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 (=CIP108541T). 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 BT 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_19977T [20]) and 96.73% to M. abscessus subsp. massiliense (complete genome of strain JCM_15300T [7]). GGD-estimated DDH values between strains BT T and ATCC_19977T, strains ATCC_19977T and ATCC_19977T.

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