

Technical University of Denmark



Draft Genome Sequences of Enterococcus mundtii Strains Isolated from Beef Slaughterhouses in Kenya

Wambui, Joseph; Stevens, Marc; Njage, Patrick Murigu Kamau; Wüthrich, Daniel; Egli, Adrian; Stephan, Roger; Tasara, Taurai

Published in:
Genome Announcements

Link to article, DOI:
[10.1128/genomeA.00446-18](https://doi.org/10.1128/genomeA.00446-18)

Publication date:
2018

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

[Link back to DTU Orbit](#)

Citation (APA):
Wambui, J., Stevens, M., Njage, P. M. K., Wüthrich, D., Egli, A., Stephan, R., & Tasara, T. (2018). Draft Genome Sequences of Enterococcus mundtii Strains Isolated from Beef Slaughterhouses in Kenya. Genome Announcements, 6(21), [e00446-18-e00446-18]. DOI: 10.1128/genomeA.00446-18

DTU Library

Technical Information Center of Denmark

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.



Draft Genome Sequences of *Enterococcus mundtii* Strains Isolated from Beef Slaughterhouses in Kenya

Joseph Wambui,^{a,b} Marc Stevens,^a Patrick Murigu Kamau Njage,^c Daniel Wüthrich,^{d,e} Adrian Egli,^{d,e} Roger Stephan,^a Taurai Tasara^a

^aInstitute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland

^bDepartment of Food Science, Nutrition and Technology, University of Nairobi, Nairobi, Kenya

^cDivision for Epidemiology and Microbial Genomics, National Food Institute, Technical University of Denmark, Kongens Lyngby, Denmark

^dDivision of Clinical Microbiology, University Hospital Basel, Basel, Switzerland

^eApplied Microbiology Research, Department of Biomedicine, University of Basel, Basel, Switzerland

ABSTRACT We present here draft genome sequences of *Enterococcus mundtii* strains K7-EM, P2-EM, C11-EM, and H18-EM, which were isolated from slaughterhouse equipment, carcasses, and personnel of small- and medium-sized beef slaughterhouses in Kenya.

Enterococcus mundtii strains are bacteriocin-producing enterococci that occur in natural environments, humans, and various animal species (1, 2). We report here the draft genome sequences determined for *E. mundtii* strains K7-EM, P2-EM, C11-EM, and H18-EM, which were isolated from equipment, personnel, and carcasses sampled in small- and medium-sized beef slaughterhouses in Kenya.

Genomic DNA isolated from the *E. mundtii* strains was sequenced on the MiSeq platform (Illumina, San Diego, CA, USA). The resulting genome sequences were assembled *de novo* using SPAdes genome assembler version 3.11 (3) and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (4). The draft genome sequences determined in the four strains are between 3.12 Mb and 3.23 Mb in size with GC contents of 37%. Overall, there were 2,991, 3,023, 2,901, and 3,052 genes and 2,927, 2,975, 2,834, and 3,004 protein-coding sequences identified in the K7-EM, P2-EM, H18-EM, and C11-EM strains, respectively.

The numbers of RNAs predicted using the Rapid Annotations using Subsystems Technology (RAST) server (<http://rast.nmpdr.org>) were 62, 44, 60, and 58, while those for tRNAs predicted using tRNAscan-SE version 2.0 (5) were 53, 35, 55, and 49 in strains K7-EM, P2-EM, H18-EM, and C11-EM, respectively. In each strain, the presence of one transfer-messenger RNA was predicted using ARAGORN version 1.2.38 (6). At least four multidrug efflux pump proteins were identified in each strain using the RAST server. The macrolide resistance determinant, *ermB*, was found in strains P2-EM and C11-EM using ResFinder version 3.0 (7).

No virulence factors or phages were detected in any of the strains using VirulenceFinder version 1.5 and PHASTER, respectively (8, 9). However, the four putative hemolysin genes (hemolysin, hemolysin III, hemolysin A, and α -hemolysin), which were previously identified in *E. mundtii* QU 25 (10), were identified in all four strains using BLAST searches (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Clustered regularly interspaced short palindromic repeats (CRISPRs) were identified using CRISPRfinder (11). H18-EM had one confirmed CRISPR, which was linked to the CRISPR-associated (*cas*) genes *cas1*, *cas2*, *cas4*, *cas9*, and *csn2*, classifying this array as a type II-A system (12). The other three strains were predicted to have between one and three unconfirmed CRISPRs.

Received 17 April 2018 Accepted 18 April 2018 Published 24 May 2018

Citation Wambui J, Stevens M, Njage PMK, Wüthrich D, Egli A, Stephan R, Tasara T. 2018. Draft genome sequences of *Enterococcus mundtii* strains isolated from beef slaughterhouses in Kenya. Genome Announc 6:e00446-18. <https://doi.org/10.1128/genomeA.00446-18>.

