



Complete Genome Sequence of *Aureimonas* sp. Strain OT7, Isolated from Human Skin

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ABSTRACT *Aureimonas* sp. strain OT7 was isolated from human skin. This strain can grow on Triton X-100. Here, we present the complete whole-genome sequence of this species, which has one chromosome of 4,181,223 bp (G+C content, 65.05%). Analysis of the *Aureimonas* sp. strain OT7 genome sequence indicated potential for autotrophic growth.

Strains of Gram-negative *Aureimonas altamirensis* have been isolated from diverse environments and human skin (1, 2) and have been also implicated in human infections (3, 4). In most cases, identification of the species of the clinical isolates has been based on the 16S rRNA gene sequence identities. Two genome assemblies of *A. altamirensis* from strains DSM 21988^T and ON-56566 are publicly available in the NCBI database. These strains were isolated from a subterranean environment and the blood culture of a patient with cellulitis, respectively (1, 4). In this study, we isolated *Aureimonas* sp. strain OT7 from human skin for its ability to grow on Triton X-100, a nonionic detergent.

A swab sample from the skin of the back of a male college student's ear was directly streaked onto minimal salts basal medium (MSB) agar (5) containing 0.5% Triton X-100 as a source of carbon and energy. The agar medium was aerobically incubated for 1 week at 28°C for growth. One strain, named OT7, was further purified by streaking on nutrient broth agar (Difco Co.) with 0.1% sodium pyruvate and then incubated at 28°C for 2 days. This strain was deposited in the Korean Collection for Type Cultures as KCTC 82307. Ethical approval for subject sampling was granted by the institutional review board of Changwon National University. The 16S rRNA gene of strain OT7 was amplified from lysed colony material by PCR with the universal primers 27F and 1492R (6) using *Taq* DNA polymerase (Bioneer, Republic of Korea). Following Sanger sequencing, a similarity search with the sequences of type strains using BLASTn v.2.11.0 with default settings in NCBI (rRNA/ITS databases) (7) revealed the highest sequence identity to *A. altamirensis* DSM 21988^T (99.47%). Strain OT7 has been further characterized by genomic sequencing.

For DNA extraction, cells were cultured in a flask on nutrient broth with 0.1% sodium pyruvate for 48 h at 28°C with shaking at 140 rpm. Total genomic DNA was purified using the phenol extraction method (8). The DNA was quantified with NanoDrop UV-visible spectroscopy (S-3100; Sinco, Republic of Korea) and spectrofluorimetry (Qubit 4; Thermo Fisher Scientific, USA). For genomic DNA sequencing, 5 μg genomic DNA was sheared into 20-kb fragments using a g-TUBE device (Covaris, USA) and purified using the AMPure XP bead purification system (Beckman Coulter, USA) according to the manufacturers' protocols. A DNA library with an insert size of 20 kbp was prepared using the SMRTbell template prep kit 1.0 (PN 100-259-100) and the PacBio DNA/polymerase binding kit P6 according to the manufacturers' protocols. The Pacific Biosciences RS II platform with SMRT Analysis 2.3.0 p4 software with default settings was utilized for library sequencing (9), read filtering, and genome assembly at DNA Link Co.

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(Seoul, Republic of Korea). With a minimum polymerase read quality of 0.8, the OT7 genome yielded 105,216 reads encompassing 1,136,303,269 bp. The postfilter with a length cutoff of 1,000 bp yielded 39,455 sequencing reads with 1,119,510,078 bp and an N_{50} value of 15,790 bp. Subsequently, the clean reads were *de novo* assembled using the Hierarchical Genome Assembly Process (RS_HGAP3_Assembly) workflow, which included consensus polishing using Quiver. Gene predictions and annotations were provided by NCBI using the NCBI Prokaryotic Genome Annotation Pipeline 4.13 (10).

The final genome assembly of *Aureimonas* sp. strain OT7 consists of one circular chromosome of 4,181,223 bp (G+C content, 65.05%), with 267.7× contig sequencing coverage. The chromosome contains 3,875 protein-coding sequences, three copies of rRNA genes (5S, 16S, and 23S), 51 tRNA coding regions, and 4 noncoding RNA (ncRNA) genes. The genome sequence of strain OT7 shared BLAST average nucleotide identity (ANIb) values, as determined by the JSpeciesWS server (11), of 91.20% and 97.46% with *A. altamirensis* DSM 21988^T (GenBank accession number [GCA_001463885.1](https://doi.org/10.1093/jgs.064397-0)) and *A. altamirensis* ON-56566 ([GCA_000800175.1](https://doi.org/10.1093/jgs.064397-0)), respectively. Based on the above 95% ANIb species-level thresholds (11), strains OT7 and ON-56566 belong to the same species clade, which is distantly related to the species *A. altamirensis*. This result deserves further taxonomic studies on these strains and clinical isolates. The *Aureimonas* sp. strain OT7 genome sequence contained genes coding for the glyoxylate cycle, required for Triton X-100 degradation by *Pseudomonas nitroreducens* TX1 (12), genes related to the Calvin-Benson cycle, and RuBisCO genes for autotrophic growth, like other skin-derived bacterial isolates (13, 14).

Data availability. The complete genome sequence of *Aureimonas* sp. strain OT7 was deposited in GenBank under the accession number [CP062167.1](https://doi.org/10.1093/jgs.064397-0). The BioProject, BioSample, and SRA accession numbers are [PRJNA665798](https://doi.org/10.1093/jgs.064397-0), [SAMN16268744](https://doi.org/10.1093/jgs.064397-0), and [SRX9198886](https://doi.org/10.1093/jgs.064397-0), respectively.

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