Complete Genome Sequence of Mycobacterium intracellulare Clinical Strain MOTT-36Y, Belonging to the INT5 Genotype

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Here we report the complete genome sequence of the Mycobacterium intracellulare clinical strain MOTT-36Y, previously grouped into the INT5 genotype among the 5 genotypes of M. intracellulare. This genome sequence will serve as a valuable reference for understanding the disparity in virulence and epidemiologic traits between M. intracellulare-related strains.

Traditionally, Mycobacterium avium complex (MAC) includes two species, Mycobacterium avium and Mycobacterium intracellulare (1, 9). M. intracellulare has been reported to be isolated more frequently than M. avium in Korea (5, 6, 8). Previously, we reported that the 94 M. intracellulare clinical isolates from Korean patients were divided into 5 genotypes (INT1, INT2, INT3, INT4, and INT5) (7). Recently we introduced the complete genome sequences of three M. intracellulare strains, one strain of the INT1 genotype (the MOTT-64 clinical strain [GenBank accession no. CP003324] [2]) and two strains of the INT2 genotype (ATCC 13950T [GenBank accession no. CP003322] [4] and the MOTT-02 clinical strain [GenBank no. CP003323] [3]).

The aim of the present study was to introduce the complete genome sequence of M. intracellulare clinical strain MOTT-36Y, belonging to the INT5 genotype (7). The MOTT-36Y genome was sequenced by a standard shotgun strategy using GS FLX pyro-sequencing technology. Sequencing analysis was performed in National Instrumentation Center for Environmental Management (NICEM) (Genome Analysis Unit) at Seoul National University. A total of 994,572 reads were generated, with an average read length of 341, yielding 339,374,044 bp of total sequences. This represents ~62× coverage for the estimated 5.6-Mb genome size. The obtained contigs were compared for mapping to the whole-genome sequences of the reference strain 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).

The MOTT-36Y genome reveals a circular DNA of 5,613,626 bp with no plasmid, larger than the genome sizes of M. intracellulare ATCC 13950T (4), MOTT-02 (3), and MOTT-64 (2). It contains larger amounts of protein-coding genes (5,381 open reading frames [ORFs]) than M. intracellulare ATCC 13950T (5,145 ORFs) and MOTT-64 (5,251 ORFs), but it has a lower number of tRNA genes (46 tRNA genes) than M. intracellulare ATCC 13950T (47 tRNA genes). The genome of MOTT-36Y has a G+C content of 67.91%. Comparison of predicted ORFs of MOTT-36Y with those of M. intracellulare ATCC 13950T showed that they shared 4,723 ORFs (average identity, 96.1%). The 476 ORFs (9.3%) and 657 ORFs (12.2%) were specific to M. intracellulare ATCC 13950T and MOTT-36Y, respectively. Our phylogenetic analysis based on the complete genome sequences from the NCBI microbial sequence databases also shows that MOTT-36Y, a member of the INT5 genotype, is phylogenetically separated from other three M. intracellulare strains (ATCC 13950T, MOTT-02, and MOTT-64), suggesting that the INT5 strain may be a novel mycobacterial species distinct from M. intracellulare. This genome sequence will serve as a valuable reference for understanding the disparity in the virulence and epidemiologic traits between M. intracellulare genotypes.

Nucleotide sequence accession number. The whole-genome sequence of Mycobacterium intracellulare strain MOTT-36Y has been deposited in GenBank under the accession number CP003491.

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