

Draft Genome Sequence of *Corynebacterium variabile* Mu292, Isolated from Munster, a French Smear-Ripened Cheese

Eric Dugat-Bony,^a Anne-Sophie Sarthou,^a Valentin Loux,^b Marie Vidal,^{c,d} Pascal Bonnarne,^a Françoise Irlinger,^a Séverine Layec^a

UMR Génie et Microbiologie des Procédés Alimentaires, GMPA, AgroParisTech, INRA, Université Paris-Saclay, Thiverval-Grignon, France^a; MalAGE, INRA, Université Paris-Saclay, Jouy-en-Josas, France^b; INRA, GeT-PlaGe, Genotoul, Castanet-Tolosan, France^c; INRA, UAR1209, Castanet-Tolosan, France^d

Here, we report the draft genome sequence of *Corynebacterium variabile* Mu292, which was originally isolated from the surface of Munster, a French smear-ripened cheese. This genome investigation will improve our knowledge on the molecular determinants potentially involved in the adaptation of this strain during the Munster-type cheese manufacturing process.

Received 26 May 2016 Accepted 1 June 2016 Published 21 July 2016

Citation Dugat-Bony E, Sarthou A-S, Loux V, Vidal M, Bonnarne P, Irlinger F, Layec S. 2016. Draft genome sequence of *Corynebacterium variabile* Mu292, isolated from Munster, a French smear-ripened cheese. *Genome Announc* 4(4):e00669-16. doi:10.1128/genomeA.00669-16.

Copyright © 2016 Dugat-Bony et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](http://creativecommons.org/licenses/by/4.0/).

Address correspondence to Séverine Layec, severine.layec@grignon.inra.fr.

Smear-ripened cheeses harbor complex microbial consortia that are mainly responsible for the production of typical sensory properties (1). Their activities are influenced by the technological processes and manufacturing environment. *Corynebacterium* species are commonly involved in the cheese-ripening process (2–4) and contribute to the flavor and texture of the final product. Three sequenced genomes are currently available for cheese isolates belonging to the *Corynebacterium* genus. Two are affiliated with *Corynebacterium casei* and were isolated from a French (5) and an Irish smear-ripened cheese (6), respectively. The third one is affiliated with *Corynebacterium variabile* and was isolated from Gubbeen (7).

We report here the genome sequence of *Corynebacterium variabile* Mu292, isolated in 1989 from Munster, a soft smear-ripened cheese. Sequencing was performed using Illumina MiSeq technology. After filtering, a total of 1,169,642 paired-ends reads of 250 bp in length were generated and merged using FLASH (8). *De novo* assembly was performed using SPAdes (version 3.1.1, with default parameters) (9), which generated 66 large contigs ($\geq 1,000$ bp), with an average sequencing coverage of 100-fold. The unclosed draft genome is 3,185,550 bp in length and has a G+C content of 67.3%. Gene prediction and annotation were performed using the IMG system, as described previously (10). This genome encompasses 3,007 genes, including 2,942 coding DNA sequences, 7 rRNAs, and 58 tRNAs.

Comparative analysis of the genome of *C. variabile* Mu292 with the genome of *C. variabile* strain DSM 44702, isolated from Gubbeen cheese (7), will provide valuable insights into the adaptation of *C. variabile* strains to different cheese technologies. Indeed, Gubbeen and Munster cheeses are differentiated by their technological characters, such as pH of the curd and NaCl and dry-matter contents (11, 12). Interestingly, the presence of a type I restriction-modification system in the genome of *C. variabile* Mu292 might explain why it is devoid of the phage-related chromosomal island of *C. variabile* DSM 44702 (7, 13).

Another feature in the genome of *C. variabile* Mu292 is the presence of a gene coding for a putative arylsulfatase (EC 3.1.6.1),

sharing 82% sequence identity (protein level) with the sequence of *Corynebacterium terpenotabidum* Y-11^T (NCBI accession no. WP_020440046), a bacterium isolated from soil and which is phylogenetically close to *C. variabile* (14, 15). This enzyme has been previously described in various soil bacteria and is considered as a key enzyme in sulfur metabolism (16, 17). In the cheese habitat, arylsulfatase may be involved in the release of molecules conjugated with sulfate, such as alkylphenols, which contribute to sheep-like flavors of the cheeses manufactured from sheep's milk (18). Thus, this specificity found in the genome of *C. variabile* Mu292 might be of interest for understanding sulfur metabolism in cheese, which is of great importance for the cheese-making process (19).

This second genome sequence of *Corynebacterium variabile* will allow deeper comparative genomic studies among *Corynebacterium* species and other *Actinobacteria*, provides new elements for understanding the adaptation strategies of cheese bacteria to the cheese habitat, and potentially aids in discovering novel technological properties for the food industry.

Nucleotide sequence accession numbers. The draft genome sequences of *Corynebacterium variabile* Mu292 have been deposited at the EMBL database under accession numbers FAUH01000001 to FAUH01000066.

ACKNOWLEDGMENTS

We thank the INRA GeT-PlaGe platform (<http://get.genotoul.fr>) for sequencing the genome, the INRA MIGALE bioinformatics platform (<http://migale.jouy.inra.fr>) for providing computational resources and support, and the IMG-ER pipeline for generating annotations.

REFERENCES

- Irlinger F, Layec S, Hélinck S, Dugat-Bony E. 2015. Cheese rind microbial communities: diversity, composition and origin. *FEMS Microbiol Lett* 362:1–11. <http://dx.doi.org/10.1093/femsle/fnu015>.
- Feurer C, Irlinger F, Spinnler HE, Glaser P, Vallaeys T. 2004. Assessment of the rind microbial diversity in a farmhouse-produced vs a pasteurized industrially produced soft red-smear cheese using both cultivation and rDNA-based methods. *J Appl Microbiol* 97:546–556. <http://dx.doi.org/10.1111/j.1365-2672.2004.02333.x>.

