



HAL
open science

Draft Genome Sequence of *Enterococcus mundtii* QAUEM2808, Isolated from Dahi, a Fermented Milk Product

N. Farah, A. Mehdi, S.I. Soomro, N.I. Soomro, R. Tareb, N. Desmasures,
Jean-Paul Vernoux, S. Bakhtiar, M. Imran

► **To cite this version:**

N. Farah, A. Mehdi, S.I. Soomro, N.I. Soomro, R. Tareb, et al.. Draft Genome Sequence of *Enterococcus mundtii* QAUEM2808, Isolated from Dahi, a Fermented Milk Product. *Genome Announcements*, 2016, 4 (5), pp.e00995-16. 10.1128/genomeA.00995-16 . hal-02086934

HAL Id: hal-02086934

<https://normandie-univ.hal.science/hal-02086934v1>

Submitted on 2 Jul 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Draft Genome Sequence of *Enterococcus mundtii* QAUEM2808, Isolated from Dahi, a Fermented Milk Product

N. Farah,^a A. Mehdi,^a S. I. Soomro,^b N. I. Soomro,^b R. Tareb,^c N. Desmaures,^c J. P. Vernoux,^c S. M. Bakhtiar,^{id} M. Imran^{a,c}

Department of Microbiology, Faculty of Biological Sciences, Quaid-i-Azam University, Islamabad, Pakistan^a; Department of Bioinformatics and Biosciences, Capital University of Science and Technology, Islamabad, Pakistan^b; Normandie Université, UNICAEN, UNIROUEN, ABTE, Caen, France^c

***Enterococcus mundtii* QAUEM2808 has been isolated from dahi, an indigenous fermented milk product of Pakistan. Here, we report the draft genome sequence for this strain, which consists of 160 contigs corresponding to 2,957,514 bp and a G+C content of 38.5%.**

Received 24 July 2016 Accepted 26 July 2016 Published 15 September 2016

Citation Farah N, Mehdi A, Soomro SI, Soomro NI, Tareb R, Desmaures N, Vernoux JP, Bakhtiar SM, Imran M. 2016. Draft genome sequence of *Enterococcus mundtii* QAUEM2808, isolated from dahi, a fermented milk product. *Genome Announc* 4(5):e00995-16. doi:10.1128/genomeA.00995-16.

Copyright © 2016 Farah 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 M. Imran, mmimran@qau.edu.pk.

Enterococcus mundtii is a Gram-positive, facultative, anaerobic, yellow-pigmented, nonmotile bacterium typically isolated from soil, plant surfaces, cows' teats, and milkers' hands (1). This bacterium does not have catalase and cytochrome oxidase enzymes. It can ferment carbohydrates via homolactic glucose metabolism (2) and has a low G+C content ranging between 38 and 39% (3). It is rarely associated with human infection (4). Some strains have been proposed to be used as probiotics to prevent mastitis in cows (5). Coculture of *E. mundtii* and *Lactobacillus plantarum* prevented the growth of *Listeria monocytogenes* ScottA under a simulated gastrointestinal model with infant milk formulations as substrates (6, 7). Here, we present the draft genome sequence of a unique strain, *E. mundtii* QAUEM2808, which was isolated from the fermented milk product dahi.

The genome sequencing of QAUEM2808 was performed using a HiSeq 2000 system (Macrogen, South Korea) to generate Illumina paired-end reads with a coverage of >100×. The resulted HiSeq reads were assembled using Velvet software (8). The assembly gave rise to a draft genome that consists of 160 contigs corresponding to 2,957,514 bp and a G+C content of 38.5%. These data are comparable to genomes that have already been reported (9). Genome annotation of QAUEM2808 was performed using the RAST server (10) and the NCBI Prokaryotic Genome Annotation Pipeline. The genome was predicted to contain a total of 2,701 genes, having 2,586 coding sequences, 24 RNAs, and 91 pseudogenes.

A preliminary analysis of this draft genome enabled us to identify a bile salt hydrolase belonging to the choloylglycine hydrolase family of enzymes, which indicates the potential ability to survive in the gastrointestinal tract (11). Although some strains of *E. mundtii* can produce bacteriocin, the genome of the present strain did not have genes related to known bacteriocin production. The presence of a high number of pseudogenes indicates the adaptation of this strain in microbial communities and in the nutritional-rich dairy matrix, as reported for dairy lactic acid bacteria (12). Regarding biogenic amines, two copies of each tyrosine and lysine decarboxylase were identified, but the histidine decar-

boxylase gene was not found. Genomic islands and virulence/resistance gene annotation were analyzed through VFDB (13) and ARDB (14). It was found that most significant virulence factors frequently associated with clinical isolates of enterococci are not present in our genome, as reported earlier for *E. mundtii* (15). A more comprehensive safety assessment for this strain will be reported in a future publication.

Draft genome sequences of some *E. mundtii* originating from both dairy and nondairy sources have been published in recent years (9, 16, 17).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [LSMC00000000](https://www.ncbi.nlm.nih.gov/nuccore/LSMC00000000). The version described in this paper is the first version, LSMC0100000.

