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Whole-Genome Sequence of *Mycobacterium intracellulare* Clinical Strain MOTT-H4Y, Belonging to INT5 Genotype

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Here, we report the draft genome sequence of the *Mycobacterium intracellulare* clinical strain MOTT-H4Y, grouped previously into the INT5 genotype of the 5 genotypes of *M. intracellulare*.

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Of members of the *Mycobacterium avium* complex (MAC), *Mycobacterium intracellulare* has been reported to be isolated more frequently than is *M. avium* in Korea (1–3). Previously, we reported that the 94 *M. intracellulare* clinical isolates from Korean patients were divided into 5 genotypes (INT1, INT2, INT3, INT4, and INT5) (4). Recently, we introduced the complete genome sequences of four *M. intracellulare* strains: two INT2 strains (ATCC 13950^T [GenBank accession no. CP003322] [5] and MOTT-02 [GenBank accession no. CP003323] [6]), one INT1 strain (MOTT-64 [GenBank accession no. CP003324] [7]), and one INT5 strain (MOTT-36Y [GenBank accession no. CP003491] [8]). To understand the phylogenetic and genetic backgrounds of INT5 strains showing phylogenetic distinctness from other *M. intracellulare* genotypes, whole-genome sequencing of another *M. intracellulare* INT5 clinical strain, MOTT-H4Y, was performed in this study.

The *Mycobacterium* sp. MOTT-H4Y 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. A total of 787,165 reads were generated, with an average read length of 429, yielding 337,397,625 bp of the total sequences. This represents ~62× coverage for the estimated 5.4 Mb genome size. The assembled sequences contained three contigs (3,099,687 bp, 1,499,525 bp, and 819,111 bp) with a G+C content of 68.09% and a plasmid sequence (24,702 bp) with a G+C content of 65.4%. The obtained contigs were compared for mapping to the whole-genome sequences of the 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).

A comparison of the *Mycobacterium* sp. MOTT-H4Y genome with the *M. intracellulare* ATCC 13950^T and *Mycobacterium* sp. MOTT-36Y genomes (5, 8) reveals it to have a circular DNA of 5,418,323 bp with a plasmid of 24,702 bp. The genome of *Mycobacterium* sp. MOTT-H4Y contains similar numbers of protein-coding genes (5,233 open reading frames [ORFs]) as *M. intracellulare* ATCC 13950^T (5,145 ORFs) and *Mycobacterium* sp. MOTT-36Y (5,381 ORFs); however, the number of tRNA genes (48 tRNA genes) was greater than those of *M. intracellulare* ATCC 13950^T (47 tRNA genes) and *Mycobacterium* sp. MOTT-36Y (46 tRNA genes). The genome of *Mycobacterium* sp. MOTT-H4Y has a G+C content of 68.09%, and a plasmid was found in its genome with a G+C content of 65.4%. A comparison of predicted ORFs of *Mycobacterium* sp. MOTT-H4Y with *M. intracellulare* ATCC 13950^T and *Mycobacterium* sp. MOTT-36Y showed that they shared 4,685 ORFs (average identity, 95.9%) and 4,988 ORFs (average identity, 98.1%), respectively. Five hundred one ORFs (9.7%) and 547 ORFs (10.5%) were specific to *M. intracellulare* ATCC 13950^T and *Mycobacterium* sp. MOTT-H4Y, respectively, and 326 ORFs (6.1%) and 244 ORFs (4.7%) were specific to *Mycobacterium* sp. MOTT-36Y and *Mycobacterium* sp. MOTT-H4Y, respectively.

Nucleotide sequence accession number. Nucleotide sequences of the chromosome and plasmid of *Mycobacterium* sp. MOTT-H4Y have been deposited in GenBank under the accession no. AKIG00000000.

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REFERENCES

1. **Koh WJ, Kwon OJ, Jeon K, Kim TS, Lee KS, Park YK, Bai GH.** 2006. Clinical significance of nontuberculous mycobacteria isolated from respiratory specimens in Korea. Chest **129**:341–348.
2. **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.

3. **Ryoo SW, Shin S, Shim MS, Park YS, Lew WJ, Park SN, Park YK, Kang S.** 2008. Spread of nontuberculous mycobacteria from 1993 to 2006 in Koreans. J. Clin. Lab. Anal. **22**:415–420.
4. **Park JH, Shim TS, Lee SA, Lee H, Lee IK, Kim K, Kook YH, Kim BJ.** 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.
5. **Kim BJ, Choi BS, Lim JS, Choi IY, Lee JH, Chun J, Kook YH, Kim BJ.** 2012. Complete genome sequence of *Mycobacterium intracellulare* ATCC 13950^T. J. Bacteriol. **194**:2750.
6. **Kim BJ, Choi BS, Lim JS, Choi IY, Lee JH, Chun J, Kook YH, Kim BJ.** 2012. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-02. J. Bacteriol. **194**:2771.
7. **Kim BJ, Choi BS, Lim JS, Choi IY, Kook YH, Kim BJ.** 2012. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-64, belonging to the INT1 genotype. J. Bacteriol. **194**:3268.
8. **Kim BJ, Choi BS, Choi IY, Lee JH, Chun J, Hong SH, Kook YH, Kim BJ.** 2012. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-36Y, belonging to the INT5 genotype. J. Bacteriol. **194**: 4141–4142.