



Københavns Universitet

**Genome sequences of two *Leuconostoc pseudomesenteroides* strains isolated from Danish dairy starter cultures**

Pedersen, Thomas Bæk; Kot, Witold Piotr; Hansen, L.H.; Sørensen, Søren Johannes; Broadbent, J.R.; Vogensen, Finn Kvist; Ardö, Ylva Margareta

*Published in:*  
Genome Announcements

*DOI:*  
[10.1128/genomeA.00484-14](https://doi.org/10.1128/genomeA.00484-14)

*Publication date:*  
2014

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

*Citation for published version (APA):*  
Pedersen, T. B., Kot, W. P., Hansen, L. H., Sørensen, S. J., Broadbent, J. R., Vogensen, F. K., & Ardö, Y. M. (2014). Genome sequences of two *Leuconostoc pseudomesenteroides* strains isolated from Danish dairy starter cultures. *Genome Announcements*, 2(3), 2. [e00484-14]. <https://doi.org/10.1128/genomeA.00484-14>

# Genome Sequences of Two *Leuconostoc pseudomesenteroides* Strains Isolated from Danish Dairy Starter Cultures

T. B. Pedersen,<sup>a</sup> W. P. Kot,<sup>b</sup> L. H. Hansen,<sup>d</sup> S. J. Sørensen,<sup>b</sup> J. R. Broadbent,<sup>c</sup> F. K. Vogensen,<sup>a</sup> Y. Ardö<sup>a</sup>

Department of Food Science, Faculty of Science, University of Copenhagen, Copenhagen, Denmark<sup>a</sup>; Department of Biology, Faculty of Science, University of Copenhagen, Copenhagen, Denmark<sup>b</sup>; Department of Nutrition, Dietetics, and Food Sciences, Utah State University, Logan, Utah, USA<sup>c</sup>; Department of Environmental Science, Aarhus University, Roskilde, Denmark<sup>d</sup>

**The lactic acid bacterium *Leuconostoc pseudomesenteroides* can be found in mesophilic cheese starters, where it produces aromatic compounds from, e.g., citrate. Here, we present the draft genome sequences of two *L. pseudomesenteroides* strains isolated from traditional Danish cheese starters.**

Received 5 May 2014 Accepted 14 May 2014 Published 5 June 2014

**Citation** Pedersen TB, Kot WP, Hansen LH, Sørensen SJ, Broadbent JR, Vogensen FK, Ardö Y. 2014. Genome sequences of two *Leuconostoc pseudomesenteroides* strains isolated from Danish dairy starter cultures. *Genome Announc.* 2(3):e00484-14. doi:10.1128/genomeA.00484-14.

**Copyright** © 2014 Pedersen et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to T. B. Pedersen, [tbpe@food.ku.dk](mailto:tbpe@food.ku.dk).

Here, we present the draft genome sequences of two *Leuconostoc pseudomesenteroides* strains, PS12 and 1159, which were isolated from two different Danish mesophilic undefined cheese starters (1). *L. pseudomesenteroides* is a versatile organism that has been isolated from various food sources (2, 3). It produces diacetyl and contributes to the eye formation in Gouda type cheese via its heterofermentative metabolism and ability to degrade citrate (4). Currently, there are two publicly available *L. pseudomesenteroides* draft sequences: those of strain 4882, isolated from a French dairy starter culture (5), and strain 3652<sup>T</sup>, isolated from cane juice (6). Sequencing libraries were prepared using the Nextera XT kit (Illumina, USA), according to the manufacturer's recommendations, followed by sequencing as a part of the flowcell, as 2 × 250-base paired-end reads using the Illumina MiSeq (Illumina, USA) technology. The reads were trimmed and assembled with the CLC Genomics Workbench 6.5.1 (CLC bio, Denmark). The resulting contigs were annotated using the RAST server (7). The two strains have similar sizes and genomic features (Table 1) and share a number of conserved functions, including genes for central carbohydrate metabolism and protein degradation. Both strains also contain clustered regularly interspaced short palindromic repeat (CRISPR) elements, which were also found in *L. pseudomesenteroides* strain 4882 but not

in strain 3652<sup>T</sup>. The finding that the main differences between the two genomes were coding sequences (CDS) for CRISPR elements and different phage genes indicates a prominent influence of phage exposure on the adaptation of these strains in dairy environments. Future work with the four genomes will give more insight on the evolution and adaptation of *L. pseudomesenteroides* to different environments.

