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Genome Sequence of *Mycobacterium abscessus* Strain M152

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***Mycobacterium abscessus* is an environmental bacterium with increasing clinical relevance. Here, we report the annotated whole-genome sequence of *M. abscessus* strain M152.**

Mycobacterium abscessus is a member of the atypical mycobacteria that normally exist in soil and water but also cause human infections, particularly in immunocompromised hosts (7). This bacterium is known for its resistance to antibiotics and often has to be treated with combination drug therapy (5, 6). With the advent of molecular biology, DNA homology studies have largely replaced biochemical tests in the identification of mycobacteria (4). Among the *M. abscessus* group, gene sequencing has led to the identification of three members, *M. abscessus* sensu stricto, *M. abscessus* subsp. *massiliense*, and *M. abscessus* subsp. *bolletii* (1, 2).

M. abscessus strain M152 was isolated from the acid-fast bacillus (AFB)-positive sputum of a Malaysian man. Its genome was sequenced using the Illumina GA 2X technology, which generated 4,770,284 sequencing reads. These reads were processed and assembled using the commercial software CLC Genomics Workbench 4.9 (CLC bio), resulting in 45 contigs with an N_{75} contig size of 157,839 bp, N_{50} contig size of 319,489 bp, and N_{25} contig size of 447,369 bp. The consensus sequences were annotated with the Rapid Annotation using Subsystem Technology (RAST) pipeline (3). The draft genome sequence shows a genome size of 4,911,666 bp with G+C content of 64.2%, 46 tRNAs, and 3 rRNAs. There are 4,836 predicted coding sequences, of which 1,525 (32%) are involved mainly with amino acids and derivatives, stress response, and metabolism of RNA, DNA, protein, sulfur, phosphorus, potassium, iron, and aromatic compounds. This draft genome is 99.4% identical to that of *M. abscessus* ATCC 19977 (99% similarity by the *hsp65* gene, compared to 98% similarity to *M. abscessus* subsp. *bolletii* and *M. abscessus* subsp. *massiliense*). Although there are fewer coding sequences in M152 than in *M. abscessus* ATCC 19977, their subsystem distributions are very similar, for instance, in potassium metabolism, iron acquisition and metabolism, membrane transport, dormancy, and sporulation, as well as motility and chemotaxis. The addition of this genome sequence to the *M. abscessus* database will augment the information available for a better understanding of the biology and pathogenicity of this *Mycobacterium* species with its increasing clinical relevance.

Nucleotide sequence accession numbers. The *M. abscessus* strain M152 genome sequence and annotation data have been deposited in NCBI GenBank under the accession number AKVT00000000. The version described in this paper is the first version, AKVT01000000.

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