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GENOME ANNOUNCEMENT

Genomic Insights into the Emerging Human Pathogen *Mycobacterium massiliense*

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***Mycobacterium massiliense* (*Mycobacterium abscessus* group) is an emerging pathogen causing pulmonary disease and skin and soft tissue infections. We report the genome sequence of the type strain CCUG 48898.**

Most nontuberculous mycobacterial respiratory infections are caused by *Mycobacterium abscessus* or *Mycobacterium avium* complex in patients with cystic fibrosis or chronic pulmonary disease. *M. abscessus* includes three closely related organisms, *Mycobacterium abscessus* (sensu stricto), *Mycobacterium massiliense*, and *Mycobacterium bolletii*, with taxonomic status under debate. Interest in *M. massiliense* arose following recent postsurgical infection outbreaks and a respiratory outbreak among cystic fibrosis patients (1, 5).

The genomes of three *M. abscessus* strains and of *M. bolletii* have been released (2–4, 6) and constitute an important resource to better understand the biology of these pathogens. Here we present the draft genome of the *M. massiliense* type strain CCUG 48898 and its comparison to the other released genomes. The sequence was obtained using a combination of the 454 Titanium 3-kb paired-end and Illumina HiSeq 2000 100-bp paired-end technologies. The draft genome includes 5 contigs with a cumulative size of 5,195,205 bp and a 64.1% G+C content. It contains 5,193 predicted protein-coding genes, 47 tRNA genes, and 1 rRNA operon. Potential functions were assigned to 66.6% (3,460) of the total coding sequences, while the rest were found to be hypothetical or conserved hypothetical proteins.

A phylogenetic tree based on core genome single nucleotide polymorphisms (SNPs) that was derived from a whole-genome multiple alignment clusters *M. abscessus* 47J26 with CCUG 48898, while *M. abscessus* M93 clusters with *M. abscessus* ATCC 19977 and *M. bolletii* BD appears separately.

Strain 47J26 carries an A-to-C substitution in the 23S rRNA, presumed to confer clarithromycin resistance. Both the *M. massiliense* type strain and 47J26 have the reported 2-nucleotide (CG) deletion and the large 276-nucleotide (nt) deletion in the inducible macrolide resistance gene *erm41* as well as several shared SNPs. These features and the tree described above indicate that 47J26 is most likely a strain of *M. massiliense*.

BLASTN-based comparisons (shared genes defined by a BLASTN e value of $\leq 10^{-5}$) revealed 346 and 304 genes that are unique to CCUG 48898 and 47J26, respectively, compared to the other three genomes. A pairwise comparison of these *M. massiliense*-specific genes revealed that 128 of these genes, including 2 genes encoding virulence-related WXG/ESAT-6 family proteins, are shared by CCUG 48898 and 47J26 while 226 and 188 genes are unique to CCUG 48898 and 47J26, respectively. We also identified an ~120-kb genomic region (108 genes) in CCUG 48898, encoding a beta-lactamase and 7 TetR family regulators, that is absent in 47J26. Most of these genes, including genes encoding virulence factors such as MCE and YrbE family proteins, are absent from the 2 *M. abscessus* genomes but mostly present (100 of 108) in *M. bolletii*.

None of the recently released genomes include the 23-kb mercury resistance plasmid found in *M. abscessus* (6).

A detailed genomic study promises a better understanding of the diseases caused by the *M. abscessus* group and *M. massiliense* in particular.

Nucleotide sequence accession number. The *M. massiliense* strain CCUG 48898 genome sequence and annotation data have been deposited at NCBI GenBank under the accession number AKVF00000000.

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