

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

Ryosuke Nakai,^{a,b} Takatomo Fujisawa,^c Yasukazu Nakamura,^{c,d} Hiroyo Nishide,^e Ikuo Uchiyama,^{e,f} Tomoya Baba,^g Atsushi Toyoda,^c Asao Fujiyama,^{c,d,h} Takeshi Naganuma,ⁱ Hironori Niki^{a,d}

Genetic Strains Research Center, National Institute of Genetics, Mishima, Japan^a; Superlative Postdoctoral Research Fellow of the Japan Society for the Promotion of Science, Tokyo, Japan^b; Center for Information Biology, National Institute of Genetics, Mishima, Japan^c; The Graduate University for Advanced Studies (SOKENDAI), Mishima, Japan^d; Data Integration and Analysis Facility, National Institute for Basic Biology, National Institutes of Natural Sciences, Okazaki, Japan^e; Laboratory of Genome Informatics, National Institute for Basic Biology, National Institutes of Natural Sciences, Okazaki, Japan^f; Transdisciplinary Research Integration Center, Research Organization of Information and Systems, Tokyo, Japan^g; Principles of Informatics Research Division, National Institute of Informatics, Tokyo, Japan^h; Graduate School of Biosphere Science, Hiroshima University, Higashi-Hiroshima, Japanⁱ

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

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Address correspondence to Ryosuke Nakai, [mkai@nig.ac.jp](mailto:makai@nig.ac.jp).

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 μm³ [4]). *Aurantimicrobium minutum* type strain KNC^T was the first described strain with a validly published name within the acIII lineage of *Actinobacteria* (5) and was isolated from a 0.2 μm filtrate of river water in western Japan (6). Here, we report the whole-genome sequence of strain KNC^T, with the aim of elucidating the physiological traits that have facilitated such a wide distribution pattern.

The genomic DNA of strain KNC^T 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 KNC^T has an extremely small, streamlined genome that is consistent with other ultramicrobacteria such as “*Candidatus Pelagibacter ubique*” (8) (*Alphaproteobacteria*) and *Rhodoluna ladicola* (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 KNC^T 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 KNC^T 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. ladicola* (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* KNC^T 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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