



Draft Reference Genome Sequence of *Corynebacterium mastitidis* 16-1433, Isolated from a Mouse

Christopher Cheleuitte-Nieves,^a Christopher A. Gulvik,^b Ben W. Humrighouse,^b Melissa E. Bell,^b Aaron Villarma,^b Lars F. Westblade,^{c,d} Neil S. Lipman,^{a,c} Vincent A. Fischetti,^e John R. McQuiston^b

^aCenter of Comparative Medicine and Pathology, Memorial Sloan Kettering Cancer Center and Weill Cornell Medicine, New York, New York, USA

^bSpecial Bacteriology Reference Laboratory, Bacterial Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, New York, New York, USA

^cDepartment of Pathology and Laboratory Medicine, Weill Cornell Medicine, New York, New York, USA

^dDepartment of Medicine, Division of Infectious Diseases, Weill Cornell Medicine, New York, New York, USA

^eLaboratory of Bacterial Pathogenesis and Immunology, The Rockefeller University, New York, New York, USA

ABSTRACT We report here a nearly complete draft genome sequence for a *Corynebacterium mastitidis* isolate from a mouse. The total read coverage is 198×, and the genome size is 2,264,319 bp with a 69.04% GC content. This genome complements the only other genome available for *C. mastitidis*, which was obtained from a sheep.

Corynebacterium species are small, pleomorphic Gram-positive bacteria with coccoid, club, and rod forms (1). Many members of the genus are commensal and colonize the skin and mucous membranes of mammals. They are known to cause opportunistic infections in mammals, particularly immunocompromised subjects. *Corynebacterium mastitidis* was first isolated from the milk of a sheep (*Ovis aries*) with subclinical mastitis and was subsequently identified as part of the normal microbiota of the ocular surface in humans (2, 3). *C. mastitidis* is reported to play a key role in the development of suppurative inflammation and preputial gland abscesses associated with fight wounds in mice (*Mus musculus*) (1). It has also been identified as an ocular commensal in C57BL/6 mice that drives the release of antimicrobials into the tears to protect the eye from pathogens such as *Candida albicans* and *Pseudomonas aeruginosa* (3). The isolate described here, *C. mastitidis* strain 16-1433, was cultured from a 7-month-old female C57BL/6 mouse that presented with microphthalmia, blepharitis, and keratitis. Aerobic culture of the right eye was performed and grew *C. mastitidis* identified using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS).

The isolate was cultured on tryptic soy agar supplemented with soy lecithin and polysorbate 80 (prepared in-house at the Centers for Disease Control and Prevention) and incubated at 37°C for 48 h. Genomic DNA was extracted according to the Quick-DNA fungal/bacterial micro prep kit (Zymo Research, Irvine, CA, USA) protocol, and the library was created using the NEBNext Ultra DNA kit (New England BioLabs, Ipswich, MA, USA) and quantified using the Qubit version 1.0 fluorometer (ThermoFisher Waltham, MA, USA). Paired-end sequencing (2 × 250 bp) was performed with the Illumina MiSeq platform (Illumina, San Diego, CA, USA). PhiX was removed from the FastQ read files with BBDUK version 37.02 using a 31-mer search allowing for a single nucleotide difference in the query, and Trimmomatic version 0.36 was used to remove adapter sequences and discard low-quality nucleotides (4). Cleaned sister reads along with cleaned broken (singleton) reads were provided to SPAdes version 3.11.1 for *de novo* assembly using the “--only-assembler” option (5). To refine the genome, BWA-MEM version 0.7.16a-r1181 was used to map only the cleaned paired reads back onto

Received 12 January 2018 Accepted 16 January 2018 Published 15 February 2018

Citation Cheleuitte-Nieves C, Gulvik CA, Humrighouse BW, Bell ME, Villarma A, Westblade LF, Lipman NS, Fischetti VA, McQuiston JR. 2018. Draft reference genome sequence of *Corynebacterium mastitidis* 16-1433, isolated from a mouse. Genome Announc 6:e00050-18. <https://doi.org/10.1128/genomeA.00050-18>.

Copyright © 2018 Cheleuitte-Nieves 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 Christopher Cheleuitte-Nieves, cheleuic@mskcc.org.

the assembly with the “-x intractg” option (6), and SAMtools version 1.3.1 generated a binary alignment map (BAM) file (7). The BAM and assembly files were provided to Pilon version 1.22 and “--fix snps,indels” and “--mindepth 0.5” options were invoked to correct initial assembly errors (8). Two subsequent rounds of polishing were performed with the same parameters to correct errors that were missed due to stringent read mapping parameters and conservative correction. According to QUAST version 4.6.0 and CheckM version 1.0.8, the quality of our genome exceeds the only other assembly (GenBank accession no. NZ_AQXB01000000; 99.97% completeness) available for the species with 100% estimated completeness from 585 single-copy gene markers in the *Corynebacterium* genus (9, 10). The genome of *C. mastitidis* 16-1433 consists of 2,264,319 bp with a GC content of 69.04%, as well as 2,132 protein-coding genes, 51 tRNAs, and 57 RNAs.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. [PJAF00000000](https://doi.org/10.1093/bioinformatics/btp352). The version described in this paper is the first version, PJAF01000000.

ACKNOWLEDGMENTS

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention. The mention of company names or products does not constitute endorsement by the CDC.

REFERENCES

1. Radaelli E, Manarolla G, Pisoni G, Balloi A, Aresu L, Sparaciari P, Maggi A, Caniatti M, Scanziani E. 2010. Suppurative adenitis of preputial glands associated with *Corynebacterium mastitidis* infection in mice. *J Am Assoc Lab Anim Sci* 49:69–74.
2. Fernandez-Garayzabal JF, Collins MD, Hutson RA, Fernandez E, Monasterio R, Marco J, Dominguez L. 1997. *Corynebacterium mastitidis* sp. nov., isolated from milk of sheep with subclinical mastitis. *Int J Syst Bacteriol* 47:1082–1085. <https://doi.org/10.1099/00207713-47-4-1082>.
3. St. Leger AJ, Desai JV, Drummond RA, Kugadas A, Almaghrabi F, Silver P, Raychaudhuri K, Gadjeva M, Iwakura Y, Lionakis MS, Caspi RR. 2017. An ocular commensal protects against corneal infection by driving an interleukin-17 response from mucosal $\gamma\delta$ T cells. *Immunity* 47:148–158. <https://doi.org/10.1016/j.immuni.2017.06.014>.
4. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
5. 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. <https://doi.org/10.1089/cmb.2012.0021>.
6. Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv:1303.3997v2.
7. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics* 25:2078–2079. <https://doi.org/10.1093/bioinformatics/btp352>.
8. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One* 9:e112963. <https://doi.org/10.1371/journal.pone.0112963>.
9. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
10. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>.