**Nucleotide sequence accession numbers.** The whole-genome shotgun projects for *L. pseudomesenteroides* strains 1159 and PS12 have been deposited at DDBJ/EMBL/GenBank under the accession no. [JAUI00000000](http://www.ncbi.nlm.nih.gov/nuccore/JAUI00000000) and [JDVA00000000](http://www.ncbi.nlm.nih.gov/nuccore/JDVA00000000), respectively. The versions described in this paper are [JAUJ01000000](http://www.ncbi.nlm.nih.gov/nuccore/JAUJ01000000) and [JDVA01000000](http://www.ncbi.nlm.nih.gov/nuccore/JDVA01000000), respectively.

## ACKNOWLEDGMENTS

This work was supported by Copenhagen University.

We thank Taylor Oberg for technical assistance in genome annotation and assembly.

## REFERENCES

- Pedersen TB, Ristagno D, McSweeney PLH, Vogensen FK, Ardo Y. 2013. Potential impact on cheese flavour of heterofermentative bacteria from starter cultures. *Int. Dairy J.* 33:112–119. <http://dx.doi.org/10.1016/j.idairyj.2013.03.003>.
- Camu N, De Winter T, Verbrugge K, Cleenwerck I, Vandamme P, Takrama JS, Vancanneyt M, De Vuyst L. 2007. Dynamics and biodiversity of populations of lactic acid bacteria and acetic acid bacteria involved in spontaneous heap fermentation of cocoa beans in Ghana. *Appl. Environ. Microbiol.* 73:1809–1824. <http://dx.doi.org/10.1128/AEM.02189-06>.
- Paulo EM, Boffo EF, Branco A, Valente AM, Melo IS, Ferreira AG, Roque MR, Assis SA. 2012. Production, extraction and characterization of exopolysaccharides produced by the native *Leuconostoc pseudomesenteroides* R2 strain. *An. Acad. Bras. Cienc.* 84:495–507. <http://dx.doi.org/10.1590/S0001-37652012000200018>.
- Hemme D, Foucaud-Scheunemann C. 2004. *Leuconostoc*, characteristics, use in dairy technology and prospects in functional foods. *Int. Dairy J.* 14:467–494. <http://dx.doi.org/10.1016/j.idairyj.2003.10.005>.

TABLE 1 General features for strains 1159 and PS12

Feature	<i>L. pseudomesenteroides</i> strain:	
	1159	PS12
Genome size (bp)	2,038,943	1,935,842
No. of open reading frames	2,109	1,964
G+C content (%)	38.9	39.0
No. of RNA genes	48	47
No. of contigs	100	91
Coverage (×)	100	380

5. Meslier V, Loux V, Renault P. 2012. Genome sequence of *Leuconostoc pseudomesenteroides* strain 4882, isolated from a dairy starter culture. *J. Bacteriol.* **194**:6637. <http://dx.doi.org/10.1128/JB.01696-12>.
6. Kim DW, Choi SH, Kang A, Nam SH, Kim RN, Kim A, Kim DS, Park HS. 2011. Genome sequence of *Leuconostoc pseudomesenteroides* KCTC 3652. *J. Bacteriol.* **193**:4299. <http://dx.doi.org/10.1128/JB.05433-11>.
7. 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. <http://dx.doi.org/10.1186/1471-2164-9-75>.