Complete Genome Sequence of Mycobacterium xenopi Type Strain RIVM700367

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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Mycobacterium xenopi* Type Strain RIVM700367

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***Mycobacterium xenopi* is a slow-growing, thermophilic, water-related *Mycobacterium* species. Like other nontuberculous mycobacteria, *M. xenopi* more commonly infects humans with altered immune function, such as chronic obstructive pulmonary disease patients. It is considered clinically relevant in a significant proportion of the patients from whom it is isolated. We report here the whole genome sequence of *M. xenopi* type strain RIVM700367.**

The genus *Mycobacterium* comprises over 150 known species and 13 subspecies (3), of which nearly one-third have been associated with disease in humans. *Mycobacterium xenopi* is a slow-growing, waterborne, and scotochromogenic mycobacterium. It was first isolated from skin lesions in a clawed frog (*Xenopus laevis*) in 1959 (10). It is a well-known opportunistic pathogen commonly associated with disease in humans, notably, pulmonary infections. Along with *M. avium* and *M. kansasii*, *M. xenopi* represents one of the most common agents of mycobacterial pulmonary infections other than tuberculosis (13). The clinical presentation of the lung infection caused by *M. xenopi* mimics the disease caused by *Mycobacterium tuberculosis* complex (MTC) and *Mycobacterium avium-M. intracellulare* (4). Extrapulmonary and disseminated infections have also been reported, particularly infections involving bone, joints, and muscle (1, 5, 7, 9, 12). However, knowledge on the pathogenesis underlying *M. xenopi* infection is limited. As a first step toward elucidating the molecular basis of *M. xenopi* virulence mechanisms, we have characterized the complete genome sequence of this microorganism. Whole-genome sequencing is also important in order to facilitate more precise identification and rapid diagnosis of *M. xenopi* infections in patients. For instance, on the basis of just limited genomic information, the designation *M. noviomagense* was recently introduced to mark a subgrouping of *M. xenopi* not associated with any clinical importance.

The *M. xenopi* type strain RIVM700367 genome was sequenced by a whole-genome shotgun strategy using the Illumina Hiseq2000 platform. The genome assembly was performed using the *de novo* assembler Velvet (14) and resulted in 117 contigs with an N_{50} of 154,665 bp, comprising in total 4,434,836 bp. The overall GC content of the chromosome amounted to 66.12%. The genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). The entire genome of *M. xenopi* was predicted to encode 4,282 coding sequences (CDSs), five sets of rRNA operons, and 46 tRNA-encoding genes. It was possible to assign a biological function to 64% (2,749) of the coding sequences on the *M. xenopi* chromosome.

The RAST server annotation pipeline (2) showed that *M. xenopi* has the highest similarity with *M. avium* subsp. *paratuberculosis* (6), compared to all mycobacteria with complete genome sequences currently available. Furthermore, our characterization of the *M. xenopi* genome showed it to be smaller (4.4 Mb) than the genome of *M. avium* subsp. *paratuberculosis* (4.8 Mb) and to carry fewer genes (4,333 versus 4,399).

Previous studies hypothesized about the evolution of pathogenic nontuberculous mycobacteria from nonpathogenic forms (8, 11). In this regard, the presence of genes involved in virulence and pathogenicity are of particular interest. Careful inspection of the *M. xenopi* genome showed that this genome encodes several genes associated with pathogenicity in other mycobacteria, such as PE and PPE proteins, mammalian cell entry (MCE) family proteins, and esterases/lipases. Interestingly, the important virulence locus *esx-1* is missing in *M. xenopi*, similar to what is observed for species of the *M. avium* complex. Further manual annotation of the genome and functional analysis will provide more information regarding the possible evolution of the pathogenicity of *M. xenopi*.

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under accession number AJFI00000000. The version described in this paper is the first version, AJFI00000000.

ACKNOWLEDGMENTS

This work was supported by faculty funding to A.P. by the King Abdullah University of Science and Technology. M.R. was supported by a SABIC postdoctoral fellowship.

We thank the Dutch National Institute for Public Health and the Environment (RIVM) for providing the strain. We gratefully acknowledge

Received 26 March 2012 **Accepted** 9 April 2012

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doi:10.1128/JB.00482-12

the support of Eveline Weerdenbrug and Roy Ummels at the Department of Medical Microbiology and Infection Control, VU University Medical Centre, Amsterdam, The Netherlands, and Thomas Dan Otto from The Wellcome Trust Sanger Institute, Cambridge, United Kingdom.

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