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Draft Genome Sequence of Mycobacterium abscessus subsp. bolletii BD ^{T}

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GENOME ANNOUNCEMENT

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

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***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^T.**

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^T 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 19977^T were obtained using CLC Genomics Workbench 4.6 (CLC bio, Aarhus, Denmark). Coverage of the genome reached ~231-fold; the N_{50} 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^T includes 5,048,007 bp with a 64.0% G+C content. It contains 4,923 protein-coding genes and 47 tRNA-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^T and ATCC 19977^T 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 19977^T revealed that *M. bolletii* BD^T 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^T has been deposited in the GenBank database under accession number AHAS00000000.

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REFERENCES

1. **Adekambi T, Berger P, Raoult D, Drancourt M.** 2006. *rpoB* gene sequence-based characterization of emerging non-tuberculous mycobacteria with descriptions of *Mycobacterium bolletii sp. nov.*, *Mycobacterium phocaicum* sp. nov. and *Mycobacterium aubagnense* sp. nov. Int. J. Syst. Evol. Microbiol. **56**:133–143.
2. **Aziz RK, et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9**:75.
3. **Goris J, et al.** 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. Int. J. Syst. Evol. Microbiol. **57**:81–91.
4. **Kanehisa M, Goto S, Kawashima S, Okuno Y, Hattori M.** 2004. The KEGG resource for deciphering the genome. Nucleic Acids Res. **32**:D277–D280.
5. **Koh WJ, et al.** 2009. First case of disseminated *Mycobacterium bolletii* infection in a young adult patient. J. Clin. Microbiol. **47**:3362–3366.
6. **Leao SC, Tortoli E, Euzéby JP, Garcia MJ.** 2011. Proposal that the two species *Mycobacterium massiliense* and *Mycobacterium bolletii* be reclassified as *Mycobacterium abscessus* subsp. *bolletii* comb. nov., designation of

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Mycobacterium abscessus subsp. *abscessus* subsp. nov., and emended description of *Mycobacterium abscessus*. Int. J. Syst. Evol. Microbiol. **61**: 2311–2313.
7. **Perez E, et al.** 2004. Characterization of three glycosyltransferases involved in the biosynthesis of the phenolic glycolipid antigens from the *Mycobacterium tuberculosis* complex. J. Biol. Chem. **279**:42574–42583.
8. **Ripoll F, et al.** 2009. Non mycobacterial virulence genes in the genome of the emerging pathogen *Mycobacterium abscessus*. PLoS One **4**:e5660.
9. **Tatusov RL, et al.** 2003. The COG database: an updated version includes eukaryotes. BMC Bioinformatics **4**:41.
10. **Zelazny AM, et al.** 2009. Cohort study of molecular identification and typing of *Mycobacterium abscessus*, *Mycobacterium massiliense*, and *Mycobacterium bolletii*. J. Clin. Microbiol. **47**:1985–1995.