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GENOME ANNOUNCEMENT

Genome Analysis of *Mycobacterium massiliense* Strain M172, Which Contains a Putative Mycobacteriophage

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The genome of *Mycobacterium massiliense* M172, isolated from a human sputum sample, was sequenced using Illumina GA IIX technology and found to contain 5,204,460 bp, including putative genes for virulence and antibiotic resistance as well as a 92-kb genomic region most likely to correspond to a mycobacteriophage.

Lysogeny is found in many mycobacterial species isolated from environmental and clinical sources (6). Of more than 2,400 mycobacteriophages identified so far, only about 360, most of which are from soil samples, have been completely sequenced (Mycobacteriophage Database [http://phagesdb.org]). *Mycobacterium massiliense*, a subspecies of *Mycobacterium abscessus*, was first isolated from the sputum and bronchoalveolar fluid of a patient with hemoptoic pneumonia in Marseille, France (1). It is now known to be a frequent cause of bronchopulmonary infections in patients with compromised immunity (4).

Strain M172 is a sputum isolate from a Malaysian patient. It was identified as a *Mycobacterium massiliense* strain by its *rpoB* and *erm41* gene sequences (5, 7), which showed 99.0% and 100% similarity, respectively, to the *rpoB* and *erm41* gene sequences of the reference *M. massiliense* CIP108297 strain. Raw reads of the M172 genome were generated by using Illumina GA IIx technology, producing 17,156,157 reads. The sequences assembled with Genomics Workbench 5.0 (CLCBio, Aarhus, Denmark) produced 33 contigs, with an N50 contig size of 862,630 bp. The genome size of 5,204,460 bp and GC content of 64% were similar to those of reference *M. massiliense* strain CIP108297. Annotation results determined with Rapid Annotations using Subsystem Technology (RAST) (3) revealed 5,221 predicted coding sequences, 47 tRNAs, one tRNA pseudogene, and 2 rRNAs. In the coding sequences were 427 genes categorized for amino acids and other derivatives and 339 involved in cofactors, vitamins, prosthetic groups, and pigments. Of 38 genes involved in virulence and defenses, 25 were associated with resistance to antibiotics and toxic compounds. Two genes were associated with dormancy and sporulation, and 58 were linked to phages, prophages, and transposable elements. A large, 92-kb genomic region was observed that did not match with any region in the reference *M. abscessus* ATCC 19977 genome when sequences were aligned using BLAST program (2). RAST annotations showed the presence of many putative phage-related genes, including genes that code for phage-tail protein, phage endolysin, phage major capsid protein, phage capsid and scaffold, and phage tape measure protein. Both ends of this region were associated with putative open reading frames (ORFs) that code for phage integrase. It is likely that this genomic region belongs to a bacteriophage that had been inserted into the M172 genome. Work is ongoing to identify the origin of this phage and to examine its effect on the virulence and drug resistance of M172.

Nucleotide sequence accession numbers. The genome of *Mycobacterium massiliense* strain M172 has been deposited in NCBI GenBank/DDBJ/EMBL under accession number AJSE00000000. The version described here is the first version, which is available under accession number AJSE01000000.

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REFERENCES

1. **Adékambi T, et al.** 2004. Amoebal coculture of "*Mycobacterium massiliense*" sp. nov. from the sputum of a patient with hemoptoic pneumonia. J. Clin. Microbiol. **42**:5493–5501.
2. **Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ.** 1990. Basic local alignment search tool. J. Mol. Biol. **215**:403–410.
3. **Aziz RK, et al.** 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics **9**:75.
4. **Griffith DE, et al.** 2007. An official ATS/IDSA statement: diagnosis, treatment, and prevention of nontuberculous mycobacterial diseases. Am. J. Respir. Crit. Care Med. **175**:367–416.
5. **Kim H-Y, et al.** 2010. *Mycobacterium massiliense* is differentiated from *Mycobacterium abscessus* and *Mycobacterium bolletii* by erythromycin ribosome methyltransferase gene (*erm*) and clarithromycin susceptibility patterns. Microbiol. Immunol. **54**:347–353.
6. **McNerney R.** 1999. TB: the return of the phage. A review of fifty years of mycobacteriophage research. Int. J. Tuberculosis Dis. **3**:179–184.
7. **Zelazny AM, et al.** 2009. Cohort study of molecular identification and typing of *Mycobacterium abscessus*, *Mycobacterium massiliense*, and *Mycobacterium bolletii*. J. Clin. Microbiol. **47**:1985–1995.

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