Copyright © 2018 Wambui et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Taurai Tasara, tasarat@fsafety.uzh.ch.

Gene clusters encoding the production of secondary metabolites were predicted using the antiSMASH version 4.1.0 server (13). Two bacteriocin production gene clusters were detected in P2-EM and C11-EM, whereas no confirmed bacteriocin production gene cluster was identified in K7-EM or H18-EM. Limitations of the databases could have resulted in unknown bacteriocin production genes remaining unidentified. It is possible that strains K7-EM and H18-EM contain further novel bacteriocin production genes, given that *munA*, *munP*, and *munL* genes were identified in strain H18-EM using BLAST searches. *munA* is part of a gene cluster that is responsible for the production of mundticin KS (1), while *munP* and *munL* are part of a gene cluster that is responsible for the production of mundticin L (14).

Accession number(s). The whole-genome shotgun projects of the P2-EM, C11-EM, K7-EM, and H18-EM strains have been deposited in GenBank under the accession numbers [PYGU00000000](https://doi.org/10.1093/nar/gkw413), [PYGT00000000](https://doi.org/10.1093/nar/gkh152), [PYGS00000000](https://doi.org/10.1093/nar/gkv437), and [PYGR00000000](https://doi.org/10.1093/nar/gku241), respectively. The versions described in this paper are the first versions, [PYGU01000000](https://doi.org/10.1093/nar/gkw413), [PYGT01000000](https://doi.org/10.1093/nar/gkh152), [PYGS01000000](https://doi.org/10.1093/nar/gkv437), and [PYGR01000000](https://doi.org/10.1093/nar/gku241), respectively.

ACKNOWLEDGMENT

The research stay of the first author was supported by funding from the State Secretariat for Education, Research and Innovation, Switzerland, through the Federal Commission for Scholarships for Foreign Students.

REFERENCES

- Kawamoto S, Shima J, Sato R, Eguchi T, Ohmomo S, Shibato J, Horikoshi N, Takeshita K, Sameshima T. 2002. Biochemical and genetic characterization of mundticin KS, an antilisterial peptide produced by *Enterococcus mundtii* NFRI 7393. *Appl Environ Microbiol* 68:3830–3840. <https://doi.org/10.1128/AEM.68.8.3830-3840.2002>.
- Collins MD, Farrow JAE, Jones D. 1986. *Enterococcus mundtii* sp. nov. *Int J Syst Bacteriol* 36:8–12. <https://doi.org/10.1099/00207713-36-1-8>.
- Bankevich A, Nurk S, Antipov D, Gurevich A, Dvorkin M, Kulikov A, Lesin V, Nikolenko S, Pham S, Prjibelski A, Pyshkin A, Sirotkin A, Vyahhi N, Tesler G, Alekseyev M, Pevzner P. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. *Omics* 12:137–141. <https://doi.org/10.1089/omi.2008.0017>.
- Lowe TM, Chan PP. 2016. tRNAscan-SE on-line: integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res* 44:W54–W57. <https://doi.org/10.1093/nar/gkw413>.
- Laslett D, Canback B. 2004. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. *Nucleic Acids Res* 32:11–16. <https://doi.org/10.1093/nar/gkh152>.
- Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <https://doi.org/10.1093/jac/dks261>.
- Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM. 2014. Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic *Escherichia coli*. *J Clin Microbiol* 52:1501–1510. <https://doi.org/10.1128/JCM.03617-13>.
- Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. *Nucleic Acids Res* 44:W16–W21. <https://doi.org/10.1093/nar/gkw387>.
- Shiwa Y, Yanase H, Hirose Y, Satomi S, Araya-Kojima T, Watanabe S, Zendo T, Chibazakura T, Shimizu-Kadota M, Yoshikawa H, Sonomoto K. 2014. Complete genome sequence of *Enterococcus mundtii* QU 25, an efficient L-(+)-lactic acid-producing bacterium. *DNA Res* 21:369–377. <https://doi.org/10.1093/dnares/dsu003>.
- Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res* 35:W52–W57. <https://doi.org/10.1093/nar/gkm360>.
- Chylinski K, Makarova KS, Charpentier E, Koonin EV. 2014. Classification and evolution of type II CRISPR-Cas systems. *Nucleic Acids Res* 42:6091–6105. <https://doi.org/10.1093/nar/gku241>.
- Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res* 43:W237–W243. <https://doi.org/10.1093/nar/gkv437>.
- Feng G, Guron GKP, Churey JJ, Worobo RW. 2009. Characterization of mundticin L, a class IIa anti-*Listeria* bacteriocin from *Enterococcus mundtii* CUGF08. *Appl Environ Microbiol* 75:5708–5713. <https://doi.org/10.1128/AEM.00752-09>.