

Draft Genome Sequence of *Mycobacterium abscessus* subsp. *bolletii* INCQS 00594

Sylvia Cardoso Leão,^a Cristianne Kayoko Matsumoto,^a Cristina Viana-Niero,^a Rommel Thiago Jucá Ramos,^b Adriana Ribeiro Carneiro,^b Maria Silvanira Barbosa,^b Karla Valéria Batista Lima,^c Maria Luiza Lopes,^c Vasco Azevedo,^d Artur Silva^b

Departamento de Microbiologia, Imunologia e Parasitologia, Escola Paulista de Medicina, Universidade Federal de São Paulo, São Paulo, São Paulo, Brazil^a; Instituto de Ciências Biológicas, Universidade Federal do Pará, Belém, Pará, Brazil^b; Seção de Bacteriologia e Micologia, Instituto Evandro Chagas, Ananindeua, Pará, Brazil^c; Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil^d

An epidemic of surgical-site infections by a single strain of *Mycobacterium abscessus* subsp. *bolletii* affected >1,700 patients in Brazil from 2004 to 2008. The genome of the epidemic prototype strain *M. abscessus* subsp. *bolletii* INCQS 00594, deposited in the collection of the National Institute for Health Quality Control (INCQS), was sequenced.

Received 30 September 2013 Accepted 2 October 2013 Published 7 November 2013

Citation Leão SC, Matsumoto CK, Viana-Niero C, Ramos RTJ, Carneiro AR, Barbosa MS, Lima KVB, Lopes ML, Azevedo V, Silva A. 2013. Draft genome sequence of *Mycobacterium abscessus* subsp. *bolletii* INCQS 00594. *Genome Announc.* 1(6):e00896-13. doi:10.1128/genomeA.00896-13.

Copyright © 2013 Leão et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Artur Silva, asilva@ufpa.br.

Mycobacterium abscessus is a rapidly growing mycobacterium and an emerging human pathogen causing pulmonary infections, especially in patients with cystic fibrosis and other underlying lung disorders (1). *M. abscessus* is also a major cause of sporadic and clustered outbreaks of community-acquired and health care-associated skin and soft tissue infections (2). Recently, two subspecies were recognized within *M. abscessus*: *M. abscessus* subsp. *abscessus* and *M. abscessus* subsp. *bolletii* (3). The latter subspecies includes strains of two previously described taxa, *M. massiliense* and *M. bolletii* (4–6).

A prolonged nationwide epidemic of surgical infections related to video surgeries occurred in Brazil between 2004 and 2008 (7). The analysis of isolates obtained in different states confirmed that the epidemic was caused by a single strain of *M. abscessus* subsp. *bolletii* (8–12). One isolate, obtained from a patient who underwent laparoscopic surgery in 2004 in Belém, Pará (PA), was deposited as the epidemic prototype strain in the collection of the National Institute for Health Quality Control (INCQS) under the name INCQS 00594 (8). This isolate was shown to carry a circular plasmid of the IncP-1 β group, named pMAB01, which was the subject of a previous publication by Leão et al. (13).

The genome of *M. abscessus* subsp. *bolletii* INCQS 00594 was sequenced from a fragment library using the 454 GS FLX sequencer (Roche, Nutley, NJ) and the GS FLX Titanium sequencing kit XL+ at the Centre for Advanced Technologies in Genomics (CATG), Chemistry Institute, São Paulo University. A total of 779,074 reads (558,522,880 bp) were extracted from the .sff file with the script “sff_extract_0_2_13” (http://bioinf.comav.upv.es/sff_extract/), which represents a genomic coverage of ~111 \times . The reads were assembled using the MIRA software (14), generating 102 contigs with an N₅₀ of 664 kb. Eighteen contigs matched sequences in the plasmid pMAB01 (GenBank accession no. CP003376), and these were not considered here. The remaining sequences were annotated via RAST (15). The draft genome sequence of *M. abscessus* subsp. *bolletii* INCQS 00594 has

4,885,146 bp, an overall G+C content of 64.24%, 4,864 open reading frames (ORF), and one rRNA operon.

Nucleotide sequence accession numbers. This genome project has been deposited in DDBJ/EMBL/GenBank under the accession no. [AUVF00000000](https://www.ncbi.nlm.nih.gov/nuccore/AUVF00000000). The version described in this paper is the first version, AUVF01000000.

ACKNOWLEDGMENTS

This work was supported by grant no. 2011/18326-4 from the São Paulo Research Foundation (FAPESP). C.K.M. was the recipient of fellowship no. 2012/07335-5 from the FAPESP. This work was part of the Paraense Network of Genomics and Proteomics and was supported by the Paraense Amazonia Foundation (FAPESPA), the Amazon Center of Excellence in Genomics of Microorganisms-Centers of Excellence Support Program Pronex/CNPq/FAPESPA, the National Program for Academic Cooperation PROCAD/CAPES, the Studies and Projects Funding Agency (FINEP), and the Minas Gerais Research Foundation (FAPEMIG).

We thank Layla Farage Martins for technical assistance.

