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Complete genome sequence of *Actinomyces oris* strain MG-1: an oral commensal critical for dental plaque formation

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ABSTRACT *Actinomyces oris* MG-1 is a key oral commensal involved in dental plaque formation. We report its complete genome sequence, generated using Illumina and Oxford Nanopore sequencing. The genome consists of a single circular chromosome of 3,042,829 bp, providing a resource for future functional studies.

KEYWORDS *Actinomyces oris*, dental plaque, genome sequencing, fimbriae

Actinomyces oris is a prominent early colonizer in oral biofilms and plays a central role in dental plaque formation, largely due to its surface-associated fimbrial structures (1). Strain MG-1, acquired from ATCC (#43146) and maintained in our laboratory, has been the principal model for studying *A. oris* fimbriae and coaggregation. It was originally isolated from dental plaque and initially designated as *A. viscosus* (2), reclassified as *A. naeslundii* (3), and later recognized as *A. oris* (4). Although a draft genome sequence is available (BioProject PRJNA327886), it consists of 485 contigs and lacks the completeness required for detailed genomic and functional analyses.

Here, we report the complete genome of *A. oris* MG-1, obtained using a hybrid sequencing approach that combines both short-read Illumina and long-read Oxford Nanopore Technologies (ONT) platforms. The strain was revived from a −80°C glycerol stock by streaking on heart infusion agar and incubating at 37°C in a 5% CO_2 atmosphere for 48 h. Colonies were harvested, and genomic DNA was extracted using the ZymoBIOMICS DNA Miniprep Kit (Zymo Research, D4300), following the manufacturer's protocol. DNA quantity was measured with a Qubit 4 fluorometer (Thermo Fisher Scientific, Q33327). Sequencing was performed by SeqCenter (Pittsburgh, PA) using both Illumina and ONT platforms. Illumina libraries were prepared using the tagmentation-based Illumina DNA Prep kit with custom 10 bp unique dual indices, targeting a 280 bp insert size. Paired-end (2 × 151 bp) sequencing was conducted on a NovaSeq X Plus instrument. Raw reads were demultiplexed, adapter-trimmed, and quality-filtered using *bcl-convert* v4.2.4, yielding 6,538,956 reads totaling 887 Mbp with >Q30 quality, 50x coverage. Default parameters were used for all software unless otherwise specified. ONT libraries were prepared with the PCR-free Ligation Sequencing Kit (SQK-NBD114.96) and NEBNext Companion Module (E7180L), without additional fragmentation or size selection. Sequencing was performed on a GridION platform using R10.4.1 flow cells in 400 bp mode. Dorado v0.5.3 was used for basecalling under the super-accurate (sup) and 5mC/5hmC models. FASTQ files were extracted from BAM files using *samtools fastq* v1.20. ONT sequencing produced 269,129 reads totaling ~907 Mbp with an N50 read length of 8,690 bp. Residual adapter sequences were trimmed with *Porechop*. *De novo* assembly was performed using *Flye* v2.9 with the nano-hq model, integrating both Illumina and ONT reads (5). Assembly quality was assessed with *QUAST* v5.0.2 (6). Genome circularization was confirmed using Circlator v1.5.5 (7). Genome annotation was performed with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.2 (8). QUAST analysis confirmed a high-quality assembly: a single circular contig of 3,042,829 bp with an N50

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equal to the full genome length, a GC content of 68.47%, and no ambiguous bases (0 Ns per 100 kbp). The final sequencing depth was approximately 50×. PGAP predicted 2,446 protein-coding genes, 51 tRNAs, and 9 rRNAs. The genome was not rotated after circularization.

This complete genome sequence of *A. oris* MG-1 establishes a robust foundation for future investigations into fimbrial structure–function relationships and microbial interactions, particularly with *Fusobacterium nucleatum*.

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AUTHOR CONTRIBUTIONS

Bibek G. C., Data curation, Validation | Kexin Tan, Writing – original draft | Chenggang Wu, Conceptualization, Funding acquisition, Project administration, Supervision, Writing – review and editing

DATA AVAILABILITY

The complete genome sequence of *Actinomyces oris* MG-1 has been deposited in GenBank under accession number CP194891. Raw sequence data for Illumina and ONT reads are available in the Sequence Read Archive (SRA) under BioProject accession number PRJNA1271997.

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