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Published in: Genome Announcements

DOI: 10.1128/genomea.00097-12

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date: 2013

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):
Romano, A., Trip, H., Campbell-Sills, H., Bouchez, O., Sherman, D., Lolkema, J. S., & Lucas, P. M. (2013). Genome Sequence of Lactobacillus saerimneri 30a (Formerly Lactobacillus sp. Strain 30a), a Reference Lactic Acid Bacterium Strain Producing Biogenic Amines. Genome Announcements, 1(1), 1-2. [0097]. DOI: 10.1128/genomea.00097-12

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Genome Sequence of *Lactobacillus saerimneri* 30a (Formerly *Lactobacillus* sp. Strain 30a), a Reference Lactic Acid Bacterium Strain Producing Biogenic Amines

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*Lactobacillus* sp. strain 30a (*Lactobacillus saerimneri*) produces the biogenic amines histamine, putrescine, and cadaverine by decarboxylating their amino acid precursors. We report its draft genome sequence (1,634,278 bases, 42.6% G+C content) and the principal findings from its annotation, which might shed light onto the enzymatic machineries that are involved in its production of biogenic amines.

Received 4 November 2012 Accepted 12 December 2012 Published 7 February 2013


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L. *lactobacillus* sp. strain 30a (ATCC 33222) was isolated from horse stomach in the early 1950s as the first strain of the genus *Lactobacillus* that produced biogenic amines (1). This is the only strain described thus far that forms all three biogenic amines—histamine, putrescine, and cadaverine—from histidine, ornithine, and lysine, respectively (1, 2). *Lactobacillus* sp. 30a has been used as a reference strain in many laboratories and in many studies relating to the production of biogenic amines by lactic acid bacteria (LAB). *Lactobacillus* sp. 30a carries a pyruvoyl-dependent histidine decarboxylase and a pyridoxal-phosphate-dependent ornithine decarboxylase that have been characterized extensively (3–10). Their genes have been identified (4), but their overall genomic environment remains unknown. *Lactobacillus* sp. 30a also possesses a pyridoxal-phosphate-dependent lysine decarboxylase (10), although this enzyme has not been identified in this strain or in any other LAB. Here, we report the genome sequence of *Lactobacillus* sp. strain 30a, which was grown in deMan, Rogosa, and Sharpe (MRS) broth at 37°C. Genomic DNA was extracted using the Wizard genomic DNA purification kit (Promega). Whole-genome sequencing was performed at Genotoul (Toulouse, France) using single-read analysis of a fragment library with the 454 GS-FLX Titanium pyrosequencing system (Roche Diagnostics). A total of 213,826 reads were obtained and assembled using Newbler (454 Life Sciences), with an average coverage of 47-fold. Annotation of genes and rRNAs was performed using the Prokaryotic Genome Annotation Pipeline (PGAAP) (11). tRNAs were identified with tRNAscan-SE (12).

The draft genome has 1,634,278 bases in 24 contigs (N50, 150,234) and a G+C content of 42.6%. It contains 1,519 predicted coding sequences, two 16S–23S–5S operons, and 55 tRNAs. No plasmids were detected in the sequenced DNA. *Lactobacillus* sp. 30a was attributed to the species *Lactobacillus saerimneri* on the basis of 16S rRNA gene analysis (>99% sequence identity with that of *L. saerimneri*).

The gene encoding the histidine decarboxylase is surrounded by the three genes typically encountered in the histamine-producing pathway in LAB (13). The ornithine decarboxylase gene stands alone, in contrast to in other LAB strains, where it is associated with an ornithine/putrescine exchanger gene (14, 15). *Lactobacillus* sp. 30a also contains a biosynthetic ornithine decarboxylase, which may account for its intracellular production of putrescine (15). A third gene that codes for a putative ornithine decarboxylase is also present and is associated with a predicted amino acid transporter; this likely represents the lysine decarboxylase pathway genes (unpublished results).

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ANAG00000000. The version described in this article is the first version, ANAG01000000.

**ACKNOWLEDGMENTS**

This work was funded by the EU commission in the framework of the BIAMFOOD project (Controlling Biogenic Amines in Traditional Food Fermentations in Regional Europe) (project no. 211441).

**REFERENCES**
