CORA Cork Open Research Archive
Cartlann Taighde Oscailte Chorcaí

Title	Draft genome sequence of Lactobacillus crispatus EM-LC1, an isolate with antimicrobial activity cultured from an elderly subject
Authors	Power, Susan E.;Harris, Hugh Michael B.;Bottacini, Francesca;Ross, R. Paul;O'Toole, Paul W.;Fitzgerald, Gerald F.
Publication date	2013-12-19
Original Citation	Power, S. E., Harris, H. M. B., Bottacini, F., Ross, R. P., O'Toole, P. W. and Fitzgerald, G. F. (2013) 'Draft Genome Sequence of Lactobacillus crispatus EM-LC1, an Isolate with Antimicrobial Activity Cultured from an Elderly Subject', Genome Announcements, 1(6), e01070-13. doi:10.1128/genomeA.01070-13.
Type of publication	Article (peer-reviewed)
Link to publisher's version	10.1128/genomeA.01070-13.
Rights	© 2013 Power et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license - https://creativecommons.org/licenses/by/3.0/
Download date	2026-11-01 05:08:52
Item downloaded from	https://hdl.handle.net/10468/3396

UCC
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

genomeA
Journals.ASM.org

Draft Genome Sequence of *Lactobacillus crispatus* EM-LC1, an Isolate with Antimicrobial Activity Cultured from an Elderly Subject

Susan E. Power,[a,b] Hugh M. B. Harris,[a] Francesca Bottacini,[b] R. Paul Ross,[b,c] Paul W. O'Toole,[a,b] Gerald F. Fitzgerald[a,b]

School of Microbiology, University College Cork, Cork, Ireland[a]; Alimentary Pharmabiotic Centre, University College Cork, Cork, Ireland[b]; Teagasc Food Research Centre, Moorepark, Fermoy, County Cork, Ireland[c]

Here we report the 1.86-Mb draft genome sequence of *Lactobacillus crispatus* EM-LC1, a fecal isolate with antimicrobial activity. This genome sequence is expected to provide insights into the antimicrobial activity of *L. crispatus* and improve our knowledge of its potential probiotic traits.

Received 12 November 2013 **Accepted** 18 November 2013 **Published** 19 December 2013

Citation Power SE, Harris HMB, Bottacini F, Ross RP, O'Toole PW, Fitzgerald GF. 2013. Draft genome sequence of *Lactobacillus crispatus* EM-LC1, an isolate with antimicrobial activity cultured from an elderly subject. Genome Announc. 1(6):e01070-13. doi:10.1128/genomeA.01070-13.

Copyright © 2013 Power et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Gerald F. Fitzgerald, g.fitzgerald@ucc.ie.

Lactobacilli are subdominant members of the human gut microbiota and encompass a considerable number of different species that display a relatively high degree of diversity (1). A number of *Lactobacillus* species are considered to have probiotic properties, offering beneficial roles in maintaining the health status of the host (2). *Lactobacillus crispatus* can persist in the gastrointestinal tract (3) and is among the most prevalent species of the *Lactobacillus*-dominated human vaginal microbiota (4). *L. crispatus* EM-LC1 was isolated from a fecal sample obtained from an elderly subject and showed H_2O_2-independent antimicrobial activity in cell-free supernatant. The genome sequence of this strain will provide a genomic platform for investigation of *L. crispatus* antimicrobial activity and will elucidate the genetic basis for its potential probiotic traits.

The genome was sequenced at Macrogen (Seoul, South Korea) on the Illumina platform, generating a paired-end library containing 35,397,530 reads of 101 bp. The data were assembled into 54 scaffolds using the *de novo* assembly program Velvet (5). MAUVE was used to reorder scaffolds based on the reference genome of *L. crispatus* ST1 (6). tRNAs were identified using tRNA-scan SE (7). Protein coding regions were predicted using Metagene (8), and annotation was subsequently performed on the basis of BLASTP (9) analysis against a nonredundant protein database (nr) provided by the National Center for Biotechnology Information (NCBI). This automated annotation was then manually curated in Artemis (10). A functional classification was applied using the Clusters of Orthologous Groups (COG) database (11). rRNA operons were detected on the basis of BLASTN searches and annotated manually.

