Complete Genome Sequence of *Aurantimicrobium minutum* Type Strain KNCT, a Planktonic Ultramicrobacterium Isolated from River Water

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*Aurantimicrobium minutum* type strain KNCT is a planktonic ultramicrobacterium isolated from river water in western Japan. Strain KNCT has an extremely small, streamlined genome of 1,622,386 bp comprising 1,575 protein-coding sequences. The genome annotation suggests that strain KNCT has an actinorhodopsin-based photometabolism.

The phylum *Actinobacteria* includes members that are often numerically dominant (up to 60%) in the freshwater bacterial communities (1, 2). The actinobacterial Luna2 lineage, currently classified into the acIII lineage (2), has a cosmopolitan distribution in inland freshwater ecosystems (3). The cell morphology of this lineage is typical of ultramicrobacteria (cell volume <0.1 \( \mu \)m\(^3\)) [4]. *Aurantimicrobium minutum* type strain KNCT was the first described strain with a validly published name within the acIII lineage of *Actinobacteria* (5) and was isolated from a 0.2 \( \mu \)m filter of river water in western Japan (6). Here, we report the whole-genome sequence of strain KNCT, with the aim of elucidating the physiological traits that have facilitated such a wide distribution pattern.

The genomic DNA of strain KNCT was extracted from cells grown in nutrient broth, soytone, yeast extract (NSY) liquid medium (7) using Qiagen Genomic-Tip 100/G columns. Genomic shotgun and fosmid-end sequences were determined using an ABI3730xl sequencer. De novo assembly was conducted with phrap version 1.080812, resulting in a single chromosome with 22.2-fold genome coverage. The total length of the complete genome was 1,622,386 bp with a G+C content of 52.8 mol%. Strain KNCT has an extremely small, streamlined genome that is consisient with other ultramicrobacteria such as "*Candidatus Pelagibacter ubique*" (8) (Alphaproteobacteria) and *Rhodoluna lacaica* (9) (*Actinobacteria*). The phylum *Actinobacteria* is generally considered to be comprised of high-G+C Gram-positive bacteria. However, the genomes of freshwater and marine actinobacteria were recently reported to have unusually low G+C contents (9, 10). The genomic G+C content of freshwater strain KNCT is also quite low.

The genome annotation by the Microbial Genome Annotation Pipeline online server (11) predicted one copy of 16S-23S-5S rRNA operon, 42 tRNAs, and 1,575 protein-coding sequences. The genome encoded a putative rhodopsin, known as actinorhodopsin (12), suggesting that strain KNCT has an ability to utilize light energy for supplemental energy generation. Conversely, genes encoding a cytochrome bd complex, a respiratory quinol:O2 oxidoreductase found in many prokaryotes and expressed under oxygen-limited conditions (13), were missing within the genome. Comparative genomic analysis by MBGD (14) revealed that the genomic traits described above are shared with the genome of another ultramicrosized actinobacterium *R. lacicola* (9). In summary, we sequenced the complete genome of a cosmopolitan freshwater ultramicrobacterium. This will provide new insight into genome streamlining and related missing genes of ultramicrobacteria.

**Nucleotide sequence accession number.** The complete genome sequence of *A. minutum* KNCT has been deposited in the DDBJ/ENA/GenBank database under the accession no. AP017457. Annotated genome data were deposited with the help of the Genome Refine web service (http://genome.annotation.jp/genomerefine/).

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