FUNDING INFORMATION

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

REFERENCES

- Müller T, Ulrich A, Ott EM, Müller M. 2001. Identification of plant-associated enterococci. *J Appl Microbiol* 91:268–278. [http://dx.doi.org/10.1046/j.1365-2672.2001.01373.x](https://doi.org/10.1046/j.1365-2672.2001.01373.x).
- Cai Y. 1999. Identification and characterization of *Enterococcus* species isolated from forage crops and their influence on silage fermentation. *J Dairy Sci* 82:2466–2471. [http://dx.doi.org/10.3168/jds.S0022-0302\(99\)75498-6](https://doi.org/10.3168/jds.S0022-0302(99)75498-6).
- Collins MD, Farrow JAE, Jones D. 1986. *Enterococcus mundtii* sp. nov. *Int J Syst Evol Microbiol* 36:8–12. [http://dx.doi.org/10.1099/00207713-36-1-8](https://doi.org/10.1099/00207713-36-1-8).
- Higashide T, Takahashi M, Kobayashi A, Ohkubo S, Sakurai M, Shirao Y, Tamura T, Sugiyama K. 2005. Endophthalmitis caused by *Enterococcus mundtii*. *J Clin Microbiol* 43:1475–1476. [http://dx.doi.org/10.1128/JCM.43.3.1475-1476.2005](https://doi.org/10.1128/JCM.43.3.1475-1476.2005).
- Espeche MC, Otero MC, Sesma F, Nader-Macias ME. 2009. Screening of surface properties and antagonistic substances production by lactic acid bacteria isolated from the mammary gland of healthy and mastitic cows. *Vet Microbiol* 135:346–357. [http://dx.doi.org/10.1016/j.vetmic.2008.09.078](https://doi.org/10.1016/j.vetmic.2008.09.078).
- Botes M, van Reenen CA, Dicks LM. 2008. Evaluation of *Enterococcus mundtii* ST4SA and *Lactobacillus plantarum* 423 as probiotics by using

- a gastro-intestinal model with infant milk formulations as substrate. *Int J Food Microbiol* 128:362–370. <http://dx.doi.org/10.1016/j.ijfoodmicro.2008.09.016>.
7. Botes M, Loos B, van Reenen CA, Dicks LM. 2008. Adhesion of the probiotic strains *Enterococcus mundtii* ST4SA and *Lactobacillus plantarum* 423 to Caco-2 cells under conditions simulating the intestinal tract, and in the presence of antibiotics and anti-inflammatory medicaments. *Arch Microbiol* 190:573–584. <http://dx.doi.org/10.1007/s00203-008-0408-0>.
 8. Zerbino DR. 2010. Using the Velvet de novo assembler for short-read sequencing technologies. *Curr Protoc Bioinform Chapter 11:Unit 11.15*. <http://dx.doi.org/10.1002/0471250953.bi1105s31>.
 9. 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. <http://dx.doi.org/10.1093/dnares/dsu003>.
 10. 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>.
 11. Begley M, Hill C, Gahan CGM. 2006. Bile salt hydrolase activity in probiotics. *Appl Environ Microbiol* 72:1729–1738. <http://dx.doi.org/10.1128/AEM.72.3.1729-1738.2006>.
 12. Schroeter J, Klaenhammer T. 2009. Genomics of lactic acid bacteria. *FEMS Microbiol Lett* 292:1–6. <http://dx.doi.org/10.1111/j.1574-6968.2008.01442.x>.
 13. Chen L, Yang J, Yu J, Yao Z, Sun L, Shen Y, Jin Q. 2005. VFDB: a reference database for bacterial virulence factors. *Nucleic Acids Res* 33:D325–D328. <http://dx.doi.org/10.1093/nar/gki008>.
 14. Liu B, Pop M. 2009. ARDB—Antibiotic Resistance Genes Database. *Nucleic Acids Res* 37:D443–D447. <http://dx.doi.org/10.1093/nar/gkn656>.
 15. Repizo GD, Espariz M, Blancato VS, Suárez CA, Esteban L, Magni C. 2014. Genomic comparative analysis of the environmental *Enterococcus mundtii* against enterococcal representative species. *BMC Genomics* 15:489. <http://dx.doi.org/10.1186/1471-2164-15-489>.
 16. Magni C, Espeche C, Repizo GD, Saavedra L, Suárez CA, Blancato VS, Espariz M, Esteban L, Raya RR, Font de Valdez G, Vignolo G, Mozzi F, Taranto MP, Hebert EM, Nader-Macías ME, Sesma F. 2012. Draft genome sequence of *Enterococcus mundtii* CRL1656. *J Bacteriol* 194:550. <http://dx.doi.org/10.1128/JB.06415-11>.
 17. Bonacina J, Saavedra L, Suárez NE, Sesma F. 2014. Draft genome sequence of the nonstarter bacteriocin-producing strain *Enterococcus mundtii* CRL35. *Genome Announc* 2(3):e00444-14. <http://dx.doi.org/10.1128/genomeA.00444-14>.