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GENOME SEQUENCES

Draft Whole-Genome Sequences of *Microbacterium oxydans* and *Microbacterium maritypicum* Strains

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ABSTRACT *Microbacterium* spp. are a group of microbes that have been recovered from a wide variety of environments in nature. Here, I report the complete genomic data for *Microbacterium oxydans* and *Microbacterium maritypicum* type strains that are already present in public culture repositories. The genome of the *M. oxydans* strain was 3,894,869 bp long, with a G+C content of 68.26%. The genome of the *M. maritypicum* strain was 3,668,377 bp long, with a G+C content of 68.44%.

Microbacterium spp. are aerobic, Gram-stain-positive, rod-shaped bacteria. Widespread in nature, the genus *Microbacterium* comprises bacterial species relevant to humans, animals, plants, and the environment (1–3). In the present work, I report the whole-genome sequences of pure cultures of *Microbacterium oxydans* LMG 23389^T (= DSM 20578^T), which was isolated from contaminated hospital material (4), and *Microbacterium maritypicum* LMG 8374^T (= DSM 12512^T), which was isolated from seawater and marine mud (5), that were retrieved from the Belgian Coordinated Collections of Microorganisms (BCCM)/Laboratorium voor Microbiologie, University of Ghent (LMG).

Strains as dried material were cultivated and checked for purity after incubation at 28°C under aerobic conditions on Trypticase soy agar (TSA) (BBL 11768). Genomic DNA was isolated from isolated colonies using a Maxwell 16 tissue DNA purification kit (Promega) and a Maxwell 16 instrument (Promega) after a prior enzymatic lysis step with lysozyme (Sigma-Aldrich 62971) and mutanolysin (Sigma-Aldrich M9901). The integrity and purity of the DNA were evaluated with a 1.0% (wt/vol) agarose gel and spectrophotometric measurements at 234, 260, and 280 nm. A Quantus fluorimeter and a QuantiFluor ONE double-stranded DNA (dsDNA) system (Promega) were used to estimate the DNA concentrations.

Whole-genome sequencing (WGS) analyses were subsequently performed on each isolated strain. Accordingly, library preparation and WGS analyses of *M. oxydans* and *M. maritypicum* were performed by the Oxford Genomics Center (University of Oxford, Oxford, UK). Library preparation was performed using an adapted protocol for the NEBNext DNA preparation kit (New England BioLabs). Paired-end 150-bp sequence reads were generated using the NovaSeq 6000 platform (Illumina). Quality checks, trimming of the raw sequence reads, and *de novo* genome assembly were performed using the Shovill v0.9.0 pipeline (https://github.com/tseemann/shovill), which used SPAdes (6) as its core and aimed at a sequencing depth of 100×. Contigs shorter than 500 bp were excluded from the final assembly. Quality checks of the assemblies were performed using QUAST (7).

The assembled draft genomes of *M. oxydans* and *M. maritypicum* yielded 4 contigs (N_{50}, 1,058,097 bp; L_{50}, 2) and 5 contigs (N_{50}, 2,227,735 bp; L_{50}, 1), respectively. The genome of the *M. oxydans* strain was 3,894,869 bp long, with a G+C content of 68.26%. The genome of the *M. maritypicum* strain was 3,668,377 bp long, with a G+C content of 68.44%.

The draft genomes were then annotated using NCBI PGAP (https://www.ncbi.nlm.nih.gov/genome/annotation_prok), and secondary metabolites were predicted using antiSMASH v5.0.0 (https://antismash.secondarymetabolites.org) (8). Genome annotation by NCBI PGAP

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predicted 3,808 genes, including 3,751 coding sequences (CDSs) and 57 RNA genes (4 rRNAs, 50 tRNAs, and 3 noncoding RNAs [ncRNAs]), and 51 pseudogenes for the *M. oxydans* genome, whereas analyses of the *M. maritypicum* genome predicted 3,541 genes, including 3,488 CDSs and 53 RNA genes (3 rRNAs, 47 tRNAs, and 3 ncRNAs), and 36 pseudogenes.

Secondary metabolite cluster identification by antiSMASH predicted that the most similar cluster was the carotenoid biosynthetic gene cluster for both *Microbacterium* strains. In bacteria, carotenoids are involved in the mechanisms of membrane fluidity (9, 10) and protection of cells from oxidative damage and UV radiation (11, 12). In addition, both strains contain the ulleugmycine nonribosomal peptide synthetase (NRPS).

Data availability. The WGS shotgun projects have been deposited in DDBJ/ENA/GenBank under the accession numbers WAAP00000000 (BioProject accession number PRJNA573493) and WAAQ00000000 (BioProject accession number PRJNA573495) for *Microbacterium oxydans* and *Microbacterium maritypicum*, respectively. The raw reads have been deposited in the NCBI Sequence Read Archive (SRA) under the SRA accession numbers SRR21898868 and SRR21901517 for *Microbacterium oxydans* and *Microbacterium maritypicum*, respectively.

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