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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Mycobacterium intracellulare* Strain ATCC 13950^T

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Here we report the first complete genome sequence of *Mycobacterium intracellulare* ATCC 13950^T, a *Mycobacterium avium* complex (MAC) strain. This genome sequence will serve as a valuable reference for understanding the epidemiologic, biological, and pathogenic aspects of the disparity between MAC members.

Among the slow-growing mycobacteria responsible for opportunistic infections, members of the *Mycobacterium avium* complex (MAC) are the nontuberculous mycobacteria most frequently isolated in clinical settings (5–7). Traditionally, the MAC includes two species, *M. avium* and *Mycobacterium intracellulare* (1, 3, 6). There are definitely distinct disparities between these two MAC members in epidemiologic, biological, and pathogenic aspects. Currently, of the MAC strains, the complete genome sequences of two MAC strains, *M avium* subsp. *avium* 104 (CP000479) and *M. avium* subsp. *paratuberculosis* (AE016958) (4) and the partial genome sequence of *M. colombiense* (AFVW00000000) (2), closely related to *M. avium*, are available. However, the complete genome sequence of *M. intracellulare* has not yet been determined. To better understand the pathogenic mechanism of *M. intracellulare*, we report the complete, annotated genome sequence of *M. intracellulare* ATCC 13950^T in the present study.

The *M. intracellulare* genome was sequenced by a standard shotgun strategy using GS FLX pyrosequencing technology. Sequencing analysis was performed at the National Instrumentation Center for Environmental Management (Genome Analysis Unit) at Seoul National University. A total of 921,179 reads were generated, with an average read length of 400, yielding a total sequence of 368,366,484 bp. This represents 68× coverage of the estimated 5.4-Mb genome. The obtained 124 contigs were compared for mapping to the whole-genome sequences of reference strain using the BLASTZ program (http://www.psc.edu/general/software/packages/blastz/). All of 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 (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

Our data on the *M. intracellulare* genome show it to have a circular DNA of 5,402,402 bp, which is larger than the genome of *M. avium* subsp. *paratuberculosis* (4.8 Mb) and contains more protein coding genes (5,145 versus 4,400) and more tRNA genes (47 versus 45). The genome of *M. intracellulare* ATCC 13950^T has a G+C content of 68.10%, and no plasmid was found. *M. intracellulare* is known to form a close cluster with *M. avium* in a phylogenetic analysis based on the 16S rRNA gene sequence. Our phylogenetic analysis based on the complete genome sequences in the NCBI microbial sequence database also supported the close relationships of *M. intracellulare* with *M avium* subsp. *avium* 104 and *M. avium* subsp. *paratuberculosis*. The genome sequence reported here will serve as a valuable reference for understanding the epidemiologic, biological, and pathogenic aspects of the disparity between MAC members.

Nucleotide sequence accession number. The whole-genome sequence of *M. intracellulare* ATCC 13950^T has been deposited in the GenBank database under accession number CP003322.

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