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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Mycobacterium phlei* Type Strain RIVM601174

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***Mycobacterium phlei* is a rapidly growing nontuberculous *Mycobacterium* species that is typically nonpathogenic, with few reported cases of human disease. Here we report the whole genome sequence of *M. phlei* type strain RIVM601174.**

Nontuberculous mycobacteria (NTM) are ubiquitous organisms and are increasingly recognized as an important cause of infection in immunocompromised and immunocompetent individuals. *Mycobacterium phlei* is a fast-growing, saprophytic bacterium that is widely distributed in soil and dust and on plants. It has only occasionally been associated with disease in humans with a suppressed immune system (5–7, 9) or in immunocompetent individuals (4, 8, 10). *M. phlei* was repeatedly isolated from synovial fluid and tissue in an immunocompetent pediatric patient with conjunctivitis, urethritis, and arthritis (1). Most of the existing identification methods for mycobacterial isolates rely on just a single genetic target, and often diverse variants are grouped in one (sub)species (11). Whole-genome sequencing provides the highest resolution on the DNA level and therefore is the most reliable approach for determining the genetic relatedness of mycobacteria. Information on specific genes, especially those of pathogenic mycobacteria, can be used to identify, unequivocally, subgroupings within species associated with clinical relevance. To facilitate a more reliable genetic identification between and within *Mycobacterium* species, we have characterized the complete genome sequence of *M. phlei* strain RIVM601174.

The whole-genome sequencing of the *M. phlei* type strain RIVM601174 genome was performed on the Illumina Hiseq2000 platform using a paired-end read library of read length 100 bp with insert size of 500 bp. The short sequence reads were first processed with Trimmomatic (http://www.usadellab.org/cms/index.php?page=trimmomatic) and FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) software before assembling them using the *de novo* assembler Velvet (12), resulting in 102 contigs with an N_{50} of 155,851 bp, comprising in total 5,681,954 bp. The overall GC content of the chromosome was 69.24%, one of the highest among the mycobacteria. The genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). The *M. phlei* genome was predicted to include 5,435 coding sequences (CDSs), four sets of rRNA operons, and 50 tRNA-encoding genes. It was possible to assign a biological function to 72% (3,969) of the coding sequences.

The RAST server annotation pipeline (2) was used to reveal that *M. phlei* is most closely related to *Mycobacterium* sp. strain MCS among all mycobacteria for which a complete genome sequence is available. The *M. phlei* genome was found to be smaller (5.64 Mb) than the genome of *Mycobacterium* sp. MCS (5.71 Mb) and to encode fewer genes (5,489 versus 5,698). Interestingly, unlike rapidly growing mycobacteria, our analysis of the *M. phlei* genome showed that this genome encodes a putative mammalian cell entry (MCE) operon, which was previously shown to be conserved only among slow-growing mycobacteria. This virulence factor operon in nonpathogenic *Escherichia coli* confers the ability to invade and survive inside host cells, such as macrophages and HeLa cells (3, 13). Further genomic and functional analyses are needed to investigate this observation.

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under accession number AJFJ00000000. The version described in this paper is the first version, AJFJ00000000.

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