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Complete Genome Sequence of *Mycobacterium vaccae* Type Strain ATCC 25954

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Mycobacterium vaccae is a rapidly growing, nontuberculous *Mycobacterium* species that is generally not considered a human pathogen and is of major pharmaceutical interest as an immunotherapeutic agent. We report here the annotated genome sequence of the *M. vaccae* type strain, ATCC 25954.

There is an increasing interest in the role of nontuberculous mycobacteria (NTM) as pathogens causing pulmonary disease and disseminated disease in both immunocompetent and immunocompromised individuals. NTM species previously considered nonpathogenic have now been shown to cause disease in humans. *Mycobacterium vaccae*, a rapidly growing and yellow-pigmented NTM, was first isolated, described, and named in 1962 (4). This bacterium can be isolated from the environment, including soil and water and especially in contact with cattle, as well as from bovine lactic ducts, skin nodules, and milk products (13). Because of the strong association of this *Mycobacterium* species with cattle, it was named *M. vaccae*, as vaccae is the Latin word for cow. *M. vaccae*, previously considered nonpathogenic, has been associated rarely with pulmonary infections and soft tissue infections (5). However, *M. vaccae* is mainly being studied for use as an immunotherapeutic agent together with chemotherapy in the treatment of tuberculosis and other diseases, such as cancer, asthma, atopic dermatitis, and psoriasis (2, 6, 7, 9, 10). To better understand the molecular basis of *M. vaccae* and further study phylogenetic relationships and the genetic factors responsible for pathogenicity, we determined the complete genome sequence of this microorganism. Whole-genome sequencing is also important to facilitate a more reliable genetic identification between and within *Mycobacterium* species.

The whole-genome sequencing of the *M. vaccae* type strain, ATCC 25954, was performed on the Illumina HiSeq2000 platform using a 100-bp paired-end library with an insert size of 500 bp. A total of 24.7 million Illumina sequencing reads were generated. These short sequence reads were quality trimmed before being *de novo* assembled using velvet (14). The genome was further improved with ICORN (8) and IMAGE (12) as described in PAGIT (11) before it was scaffolded with SSPACE (3). The final assembly has 33 supercontigs and an N_{50} of 383,962 bp. The genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP).

The *M. vaccae* type strain ATCC 25954 genome sequence is 6,245,372 bp in length, with 5,949 predicted coding sequences. The overall GC content of the chromosome amounted to 68.5%. There are 49 tRNA-encoding genes and six sets of rRNA operons as predicted by the PGAAP pipeline. It was possible to assign a biological function to 71% (4,220) of the coding sequences on the *M. vaccae* chromosome.

The automated annotation of this genome by the RAST server (1) revealed that *M. vaccae* is most closely related to *Mycobacterium vanbaalenii* PYR-1, compared to all mycobacteria with complete genome sequences currently available. Furthermore, RAST annotation revealed that this genome may contain many genes encoding proteins that are categorized in the subsystem category of amino acids and derivatives (583 genes), followed by cofactors, vitamins, prosthetic groups, and pigments (371 genes). There are 57 genes encoding products that may be involved in virulence, disease, and defense, of which 37 are linked with resistance to antibiotics and toxic compounds, 12 are involved in invasion and intracellular resistance, and 8 are linked with antimicrobial products, such as bacteriocins.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALQA00000000. The version described in this paper is the first version, ALQA00000000.

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