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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Mycobacterium fortuitum* subsp. *fortuitum* Type Strain DSM46621

Yung S. Ho,[a] Sabir A. Adroub,[a] Fajr Aleisa,[a] Hanan Mahmood,[a] Ghofran Othoum,[a] Fahad Rashid,[a] Manal Zaher,[a] Shahjahan Ali,[b] Wilbert Bitter,[c] Arnab Pain,[a] and Abdallah M. Abdallah[a]

Pathogen Genomics Laboratory, King Abdullah University of Science and Technology, Thuwal-Jeddah, Saudi Arabia[a]; Bioscience Core Laboratory, King Abdullah University of Science and Technology, Thuwal-Jeddah, Saudi Arabia[b]; and Department of Medical Microbiology and Infection Control, VU University Medical Center, Amsterdam, The Netherlands[c]

***Mycobacterium fortuitum* is a member of the rapidly growing nontuberculous mycobacteria (NTM). It is ubiquitous in water and soil habitats, including hospital environments. *M. fortuitum* is increasingly recognized as an opportunistic nosocomial pathogen causing disseminated infection. Here we report the genome sequence of *M. fortuitum* subsp. *fortuitum* type strain DSM46621.**

Mycobacterium fortuitum is a nonpigmented rapidly growing *Mycobacterium* classified in Runyon group IV (5), first isolated from an amphibian source in 1905 and subsequently identified as the cause of a human cutaneous infection in a patient in 1938 (3). Like many other nontuberculous mycobacteria (NTM), *M. fortuitum* is found worldwide in natural and processed water sources, including chlorine-treated water, as well as in sewage, dirt, and hospital environments (4, 8). Major types of disease caused by *M. fortuitum* include, in decreasing order of frequency, infections of postsurgical wounds, soft tissue, skin, and lung (3, 5, 11). Occasionally reported miscellaneous infections include keratitis, endocarditis, lymphadenitis, meningitis, hepatitis, peritonitis, catheter-related sepsis, and disseminated infections (3, 6, 11). The *M. fortuitum* group is attracting attention due to its increasing number of cases, its virulence, and its emerging resistance to antibiotics. However, in the genome database, there is no whole genome of this species present until now. To facilitate a more reliable genetic identification in the *M. fortuitum* complex, we have characterized the complete genome sequence of *M. fortuitum* subsp. *fortuitum* type strain DSM46621.

To sequence the genome of *M. fortuitum* subsp. *fortuitum* type strain DSM46621, we used a shotgun sequencing method and Illumina HiSeq 2000 technology using a paired-end library, with a read length of 100 bp and an insert size of 500 bp. A total of 2.95 million Illumina sequencing reads were generated. These short sequence reads were first quality trimmed before *de novo* assembled using Velvet (12). The draft genome was further improved with iCORN (7) and IMAGE (10), as described in PAGIT (9), before it was scaffolded with SSPACE (2). The final assembly has 82 supercontigs and an N_{50} of 159,889 bp. The genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP).

The *M. fortuitum* subsp. *fortuitum* type strain DSM46621 genome sequence is 6,349,738 bp in length, with 6,241 predicted coding sequences. The overall GC content of the chromosome was 66%. There are 54 tRNA genes and four sets of rRNA operons as predicted by the PGAAP pipeline. It was possible to assign a biological function to 67.7% (4,225) of the coding sequences on the *M. fortuitum* subsp. *fortuitum* chromosome.

The RAST server annotation pipeline (1) revealed that *M. fortuitum* subsp. *fortuitum* has the highest similarity with *Mycobacterium smegmatis* strain MC2 155, among all mycobacteria with complete genome sequences determined. The *M. fortuitum* subsp. *fortuitum* genome was found to be smaller (6.38 Mb) than the genome of *M. smegmatis* MC2 155 (6.99 Mb) and to contain fewer genes (6,076 versus 6,816). Comparative genomic analysis with *M. smegmatis* MC2 155 revealed that *M. fortuitum* subsp. *fortuitum* contains more virulence-associated mammalian cell entry (MCE) operons. In addition, several methyltransferases, glycosyltransferases, and dehydrogenases, which probably participate in the cell wall synthesis and modification, were present in the *M. fortuitum* genome. We expect that this genome sequence will serve as a valuable reference for understanding the disparity in virulence and epidemiologic traits in the *M. fortuitum* complex.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALQB00000000. The version described in this paper is the first version, ALQB00000000.

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Address correspondence to Abdallah M. Abdallah, Abdallah.abdallah@kaust.edu.sa.

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