3. Brennan NM, Ward AC, Beresford TP, Fox PF, Goodfellow M, Cogan TM. 2002. Biodiversity of the bacterial flora on the surface of a smear cheese. *Appl Environ Microbiol* 68:820–830. <http://dx.doi.org/10.1128/AEM.68.2.820-830.2002>.
4. Monnet C, Correia K, Sarthou A-S, Irlinger F. 2006. Quantitative detection of *Corynebacterium casei* in cheese by real-time PCR. *Appl Environ Microbiol* 72:6972–6979. <http://dx.doi.org/10.1128/AEM.01303-06>.
5. Monnet C, Loux V, Bento P, Gibrat J-F, Straub C, Bonnarme P, Landaud S, Irlinger F. 2012. Genome sequence of *Corynebacterium casei* UCMA 3821, isolated from a smear-ripened cheese. *J Bacteriol* 194:738–739. <http://dx.doi.org/10.1128/JB.06496-11>.
6. Walter F, Albersmeier A, Kalinowski J, Rückert C. 2014. Complete genome sequence of *Corynebacterium casei* LMG S-19264^T (=DSM 44701^T), isolated from a smear-ripened cheese. *J Biotechnol* 189:76–77. <http://dx.doi.org/10.1016/j.jbiotec.2014.08.038>.
7. Schröder J, Maus I, Trost E, Tauch A. 2011. Complete genome sequence of *Corynebacterium variabile* DSM 44702 isolated from the surface of smear-ripened cheeses and insights into cheese ripening and flavor generation. *BMC Genomics* 12:545. <http://dx.doi.org/10.1186/1471-2164-12-545>.
8. Magoč T, Salzberg SL. 2011. FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics* 27:2957–2963. <http://dx.doi.org/10.1093/bioinformatics/btr507>.
9. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.
10. Huntemann M, Ivanova NN, Mavromatis K, Tripp HJ, Paez-Espino D, Palaniappan K, Szeto E, Pillay M, Chen I-MA, Pati A, Nielsen T, Markowitz VM, Kyrpides NC. 2015. The standard operating procedure of the DOE-JGI microbial genome annotation pipeline (MGAP v.4). *Stand Genomic Sci* 10:86.
11. Cogan TM, Goerges S, Gelsomino R, Larpin S, Hohenegger M, Bora N, Jamet E, Rea MC, Mounier J, Vancanneyt M, Guéguen M, Desmasures N, Swings J, Goodfellow M, Ward AC, Sebastiani H, Irlinger F, Chamba J-F, Beduhn R, Scherer S. 2014. Biodiversity of the surface microbial consortia from Limburger, Reblochon, Livarot, Tilsit, and Gubbeen cheeses. *Microbiol Spectr* 2:CM-0010–2012. <http://dx.doi.org/10.1128/microbiolspec.CM-0010-2012>.
12. Leclercq-Perlat M-N, Spinnler H-E. 2010. The type of cheese curds determined the colouring capacity of *Brevibacterium* and *Arthrobacter* species. *J Dairy Res* 77:287–294. <http://dx.doi.org/10.1017/S0022029910000245>.
13. Loenen WAM, Dryden DTF, Raleigh EA, Wilson GG. 2014. Type I restriction enzymes and their relatives. *Nucleic Acids Res* 42:20–44. <http://dx.doi.org/10.1093/nar/gkt847>.
14. Rückert C, Albersmeier A, Al-Dilaimi A, Bednarz H, Niehaus K, Szczepanowski R, Kalinowski J. 2014. Genome sequence of the squalene-degrading bacterium *Corynebacterium terpenotabidum* type strain Y-11^T (=DSM 44721^T). *Stand Genomic Sci* 9:505–513. <http://dx.doi.org/10.4056/sigs.4588337>.
15. Takeuchi M, Sakane T, Nihira T, Yamada Y, Imai K. 1999. *Corynebacterium terpenotabidum* sp. nov., a bacterium capable of degrading squalene. *Int J Syst Bacteriol* 49:223–229. <http://dx.doi.org/10.1099/00207713-49-1-223>.
16. Cregut M, Piutti S, Vong P-C, Slezack-Deschaumes S, Crovisier I, Benizri E. 2009. Density, structure, and diversity of the cultivable arylsulfatase-producing bacterial community in the rhizosphere of field-grown rape and barley. *Soil Biol Biochem* 41:704–710. <http://dx.doi.org/10.1016/j.soilbio.2009.01.005>.
17. Cregut M, Piutti S, Slezack-Deschaumes S, Benizri E. 2013. Compartmentalization and regulation of arylsulfatase activities in *Streptomyces* sp., *Microbacterium* sp. and *Rhodococcus* sp. soil isolates in response to inorganic sulfate limitation. *Microbiol Res* 168:12–21. <http://dx.doi.org/10.1016/j.micres.2012.08.001>.
18. Kilic M, Lindsay RC. 2005. Enrichment of cheeses manufactured from cow's and sheep's milk blends with sheep-like species-related alkylphenols. *J Agric Food Chem* 53:1707–1712. <http://dx.doi.org/10.1021/jf0484834>.
19. Landaud S, Helinck S, Bonnarme P. 2008. Formation of volatile sulfur compounds and metabolism of methionine and other sulfur compounds in fermented food. *Appl Microbiol Biotechnol* 77:1191–1205. <http://dx.doi.org/10.1007/s00253-007-1288-y>.