REFERENCES

1. Bryant JM, Grogono DM, Greaves D, Foweraker J, Roddick I, Inns T, Reacher M, Haworth CS, Curran MD, Harris SR, Peacock SJ, Parkhill J, Floto RA. 2013. Whole-genome sequencing to identify transmission of *Mycobacterium abscessus* between patients with cystic fibrosis: a retrospective cohort study. *Lancet* 381:1551–1560.
2. Brown-Elliott BA, Wallace RJ, Jr. 2002. Clinical and taxonomic status of pathogenic nonpigmented or late-pigmenting rapidly growing mycobacteria. *Clin. Microbiol. Rev.* 15:716–746.
3. Leão SC, Tortoli E, Euzeby JP, Garcia MJ. 2011. Proposal that *Mycobacterium massiliense* and *Mycobacterium bolletii* be united and reclassified as *Mycobacterium abscessus* subsp. *bolletii* comb. nov., designation of *Mycobacterium abscessus* subsp. *abscessus* subsp. nov. and emended description of *Mycobacterium abscessus*. *Int. J. Syst. Evol. Microbiol.* 61: 2311–2313.
4. Adékambi T, Berger P, Raoult D, Drancourt M. 2006. *rpoB* gene sequence-based characterization of emerging non-tuberculous mycobacteria with descriptions of *Mycobacterium bolletii* sp. nov., *Mycobacterium phocaicum* sp. nov. and *Mycobacterium aubagnense* sp. nov. *Int. J. Syst. Evol. Microbiol.* 56:133–143.

5. Adékambi T, Reynaud-Gaubert M, Greub G, Gevaudan MJ, La Scola B, Raoult D, Drancourt M. 2004. Amoebal coculture of "*Mycobacterium massiliense*" sp. nov. from the sputum of a patient with hemoptoic pneumonia. *J. Clin. Microbiol.* 42:5493–5501.
6. Leão SC, Tortoli E, Viana-Niero C, Ueki SY, Lima KV, Lopes ML, Yubero J, Menendez MC, Garcia MJ. 2009. Characterization of mycobacteria from a major Brazilian outbreak suggests that revision of the taxonomic status of members of the *Mycobacterium chelonae*-*M. abscessus* group is needed. *J. Clin. Microbiol.* 47:2691–2698.
7. ANVISA. 2011. Descriptive Report of the investigation of cases of infection by rapidly growing nontuberculous mycobacteria in Brazil from 1998 to 2009. Escola Paulista de Enfermagem, Universidade Federal de São Paulo, Brazil. (In Portuguese.) http://www.anvisa.gov.br/hotsite/hotsite_micobacteria/relatorio_descrito_mcr_16_02_11.pdf.
8. Leão SC, Viana-Niero C, Matsumoto CK, Lima KV, Lopes ML, Palaci M, Hadad DJ, Vinhas S, Duarte RS, Lourenço MC, Kipnis A, das Neves ZC, Gabardo BM, Ribeiro MO, Baethgen L, de Assis DB, Madalosso G, Chimara E, Dalcolmo MP. 2010. Epidemic of surgical-site infections by a single clone of rapidly growing mycobacteria in Brazil. *Future Microbiol.* 5:971–980.
9. Cardoso AM, Martins de Sousa E, Viana-Niero C, Bonfim de Bortoli F, Pereira das Neves ZC, Leão SC, Junqueira-Kipnis AP, Kipnis A. 2008. Emergence of nosocomial *Mycobacterium massiliense* infection in Goiás, Brazil. *Microbes Infect.* 10:1552–1557.
10. Duarte RS, Lourenço MC, Fonseca LdeS, Leão SC, Amorim Ediel, Rocha IL, Coelho FS, Viana-Niero C, Gomes KM, da Silva MG, Lorena NS, Pitombo MB, Ferreira RM, Garcia MH, de Oliveira GP, Lupi O, Vilaça BR, Serradas LR, Chebabo A, Marques EA, Teixeira LM, Dalcolmo M, Senna SG, Sampaio JL. 2009. Epidemic of postsurgical infections caused by *Mycobacterium massiliense*. *J. Clin. Microbiol.* 47:2149–2155.
11. Monego F, Duarte RS, Nakatani SM, Araújo WN, Riediger IN, Brockelt S, Souza V, Cataldo JI, Dias RC, Biondo AW. 2011. Molecular identification and typing of *Mycobacterium massiliense* isolated from postsurgical infections in Brazil. *Braz. J. Infect. Dis.* 15:436–441.
12. Viana-Niero C, Lima KV, Lopes ML, Rabello MCdS, Marsola LR, Brilhante VC, Durham AM, Leão SC. 2008. Molecular characterization of *Mycobacterium massiliense* and *Mycobacterium bolletii* in isolates collected from outbreaks of infections after laparoscopic surgeries and cosmetic procedures. *J. Clin. Microbiol.* 46:850–855.
13. Leão SC, Matsumoto CK, Carneiro A, Ramos RT, Nogueira CL, Lima JD, Jr, Lima KV, Lopes ML, Schneider H, Azevedo VA, da Costa da Silva A. 2013. The detection and sequencing of a broad-host-range conjugative IncP-1 β plasmid in an epidemic strain of *Mycobacterium abscessus* subsp. *bolletii*. *PLoS One* 8:e60746. doi:10.1371/journal.pone.0060746.
14. Chevreur B, Pfisterer T, Drescher B, Driesel AJ, Müller WE, Wetter T, Suhai S. 2004. Using the miraEST assembler for reliable and automated mRNA transcript assembly and SNP detection in sequenced ESTs. *Genome Res.* 14:1147–1159.
15. 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. doi:10.1186/1471-2164-9-75.