

Whole-Genome Sequence of the Emerging Pathogen *Mycobacterium abscessus* Strain 47J26

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***Mycobacterium abscessus* is a rapidly growing environmental mycobacterium commonly found in soil and water which is often also associated with infections in humans, particularly of the lung. We report herein the draft genome sequence of *M. abscessus* strain 47J26.**

Mycobacterium abscessus was first described in 1953 (6) and is recognized as an emerging human pathogen (5a) which usually affects patients with bronchiectasis and cystic fibrosis (CF), where it can cause a serious lung disease, particularly following lung transplantation (1, 2). *M. abscessus* is one of the most drug-resistant mycobacterial species (4), difficult to treat even with agents (e.g., clarithromycin) to which it appears sensitive *in vitro*. It is also resistant to most disinfectants and biocides, which facilitates its survival in the hospital environment (5a). The genome sequence of the type strain ATCC 19977, isolated from a knee infection, was determined in 2009 (8). Here we present the second genome for this species, strain 47J26, isolated from a sputum sample collected from a patient with CF in December 2009.

The *M. abscessus* 47J26 genome was shotgun sequenced using Roche FLX 454, which resulted in 302,442 reads, 98.52% (297,977) of which assembled using Newbler v2.5 into 17 high-quality contigs (>500 bp and >50 reads). The draft genome size is 4,556,047 bp, with an average G+C content of 64.5%. Average coverage depth was 20×, N_{50} contig size was 1.1 Mb, and average contig size was 286 kb. Annotation with PGAAP (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) identified 4,824 predicted coding sequences (CDSs).

Comparison of *M. abscessus* 47J26 to ATCC 19977 using the BLASTN reciprocal best hit approach reveals 4,318 shared CDSs (average identity, 97.5%); 623 (12.6%) are specific to ATCC 19977 and 506 (10.4%) are specific to 47J26. Unlike *M. abscessus* ATCC 19977, strain 47J26 does not contain a copy of pMM23, the mercury resistance plasmid from *Mycobacterium marinum* (8). Over half of the chromosomal CDSs specific to strain 47J26 (315) form 12 regions of difference (RODs) of at least 10 CDSs in length. Two RODs correspond to two putative prophages predicted using Prophinder (5). A 60.2-kb ROD/prophage consists of 93 CDSs inserted into a leucyl-tRNA and shares 21 CDSs with an 81-kb prophage previously found in *M. abscessus* ATCC 19977 (8). The 47.1-kb ROD/prophage is not found in strain ATCC 19977, though 35 of the 66 predicted CDSs have homologs in previously sequenced double-stranded DNA (dsDNA)-tailed mycobacteriophages (7). Four of the RODs replace regions occupied by putative prophages in ATCC 19977. Of particular interest is a 13-kb ROD containing a putative mammalian cell entry (MCE) operon; in *Mycobacterium tuberculosis*, MCE genes confer on nonpathogenic

Escherichia coli the ability to invade and survive inside macrophages and HeLa cells (3, 9).

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AGQU00000000. The version described in this paper is the first version, AGQU01000000.

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