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Complete Genome Sequence of *Mycobacterium massiliense*

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***Mycobacterium massiliense* is a rapidly growing bacterium associated with opportunistic infections. The genome of a representative isolate (strain GO 06) recovered from wound samples from patients who underwent arthroscopic or laparoscopic surgery was sequenced. To the best of our knowledge, this is the first announcement of the complete genome sequence of an *M. massiliense* strain.**

Rapidly growing mycobacteria (RGM) have important implications in human diseases, as they are frequently associated with infections among immunocompromised patients, as well as wound, skin, and soft tissue infections (9). In addition, these bacteria are naturally resistant to several classes of antibiotics, particularly antituberculosis drugs. *Mycobacterium abscessus* is the most important pathogen among RGM; however, in 2004, Adékambi et al. (1) assigned a novel species name to a closely related isolate, *Mycobacterium massiliense*. *M. massiliense* has since been increasingly reported as causing soft tissue infection outbreaks. In Brazil, our group and others recently reported a major outbreak, with the characterization of some aspects of antibiotic resistance, as well as disinfectant resistance, that may have also contributed to the difficulty in controlling the spread of this strain (3, 5, 7, 2). The unusual clonality of the strain throughout distant states of Brazil made it especially interesting to sequence the genome of this isolate.

M. massiliense strain GO 06 was isolated from a patient who had undergone knee joint surgery (3), and its genome was sequenced by 454 GS-FLX Titanium (Roche). A total of 584,619 reads were obtained, with an average length of 428 bp. A single scaffold was assembled directly from 454 reads using MIRA software (4). It has 5,068,807 bp and an overall GC content of 64.2%. We could not detect the presence of any plasmid in the genome. Open reading frame (ORF) prediction and annotation were performed by Genome Reverse Compiler (11). Of the 4,313 ORFs present in the circular chromosome, 2,009 (46.6%) could be assigned by similarity to a known annotated protein function, 620 (14.4%) were assigned to unknown protein functions, and 1,633 (37.9%) were considered nonconserved. In addition, 2,869 ORFs (66.5%) were assigned to Clusters of Orthologous Groups categories (10). The rRNAs and tRNAs were identified using RNAmmer (6) and tRNAscan-SE (8), respectively. By these analyses, 48 tRNAs and one rRNA operon, comprising 5S, 16S, and 23S rRNA genes, could be detected in the genome.

Nucleotide sequence accession numbers. The results of this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under accession number CP003699. The version described in this paper is the first version, CP003699.

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REFERENCES

1. **Adékambi T, et al.** 2004. Amoebal coculture of "Mycobacterium massiliense" sp. nov. from the sputum of a patient with hemoptoic pneumonia. J. Clin. Microbiol. **42**:5493–5501.
2. **Cardoso AM, Junqueira-Kipnis AP, Kipnis A.** 4 January 2011, posting date. In vitro antimicrobial susceptibility of *Mycobacterium massiliense* recovered from wound samples of patients submitted to arthroscopic and laparoscopic surgeries. Minim. Invasive Surg. doi:10.1155/724635.
3. **Cardoso AM, et al.** 2008. Emergence of nosocomial *Mycobacterium massiliense* infection in Goiás, Brazil. Microbes Infect. **10**:1552–1557.
4. **Chevreux B, Wetter T, Suhai S.** 1999. Genome sequence assembly using trace signals and additional sequence information, p 45–56. *In* Proceedings of the German Conference on Bioinformatics (GCB). Universität Trier, Trier, Germany. http://www.bioinfo.de/isb/gcb99/talks/chevreux/.
5. **Duarte RS, et al.** 2009. Epidemic of postsurgical infections caused by *Mycobacterium massiliense*. J. Clin. Microbiol. **47**:2149–2155.
6. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
7. **Leao SC, et al.** 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.
8. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**:955–964.
9. **Petrini B.** 2006. *Mycobacterium abscessus*: an emerging rapid-growing potential pathogen. APMIS **114**:319–328.
10. **Tatusov RL, Galperin MY, Natale DA, Koonin EV.** 2000. The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Res. **28**:33–36.
11. **Warren AS, Setubal J.** 2009. The Genome Reverse Compiler: an explorative annotation tool. BMC Bioinformatics **10**:35. doi:10.1186/1471-2105-10-35.

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