JB Journals.ASM.org

GENOME ANNOUNCEMENT

Complete Genome Sequence of *Mycobacterium intracellulare* Clinical Strain MOTT-64, Belonging to the INT1 Genotype

Byoung-Jun Kim,[a] Beom-Soon Choi,[b] Jong-Sung Lim,[b] Ik-Young Choi,[b] Yoon-Hoh Kook,[a] and Bum-Joon Kim[a]

Department of Microbiology and Immunology, Biomedical Sciences, Institute of Endemic Diseases, Seoul National University Medical Research Center (SNUMRC), Seoul National University College of Medicine, Seoul, Republic of Korea,[a] and National Instrumentation Center for Environmental Management, Seoul National University, Seoul, Republic of Korea[b]

Here, we report the complete genome sequence of the *Mycobacterium intracellulare* clinical strain MOTT-64, previously grouped into the INT1 genotype among five genotypes of *M. intracellulare*. This genome sequence will serve as a valuable reference for understanding the disparity in the virulence and epidemiologic traits among *M. intracellulare* genotypes.

Members of the *Mycobacterium avium* complex (MAC) are the most frequently isolated nontuberculous mycobacteria (NTM) (1, 8). *Mycobacterium intracellulare* has been reported to be isolated more frequently than *M. avium* in South Korea (4, 5, 7). Previously, we reported that 94 *M. intracellulare* clinical isolates from Korean patients were divided into five genotypes (INT1, INT2, INT3, INT4, and INT5) (6). Recently, we have introduced the complete genome sequences of two *M. intracellulare* strains belonging to the INT2 genotype, *M. intracellulare* ATCC 13950^T (GenBank accession no. CP003322) (3) and MOTT-02 (GenBank accession no. CP003323) (2).

The aim of the present study is to introduce the complete genome sequence of *M. intracellulare* clinical strain MOTT-64, which belongs to INT1, the most frequently encountered genotype in South Korea (6). The MOTT-64 genome was sequenced by a standard shotgun strategy using GS FLX pyrosequencing technology. Sequencing analysis was performed in the National Instrumentation Center for Environmental Management (NICEM; genome analysis unit) at Seoul National University, Seoul, Republic of Korea. A total of 544,705 reads were generated, with an average read length of 435, yielding 236,979,211 bp of total sequence. This represents ~43× coverage for the estimated 5.5-Mb genome. The obtained contigs were compared for mapping to the whole genome sequences of reference strains using the BLASTZ program (http://www.bx.psu.edu/miller_lab/). All the remaining gaps between contigs were completely filled by ~50-fold Solexa reads and PCR amplifications. Genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

Comparison of the MOTT-64 genome with those of two *M. intracellulare* strains, *M. intracellulare* ATCC 13950^T (GenBank accession no. CP003322) (3) and MOTT-02 (GenBank accession no. CP003323) (2), shows that it has a circular DNA molecule of 5,501,090 bp with no plasmid and is thus larger than the genome of *M. intracellulare* ATCC 13950^T (5,402,402 bp) or MOTT-02 (5,409,696 bp). MOTT-64 carries more protein-encoding genes (5,251 open reading frames [ORFs]) than *M. intracellulare* ATCC 13950^T (5,145 ORFs) or MOTT-02 (5,151 ORFs), but it has fewer tRNA genes (46 tRNA genes) than *M. intracellulare* ATCC 13950^T (47 tRNA genes) or MOTT-02 (47 tRNA genes). The genome of *Mycobacterium* strain MOTT-64 has a G+C content of 68.07%. Comparison of the predicted ORFs between ATCC 13950^T and MOTT-64 shows that 295 ORFs (5.7%) and 395 ORFs (7.5%) are specific to ATCC 13950^T and MOTT-64, respectively. Comparison of the predicted ORFs between MOTT-64 and MOTT-02 shows that 400 ORFs (7.6%) and 301 ORFs (5.8%) are specific to MOTT-64 and MOTT-02, respectively. Our phylogenetic analysis based on complete genome sequences from the NCBI microbial sequence databases also shows that MOTT-64, a member of the INT1 genotype, is phylogenetically separated from two strains of the INT2 genotype, *M. intracellulare* ATCC 13950^T and MOTT-02 (2, 3). This genome sequence will serve as a valuable reference for understanding the disparity in the virulence and epidemiologic traits among *M. intracellulare* genotypes.

Nucleotide sequence accession number. The whole-genome sequence of *Mycobacterium* strain MOTT-64 has been deposited at GenBank under the accession number CP003324.

ACKNOWLEDGMENT

This work was supported by a grant (no. 2010-0014269) from the National Research Foundation of Korea (NRF), Republic of Korea.

REFERENCES

1. **Falkinham JO, III.** 1996. Epidemiology of infection by nontuberculous mycobacteria. Clin. Microbiol. Rev. **9**:177–215.
2. **Kim B-J, et al.** 2012. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-02. J. Bacteriol. **194**:2771.
3. **Kim B-J, et al.** 2012. Complete genome sequence of *Mycobacterium intracellulare* strain ATCC 13950^T. J. Bacteriol. **194**:2750.
4. **Koh WJ, et al.** 2006. Clinical significance of nontuberculous mycobacteria isolated from respiratory specimens in Korea. Chest **129**:341–348.
5. **Koh WJ, Kwon OJ, Lee KS.** 2005. Diagnosis and treatment of nontuberculous mycobacterial pulmonary diseases: a Korean perspective. J. Korean Med. Sci. **20**:913–925.
6. **Park JH, et al.** 2010. Molecular characterization of *Mycobacterium intracellulare*-related strains based on the sequence analysis of *hsp65*, internal transcribed spacer and 16S rRNA genes. J. Med. Microbiol. **59**:1037–1043.
7. **Ryoo SW, et al.** 2008. Spread of nontuberculous mycobacteria from 1993 to 2006 in Koreans. J. Clin. Lab. Anal. **22**:415–420.
8. **Turenne CY, Wallace R, Jr, Behr MA.** 2007. *Mycobacterium avium* in the postgenomic era. Clin. Microbiol. Rev. **20**:205–229.

Received 23 March 2012 **Accepted** 29 March 2012

Address correspondence to Bum-Joon Kim, kbumjoon@snu.ac.kr.

doi:10.1128/JB.00471-12