, USA) according to the manufacturer's protocol. After a quality check using the Qubit double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit (Thermo Fisher Scientific, USA) and size selection using the BluePippin system (Sage Science, USA), a library was prepared using the SMRTbell template prep kit v1.0 (Pacific Biosciences), followed by single-molecule real-time (SMRT) sequencing on the PacBio RS II platform.

Sequencing generated 149,490 subreads with a total length of 1,232,710,752 bp for a genome coverage of $\sim$300×. In total, 149,490 subreads were obtained, for which the average, N_{50}, and maximum read lengths were 8,246, 11,029, and 50,776 bp, respectively. The reads were assembled *de novo* using Canu v1.6 (2) with default settings. Briefly, Canu is capable of correcting read errors and controlling the read quality before assembling the subreads into contigs. The genome contains a single chromosome, which was assembled into one contig (reported by Canu as circular) of 4,096,020 bp, with a GC content of only 36.67%. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.6 (3). It predicted 4,117 genes, of

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Address correspondence to Jiumn-Yih Wu, wujy@nqu.edu.tw, or Tzi-Yuan Wang, tziyuan@gmail.com.

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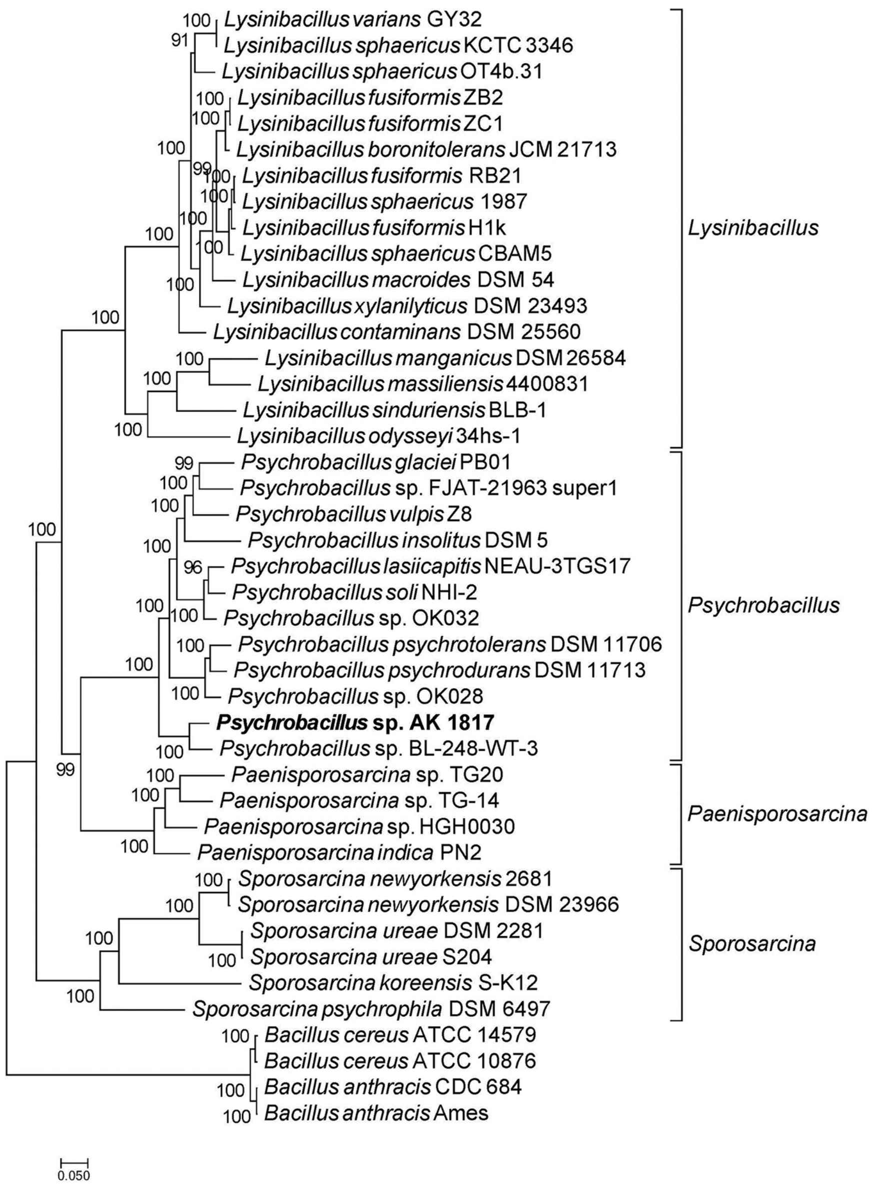

FIG 1 Phylogenomics of *Psychrobacillus* sp. strain AK 1817. This species tree was used to define the gene orthology.

which 3,907 were coding genes, 110 were RNA genes (30 rRNAs, 75 tRNAs, and 5 noncoding RNAs [ncRNAs]), and 100 were pseudogenes. A phylogenetic tree was built using ezTree v0.1 (4), which extracted single-copy marker genes from selected genomes and concatenated the marker genes to build a phylogenetic tree, with four *Bacillus* species as the outgroups using default settings. From the phylogenetic tree (Fig. 1), one can see that AK 1817 was closest to *Psychrobacillus* sp. strain BL-248-WT-3 (GenBank accession number NZ_JABAFC000000000), which was identified from domestic pig feces.

Data availability. The complete genome sequence of *Psychrobacillus* sp. strain AK 1817 is available in DDBJ/EMBL/GenBank under accession number CP031739 (BioSample accession number SAMN09845876 and BioProject accession number PRJNA486432). The filtered subreads have been submitted under SRA accession number SRX4910659.

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