Complete Genome Sequence of a Novel Clinical Isolate, the Nontuberculous Mycobacterium Strain JDM601[▽]

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Mycobacteriosis is on the increase. Nontuberculous mycobacteria (NTM) are resistant to most antituberculous drugs naturally. We determined the complete genome sequence of a novel NTM strain, JDM601, of the *Mycobacterium terrae* complex, which was isolated from a patient with tuberculosis-like disease and with various antibiotic resistances.

Mycobacterium terrae was first isolated in 1950 from radish washings and was described as an acid-fast saprophyte and nonpathogenic mycobacterium (8). Despite the common opinion that *M. terrae* complex (MTEC) isolates are nonpathogenic, these organisms are occasionally identified in the clinical laboratory in the setting of clinical disease (1, 2, 4, 10). In the past century, because of the presumed nonpathogenic nature of MTEC, there has been little effort to distinguish the species of this complex in the clinical setting. However, MTEC infection can cause debilitating disease that is relatively resistant to antibiotic therapy. *M. sensuense* and *M. paraterrae* are two novel MTEC species that were recently isolated from patients with pulmonary infection (3, 6). However, the genomic knowledge of MTEC is limited. In this study, we determined the whole genome sequence, by the 454 GS FLX system (5), of a novel pathogenic mycobacterium belonging to MTEC, which was isolated from a patient with tuberculosis-like disease and with a high level of resistance to various antibiotics.

The complete genome of *Mycobacterium* strain JDM601 contains a single, circular chromosome of 4,643,668 bp without any plasmid. The overall GC content of the chromosome is 68.4%. The entire genome of JDM601 contains 4,346 protein-coding genes, two sets of ribosome RNA operons, and 46 tRNA-encoding genes. It was possible to assign a biological function to 65.8% (2,862) of the coding sequence on the JDM601 chromosome; 28.5% (1,238) were found to be conserved hypothetical proteins, and 5.7% (246) were unique. The protein coding percentage is 92.2%.

The genes of JDM601 were most similar to those of *M. marinum* M (11) among all mycobacteria with complete genome sequences determined, and they had common insertion

sequences. Sixteen insertion sequences were found in the genome of JDM601, with five groups, four ISMyma01_aa1-like proteins, four ISMyma01_aa2-like proteins, five IS265 family transposases, an ISMsm5, and two putative transposases. No prophage was found in JDM601. There were only four integrase genes related to prophage and a gp49 without any other characteristic functional prophage genes.

Most of the slowly growing mycobacteria (SGM) had only one rRNA operon, compared with the two found in rapidly growing mycobacteria (RGM). However, *M. terrae* and JDM601, which belong to the SGM, had two rRNA operons. The two operons of the former strain were different (7), and the operons of the latter strain were the same as each other. Interestingly, the sequencing coverage of the operon contig was close to the genome average coverage, which may mean this contig had one copy in the whole genome. However, there were two copies in the genome, which was indeed confirmed by PCR. The reason for the abnormal operons requires further study.

Some reports mentioned the evolution of nontuberculous mycobacteria from nonpathogenicity toward pathogenicity (9, 11). We also found several genes coding proteins that were associated with pathogenicity, such as PE and PPE proteins, MCE family proteins, and lipases/esterases/monooxygenases. The pathogenicity and antibiotics resistance analysis of JDM601 have been described in our other work.

Nucleotide sequence accession number. Genome information for the chromosome of *Mycobacterium* strain JDM601 was deposited in GenBank under the accession number CP002329.

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