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GENOME ANNOUNCEMENT

Genome Sequence of the *Mycobacterium abscessus* Strain M93

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***Mycobacterium abscessus* is a rapid-growing species of nontuberculous mycobacteria that is frequently associated with opportunistic infections in humans. We report herein the draft genome sequence of *M. abscessus* strain M93.**

Mycobacterium abscessus, also referred to as *M. abscessus* sensu lato, is an important pathogen in immunocompromised individuals. Although it is an environmental contaminant, it is also frequently found on medical equipment in hospitals (6) and has been linked with a variety of health care-associated and community-acquired infections, ranging from superficial skin and soft tissue lesions to deep-seated and disseminated sepsis. These infections can be difficult to treat because of resistance to antimicrobial therapy (5). It is not clear how the organism's genomic composition determines its pathogenicity, virulence, and response to chemotherapy. Even its taxonomic position has not been clarified, owing to conflicting results from molecular studies using single gene sequencing (3).

The genome of the *M. abscessus*, type strain ATCC 19977, was first isolated and sequenced in 2009 (4). Here, we present another genome for this species, strain M93, isolated from a sputum sample from a Malaysian patient presenting with a prolonged productive cough suggestive of a bacterial lower respiratory tract infection.

The strain M93 genome was shotgun sequenced using the Illumina Genome Analyzer 2× technology. With this technology, we generated 22,254,280 reads. These Illumina sequences were assembled with Genomics Workbench 4.9, resulting in 42 contigs with an N_{50} contig size of 413,411 bp.

The draft genome sequence shows a genome size 5,078,984 bp. The average GC content of this genome sequence is 64%, similar to the published genome sequences of *M. abscessus* strain ATCC 19977 (4) and strain 47J26 (1). The genome sequence was annotated using NCBI Prokaryotic Genomes Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). Using this automated pipeline, we identified 4,907 predicted coding sequences. There are 46 tRNA as predicted by tRNAscan-SE (2) and 2 rRNA loci as identified by the pipeline.

Nucleotide sequence accession number. The *M. abscessus* strain M93 genome sequence and annotation data have been deposited in NCBI GenBank under the accession number AJGF00000000.

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