



Draft Genome Sequence of Methicillin-Resistant *Staphylococcus aureus* Strain LC33 Isolated from Human Breast Milk

Jéssica B. de Almeida,^a Suzi P. de Carvalho,^a Leandro M. de Freitas,^b
Ana Marcia S. Guimarães,^c Naila C. do Nascimento,^d Andrea P. dos Santos,^d
Joanne B. Messick,^d Jorge Timenetsky,^c Lucas M. Marques^{a,b,c}

State University of Santa Cruz (UESC), Campus Soane Nazaré de Andrade, Ilhéus, Brazil^a; Multidisciplinary Institute of Health, Universidade Federal da Bahia, Vitória da Conquista, Brazil^b; Department of Microbiology, Institute of Biomedical Science, University of São Paulo, São Paulo, Brazil^c; Department of Comparative Pathobiology, Purdue University, West Lafayette, Indiana, USA^d

ABSTRACT Here, we report the draft genome sequence of *Staphylococcus aureus* strain LC33, isolated from human breast milk in Brazil. This microorganism has been typed as ST1/t127/sccmecV. To our knowledge, this is the first draft genome sequence of a methicillin-resistant *S. aureus* strain isolated from human breast milk.

Human breast milk is the source of nutrition for newborns in the first months of life (1). Over the past years, the isolation of *Staphylococcus aureus* from human milk has raised concern regarding newborn infection following milk ingestion (2, 3). *S. aureus* is the second leading cause of acquired infections in neonatal intensive care units worldwide (4). The clinical importance of *S. aureus* is attributed to its high virulence, its being able to cause superficial lesions and systemic infections, and its rapid development of drug resistance (5). Accordingly, methicillin-resistant *S. aureus* (MRSA) is an important pathogen that was first detected in hospitals (HA-MRSA), but has recently emerged in the community (CA-MRSA) (6, 7).

S. aureus strain LC33 was isolated from samples of human breast milk collected from a human milk bank in Vitória da Conquista, Bahia, Brazil. The strain was characterized by multilocus sequence typing as sequence type 1 (ST1), clonal complex 1 (CC1), as t127 by *spa* typing, and as carrying a staphylococcal chromosomal cassette *mec* element (SCC*mec*) type V by PCR. DNA was extracted using a PureLink Genomic DNA minikit (Life Technologies, Inc., Brazil), and the whole genome was sequenced from a paired-end library using the Illumina HiSeq 2500 platform (Illumina, Inc., San Diego, CA, USA) at the Purdue University Genomics Core Facility. Average reads of about 100 bases were assembled using ABySS version 1.2.7. After assembly resulting from 1,641× genome coverage, first-pass annotation was achieved using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP).

A total of 39,477,532 reads were assembled into 53 contigs, resulting in a genome size of approximately 2,851 Mb with a G+C content of 32.7%. Annotation resulted in 2,860 protein-coding genes, 47 RNA-coding genes (39 tRNAs, four rRNAs, and four ncRNAs), and 84 pseudogenes. The resistome was analyzed using ResFinder version 2.1 (<http://cbs.dtu.dk/services/ResFinder>), and the following resistance genes were identified: *aph(3')-III* (aminoglycoside resistance); *mecA* (β -lactam resistance); *blaZ* (β -lactam resistance) and *norA* (fluoroquinolone resistance). To our knowledge, the draft genome sequence presented here is the first for an *S. aureus* strain isolated from human breast milk. Further analyses of these data may contribute to a better understanding of the molecular mechanisms involved in antibiotic resistance, pathogenicity, and dissemination.

Received 9 February 2017 Accepted 14 February 2017 Published 13 April 2017

Citation de Almeida JB, de Carvalho SP, de Freitas LM, Guimarães AMS, do Nascimento NC, dos Santos AP, Messick JB, Timenetsky J, Marques LM. 2017. Draft genome sequence of methicillin-resistant *Staphylococcus aureus* strain LC33 isolated from human breast milk. *Genome Announc* 5:e00154-17. <https://doi.org/10.1128/genomeA.00154-17>.

Copyright © 2017 de Almeida 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 Lucas M. Marques, lucasm@ufba.br.

Accession number(s). The genome sequence of methicillin-resistant *S. aureus* strain LC33 has been deposited in GenBank under the accession no. [MSFD00000000](https://doi.org/10.1093/nar/gkz119).

ACKNOWLEDGMENTS

We are extremely grateful to the Genomics Core Facility at Purdue University for constructing the library, running the HiSeq 2500 platform, and performing the ABySS assembly. This study was supported by PROPI/UFBA (01/2013).

REFERENCES

1. Jeurink PV, van Bergenhenegouwen J, Jiménez E, Knippels LM, Fernández L, Garssen J, Knol J, Rodríguez JM, Martín R. 2013. Human milk: a source of more life than we imagine. *Benef Microbes* 4:17–30. <https://doi.org/10.3920/BM2012.0040>.
2. Novak FR, Almeida JA, Warnken MB, Ferreira-Carvalho BT, Hagler AN. 2000. Methicillin-resistant *Staphylococcus aureus* in human milk. *Mem Inst Oswaldo Cruz* 95:29–33. <https://doi.org/10.1590/S0074-0276200000100003>.
3. Kayıran PG, Can F, Kayıran SM, Ergonul O, Gürakan B. 2014. Transmission of methicillin-sensitive *Staphylococcus aureus* to a preterm infant through breast milk. *J Matern Fetal Neonatal Med* 27:527–529. <https://doi.org/10.3109/14767058.2013.819332>.
4. Carey AJ, Duchon J, Della-Latta P, Saiman L. 2010. The epidemiology of methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* in a neonatal intensive care unit, 2000–2007. *J Perinatol* 30:135–139. <https://doi.org/10.1038/jp.2009.119>.
5. Machuca MA, Sosa LM, González CI. 2013. Molecular typing and virulence characteristic of methicillin-resistant *Staphylococcus aureus* isolates from pediatric patients in Bucaramanga, Colombia. *PLoS One* 8:e73434. <https://doi.org/10.1371/journal.pone.0073434>.
6. Stefani S, Chung DR, Lindsay JA, Friedrich AW, Kearns AM, Westh H, Mackenzie FM. 2012. Methicillin-resistant *Staphylococcus aureus* (MRSA): global epidemiology and harmonisation of typing methods. *Int J Antimicrob Agents* 39:273–282. <https://doi.org/10.1016/j.ijantimicag.2011.09.030>.
7. Andrade-Figueiredo M, Leal-Balbino TC. 2016. Clonal diversity and epidemiological characteristics of *Staphylococcus aureus*: high prevalence of oxacillin-susceptible mecA-positive *Staphylococcus aureus* (OS-MRSA) associated with clinical isolates in Brazil. *BMC Microbiol* 16:115. <https://doi.org/10.1186/s12866-016-0733-4>.