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Title	Draft genome sequences of three Lactobacillus paracasei strains, members of the nonstarter microbiota of mature cheddar cheese
Authors	Stefanovic, Ewelina;Fitzgerald, Gerald F.;McAuliffe, Olivia
Publication date	2017-01-01
Original Citation	Stefanovic, E., Fitzgerald, G. and McAuliffe, O. (2017) 'Draft genome sequences of three Lactobacillus paracasei strains, members of the nonstarter microbiota of mature cheddar cheese', Genome Announcements, 5(29), e00655-17 (2pp). doi: 10.1128/genomeA.00655-17
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://genomea.asm.org/content/5/29/e00655-17 - 10.1128/genomeA.00655-17
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Download date	2026-11-06 12:02:55
Item downloaded from	https://hdl.handle.net/10468/4883

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PROKARYOTES

Draft Genome Sequences of Three *Lactobacillus paracasei* Strains, Members of the Nonstarter Microbiota of Mature Cheddar Cheese

Ewelina Stefanovic,[a,b] Gerald Fitzgerald,[b] Olivia McAuliffe[a]

Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland[a]; School of Microbiology, University College Cork, Cork, Ireland[b]

ABSTRACT *Lactobacillus paracasei* strains are common members of the nonstarter microbiota present in various types of cheeses. The draft genome sequences of three strains isolated from mature cheddar cheeses are reported here.

Received 30 May 2017 **Accepted** 31 May 2017 **Published** 20 July 2017

Citation Stefanovic E, Fitzgerald G, McAuliffe O. 2017. Draft genome sequences of three *Lactobacillus paracasei* strains, members of the nonstarter microbiota of mature cheddar cheese. Genome Announc 5:e00655-17. https://doi.org/10.1128/genomeA.00655-17.

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Address correspondence to Ewelina Stefanovic, ewelina.stefanovic@teagasc.ie.

Lactic acid bacteria (LAB) are Gram-positive aerotolerant bacteria with a wide spectrum of practical applications, including food production, biotechnology, and medicine-related fields (1). Strains of the genus *Lactobacillus* have been isolated from diverse habitats, such as fermented products, plant materials, and human and animal gastrointestinal tracts (2). In cheese, *Lactobacillus paracasei* forms part of the nonstarter microbiota and is considered to have an important role in the ripening process and flavor development (3). The three *Lactobacillus paracasei* strains (DPC2071, DPC4206, and DPC4536) analyzed in this study were isolated from mature cheddar cheeses as part of the nonstarter LAB population.

Bacterial DNA was isolated from all three strains, and genomic libraries were prepared with the Nextera XT DNA library preparation kit (Illumina, Inc., USA). The 2 × 250-bp paired-end read sequencing was performed on an Illumina MiSeq platform (MicrobesNG, University of Birmingham, United Kingdom). The assembly of each genome was performed using the SeqMan NGen application of the DNAStar Lasergene Genomics Suite (DNAStar, Inc., Madison, WI, USA). Glimmer version 3.02 (4) and RAST (5) were used to predict open reading frames (ORFs). Initially, the RAST server was used to annotate each genome, and the annotations were verified and manually curated using BLASTp (6) and Artemis (7).

Sequence assemblies for the three strains indicated coverages of 88×, 70×, and 101× for DPC2071, DPC4206, and DPC4536, respectively. The length of the DPC2071 genome was 2,936,872 bp, consisting of 41 nonoverlapping contigs, with a contig N_{50} of 300,051 bp, a maximum contig size of 536,232 bp, and a total of 2,827 protein-coding genes. In the case of strain DPC4206, the assembly yielded a genome sequence of 3,095,268 bp, consisting of 49 contigs. The maximum contig size was 322,047 bp, and the contig N_{50} was 142,300 bp, while a total of 2,951 protein-coding genes were identified. The draft genome sequence of strain DPC4536 was 3,078,575 bp long, and it consisted of 35 contigs and 2,931 genes encoding proteins. The maximum contig size was 426,277 bp, and the contig N_{50} was 191,696 bp. The G+C content of all three genomes was 46.3%, which corresponds to the usual G+C content of *L. paracasei* genomes.

These sequencing data will contribute to the pool of available *Lactobacillus paracasei* genomes and enable further comparative genome analysis of strains of this species.

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Accession number(s). The whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers NCSN00000000, NCSO00000000, and NCSP00000000, while the versions described in this paper are versions NCSN01000000, NCSO01000000, and NCSP01000000 for strains DPC2071, DPC4206, and DPC4536, respectively.

ACKNOWLEDGMENTS

E. Stefanovic is the recipient of the Teagasc Walsh Fellowship. This work was funded by Teagasc (grant 6224).

REFERENCES

1. Makarova K, Slesarev A, Wolf Y, Sorokin A, Mirkin B, Koonin E, Pavlov A, Pavlova N, Karamychev V, Polouchine N, Shakhova V, Grigoriev I, Lou Y, Rohksar D, Lucas S, Huang K, Goodstein DM, Hawkins T, Plengvidhya V, Welker D, Hughes J, Goh Y, Benson A, Baldwin K, Lee JH, Díaz-Muñiz I, Dosti B, Smeianov V, Wechter W, Barabote R, Lorca G, Altermann E, Barrangou R, Ganesan B, Xie Y, Rawsthorne H, Tamir D, Parker C, Breidt F, Broadbent J, Hutkins R, O'Sullivan D, Steele J, Unlu G, Saier M, Klaenhammer T, Richardson P, Kozyavkin S, Weimer B, Mills D. 2006. Comparative genomics of the lactic acid bacteria. Proc Natl Acad Sci U S A 103:15611–15616. https://doi.org/10.1073/pnas.0607117103.
2. Smokvina T, Wels M, Polka J, Chervaux C, Brisse S, Boekhorst J, van Hylckama Vlieg JE, Siezen RJ. 2013. *Lactobacillus paracasei* comparative genomics: towards species pan-genome definition and exploitation of diversity. PLoS One 8:e68731. https://doi.org/10.1371/journal.pone.0068731.
3. Gobbetti M, De Angelis M, Di Cagno R, Mancini L, Fox PF. 2015. Pros and cons for using non-starter lactic acid bacteria (NSLAB) as secondary/adjunct starters for cheese ripening. Trends Food Sci Technol 45:167–178. https://doi.org/10.1016/j.tifs.2015.07.016.
4. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics 23:673–679. https://doi.org/10.1093/bioinformatics/btm009.
5. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.
6. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic Local Alignment Search Tool. J Mol Biol 215:403–410. https://doi.org/10.1016/S0022-2836(05)80360-2.
7. Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B. 2000. Artemis: sequence visualization and annotation. Bioinformatics 16:944–945. https://doi.org/10.1093/bioinformatics/16.10.944.

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