**Draft Genome Sequence of Mycobacterium abscessus subsp. bolletii BD**

Go-Eun Choi,a Yong-Joon Cho,b,c Won-Jung Koh,d Jongsik Chun,b,c,e Sang-Nae Cho,f and Sung Jae Shinf

Department of Microbiology and Research Institute for Medical Sciences, College of Medicine, Chungnam National University, Daejeon, Republic of Korea; Chunlab, Inc.,b and School of Biological Sciences, Seoul National University,c Seoul, Republic of Korea; Division of Pulmonary and Critical Care Medicine, Department of Medicine, Samsung Medical Center, Sungkyunkwan University, School of Medicine, Seoul, Republic of Korea; and Department of Microbiology, Yonsei University College of Medicine, Seoul, Republic of Koreaf

**Mycobacterium abscessus subsp. bolletii** is an increasing cause of human pulmonary disease and infections of the skin and soft tissues. Consistent reports of human infections indicate that *M. bolletii* is a highly pathogenic, emerging species of rapidly growing mycobacteria (RGM). Here we report the first whole-genome sequence of *M. abscessus subsp. bolletii BD*.  

*Mycobacterium abscessus subsp. bolletii* belongs to a group of rapidly growing mycobacteria (RGM) (10). However, *M. bolletii* has been shown to be highly resistant to clarithromycin, unlike other RGM. *Mycobacterium bolletii* was first isolated in 2006 from the sputum of a patient with chronic pneumonia and later from a group of patients with cystic fibrosis (1). Consistent reports of human infections and several recent outbreaks indicate that *M. bolletii* is a highly pathogenic, emerging RGM species (5, 10). Historically, *M. bolletii* was recognized as separate from the *Mycobacterium chelonae-Mycobacterium abscessus* complex (1). However, the reclassification of *M. bolletii* as *Mycobacterium abscessus* subsp. *bolletii* was proposed in accordance with the rules of the Bacteriological Code (6).  

To understand the genetics of *M. bolletii* in detail, the complete genome of the *M. abscessus* subsp. *bolletii BD* type strain (=CIP108541) was obtained from the Collection of Institute Pasteur (Paris, France). The genome was sequenced and annotated.  

The sequence data were obtained using Illumina GA IIx (San Diego, CA) with 100-bp single-end information (13,144,849 reads, ~1,165.9 Mb). All reads were assembled into 22 contigs by de novo assembly. Reference mapping results for *Mycobacterium abscessus* subsp. *abscessus* ATCC 19977T were obtained using CLC Genomics Workbench 4.6 (CLC bio, Aarhus, Denmark). Coverage of the genome reached ~231-fold; the N50 contig size was 462.2 kb. The functional annotation of predicted coding regions was achieved using the RAST server (2) and BLASTP-based comparisons with the KEGG (4) and COG (9) databases.  

The draft genome of *M. bolletii BD* includes 5,048,007 bp with a 64.0% G+C content. It contains 4,923 protein-coding genes and 47 rRNA-encoding genes. Judging from coverage, two rRNA operons exist in the genome. Functions were assigned to 56.1% (2,782) of the total coding sequences; 8.7% (428) were found to be hypothetical proteins that are unique to this strain.  

The average nucleotide identity (ANI) values between strain BD and ATCC 19977T were 96.64 and 96.7%, respectively, from comparisons in each direction. These correspond to DNA-DNA hybridization values of over 70% and agree with the classical species cutoff point (3).  

We also detected the presence of a 63-kb prophage, but functional genes were not found. Comparative genomic analysis with *M. abscessus* ATCC 19977T revealed that *M. bolletii BD* contains more virulence factor mammalian cell entry (MCE) operons. These proteins have high similarity to those from *Mycobacterium* sp. strain KMS, which supports the possibility of horizontal gene transfer between mycobacteria (8). In addition, several methyltransferases, glycosyltransferases, and dehydrogenases, which participate in cell wall synthesis and modification (7), were detected in insertion regions. We expect that the complete, annotated genomic sequence of *M. bolletii* will facilitate the future understanding of this bacterium’s pathogenic properties.  

**Nucleotide sequence accession number.** The draft genome sequence of *M. abscessus subsp. bolletii BD* has been deposited in the GenBank database under accession number AHAS00000000.

**ACKNOWLEDGMENT**

This study was supported by a grant of the Korea Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea (A101750).

**REFERENCES**


Received 5 March 2012 Accepted 7 March 2012

Address correspondence to Sung Jae Shin, sjshin05@gmail.com.

G.-E.C. and Y.-J.C. contributed equally to this article.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.00354-12