The draft genome sequence of *L. crispatus* EM-LC1 consists of 1,862,161 bp, with a G+C content of 37%, which is similar to those of other *Lactobacillus* genomes (6, 12). All predicted genes, proteins, enzymes, and their functions are putative. The draft genome sequence contains 1,827 protein-encoding genes, representing a coding density of 87.6%, with an average gene length of 893 bp. No rRNA locus was assembled due to exclusion of repetitive sequences from the assembly. Forty-five tRNA genes and 27 transposase-encoding genes were identified. No complete prophages were found in the genome sequence, but a number of single open reading frames (ORFs) with similarity to phage genes were identified. Genes encoding a helveticin-like bacteriocin and a class II bacteriocin-like product were also identified.

Functional classification of the predicted genes by COG (11) showed that 1,383 predicted protein-encoding genes (75.7%) were homologous to members of known gene families, including 155 (8.5%) identified as "general function prediction only" and 130 (7.1%) with poorly characterized gene functions designated "function unknown."

Nucleotide sequence accession numbers. This draft whole-genome shotgun project has been deposited in GenBank under the accession no. AXLM00000000. The version described in this paper is the first version, AXLM01000000.

ACKNOWLEDGMENTS

S.E.P. is supported by the Irish Research Council postgraduate scholarship Enterprise Partnership Scheme (in collaboration with Alimentary Health, Ltd.) and by the Alimentary Pharmabiotic Centre (SFI grant no. 07/CE/B1368). This work was also supported by a Principal Investigator award (07/IN.1/B1780) from Science Foundation Ireland to P.W.O.

REFERENCES

1. **Claesson MJ, van Sinderen D, O'Toole PW.** 2007. The genus *Lactobacillus*—a genomic basis for understanding its diversity. FEMS Microbiol. Lett. **269:**22–28.
2. **Goldin BR.** 2011. Probiotics and health: from history to future, p 1–16. *In* Kneifel W, Salminen S (ed), Probiotics and health claims, 1st ed. Wiley-Blackwell, Oxford, United Kingdom.
3. **Walter J.** 2008. Ecological role of lactobacilli in the gastrointestinal tract: implications for fundamental and biomedical research. Appl. Environ. Microbiol. **74:**4985–4996.
4. **Ma B, Forney LJ, Ravel J.** 2012. Vaginal microbiome: rethinking health and disease. Annu. Rev. Microbiol. **66:**371–389.
5. **Zerbino DR, Birney E.** 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. **18:**821–829.
6. **Ojala T, Kuparinen V, Koskinen JP, Alatalo E, Holm L, Auvinen P, Edelman S, Westerlund-Wikström B, Korhonen TK, Paulin L,**

Downloaded from http://genomea.asm.org/ on December 14, 2016 by IRIS

Kankainen M. 2010. Genome sequence of *Lactobacillus crispatus* ST1. J. Bacteriol. **192:**3547–3548.
7. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25:**955–964.
8. **Noguchi H, Park J, Takagi T.** 2006. Metagene: prokaryotic gene finding from environmental genome shotgun sequences. Nucleic Acids Res. **34:** 5623–5630.
9. **Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ.** 1990. Basic local alignment search tool. J. Mol. Biol. **215:**403–410.
10. **Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B.** 2000. Artemis: sequence visualization and annotation. Bioinformatics **16:**944–945.
11. **Tatusov RL, Natale DA, Garkavtsev IV, Tatusova TA, Shankavaram UT, Rao BS, Kiryutin B, Galperin MY, Fedorova ND, Koonin EV.** 2001. The COG database: new developments in phylogenetic classification of proteins from complete genomes. Nucleic Acids Res. **29:**22–28.
12. **Cremonesi P, Chessa S, Castiglioni B.** 2012. Genome sequence and analysis of *Lactobacillus helveticus*. Front. Microbiol. **3:**1–13.

Downloaded from http://genomea.asm.org/ on December 14, 2016 by IRIS