Complete Genome Sequence of a Type Strain of *Mycobacterium abscessus* subsp. *bolletii*, a Member of the *Mycobacterium abscessus* Complex

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ABSTRACT *Mycobacterium abscessus* subsp. *bolletii* is a rapidly growing mycobacterial organism for which the taxonomy is unclear. Here, we report the complete genome sequence of a *Mycobacterium abscessus* subsp. *bolletii* type strain. This sequence will provide essential information for future taxonomic and comparative genome studies of these mycobacteria.

The number of cases of nontuberculosis mycobacteria (NTM) is increasing, especially in developed countries. In our hospital-based survey of pulmonary NTM disease patients in Japan, the number of pulmonary *Mycobacterium abscessus* disease cases increased 5-fold relative to a survey conducted 7 years earlier (1). Moreover, the finding that the multidrug-resistant *M. abscessus* complex (MABC) is transmissible between patients with conditions such as cystic fibrosis provided a radical shift in thinking about MABC acquisition, which was previously thought to be environmental (2–4). Despite advances made in the genomics and documentation of clinical phenotypical differences among MABCs, discrepancies in conventional DNA-DNA hybridization (DDH) results led to debate about MABC taxonomic differentiation (3, 5–9).

Here, we report the complete genome sequence of *M. abscessus* subsp. *bolletii* BD^T (=CIP108541^T). The strain was grown in Middlebrook 7H9 medium, and DNA was extracted using a standard phenol-chloroform method. The genome sequence was determined using PacBio reads (112,992 reads) obtained with the RS II system (Pacific Biosciences, Menlo Park, CA, USA) (10–12). The reads were *de novo* assembled with Canu version 1.5 (13), and the assembled genome was circularized by manually trimming the repeated sequences. Illumina 2 × 300-bp paired-end reads (100,578,382 reads) were obtained with the MiSeq system (Illumina, San Diego, CA, USA) and mapped to the assembly using the Burrows-Wheeler aligner (14) for sequence and assembly error correction with Pilon (15). The DDBJ Fast Annotation and Submission Tool (DFAST) (https://dfast.nig.ac.jp/) was used for annotation (16). Average nucleotide identity (ANI), genome-to-genome distance (GGD), and genomic signature-delta distance (GS-DD) were calculated by JSpeciesWS, Genome-to-Genome Distance Calculator 2.1 (http://ggdc.dsmz.de/ggdc.php), and δ*-differences (http://www.cmbl.uga.edu/software/delta-differences.html), respectively (17–19).

The length of the *M. abscessus* subsp. *bolletii* BD^T genome is 5,080,450 bp (64.1% G+C content). Mycobacterium-related ANI was 96.95% to *M. abscessus* subsp. *abscessus* (complete genome of strain ATCC_19977^T [20]) and 96.73% to *M. abscessus* subsp. *massiliense* (complete genome of strain JCM_15300^T [7]). GGD-estimated DDH values between strains BD^T and ATCC_19977^T, strains ATCC_19977^T and

JCM_15300, and strains JCM_15300 and BD^T were 87.0%, 86.0%, and 88.1%, respectively. The GS-DD was 23 for these 3 comparisons. These values support the proposed taxonomic position of *M. abscessus* subsp. *bolletii* (3). The number of predicted protein-coding sequences in the genome (*n* = 4,976) is nearly equivalent to those of *M. abscessus* subsp. *abscessus* (*n* = 4,920) and *M. abscessus* subsp. *massiliense* (*n* = 4,857) (7, 20). The numbers of rRNA operons (*n* = 3) and tRNA genes (*n* = 49) are similar or equivalent to those of close relatives. Although a draft genome sequence for *Mycobacterium abscessus* subsp. *bolletii* BD^T was previously determined (21), the number of predicted genes differed significantly from that obtained here. We also identified a 97.1-kb prophage that was longer than that seen in a previous study (63 kb) (21). The complete genome sequence of *M. abscessus* subsp. *bolletii* BD^T represents essential data for future taxonomic and comparative genome studies.

Accession number(s). The chromosome sequence was deposited in DDBJ/ENA/GenBank under accession no. AP018436.

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