

Genome Sequence of *Citromicrobium* Strain JLT1363, Isolated from the South China Sea[∇]

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***Citromicrobium* is a member of the alpha-4 subcluster in the *Alphaproteobacteria* and is identified as a typical aerobic anoxygenic phototrophic bacterium (AAPB). Here we report the draft genome sequence of a non-AAPB strain, *Citromicrobium* sp. JLT1363. The genome sequence reveals a multimechanism of horizontal gene transfer, as well.**

The genus *Citromicrobium* was first named by Yurkov et al. in 1999, and it is one clade of the alpha-4 subcluster in the *Alphaproteobacteria* (14). Currently, this genus contains only one species, *Citromicrobium bathyomarinum*. The type strain *C. bathyomarinum* JF-1 was isolated from deep-sea hydrothermal vent plume waters. *C. bathyomarinum* JF-1 and other *Citromicrobium* spp. were identified as aerobic anoxygenic phototrophic bacteria (AAPB) (6, 11, 14). We isolated a *Citromicrobium* sp. strain, JLT1363 (98.0% sequence similarity of 16S rRNA gene with that of JF-1), not showing phototrophic growth, from the surface water of the South China Sea. Here we report the whole-genome sequence of *Citromicrobium* sp. JLT1363.

Whole-genome shotgun sequencing was performed on JLT1363 using 454 pyrosequencing technologies, which produced 362,544 reads and 154,451,585 bp sequences. We used 355,141 high-quality reads to assemble the genome and obtained a 49.5-fold coverage of the genome. The complete sequence was analyzed using the Glimmer 3.02 software program (4) for the protein-coding genes, tRNAscan-SE (9) for the tRNA, and RNAmmer (8) for the rRNA. The functions of predicted protein-coding genes were then annotated through comparisons with the NCBI-NR (1), COG (12), and KEGG (7) databases.

The *Citromicrobium* sp. JLT1363 draft genome sequence has a total of 3,117,324 bp (3,198 open reading frames [ORFs]) distributed in 26 contigs with an average GC content of 64.9%. One 16S-23S-5S operon and 46 tRNAs on the draft assembly were identified, as were complete sets of genes for the synthesis of amino acids and nucleotides. A detailed inspection of the genome sequence revealed the presence of complete sets of genes encoding flagellum formation and the complete tricarboxylic acid cycle.

In particular, the *Citromicrobium* sp. JLT1363 genome showed various mechanisms for horizontal gene transfer. An integrative conjugative element (ICE) (about 100 kb) was observed in the *Citromicrobium* sp. JLT1363 genome (2, 5). Two

regions carrying exogenous DNA were discovered in the ICE. We further found a nearly complete gene transfer agent (GTA) (about 15 kb) gene cluster. In addition, seven genes (*virB2B3B4-virB6-virB9B10B11*) of the type IV secretion system (T4SS) (about 7 kb) existed in the genome.

In the JLT1363 genome, we found exactly the same genes as those located upstream and downstream of the photosynthetic gene cluster (PGC) of JL354 (6). Their order and direction are the same as well. This suggests a loss of PGC in *Citromicrobium* sp. JLT1363 (10). So far, JLT1363 is the only isolate in the *Citromicrobium* genus without phototrophic capability.

The exchange of genetic information by horizontal gene transfer plays important roles in the evolution of bacteria (3, 13). A multimechanism of horizontal gene transfer and the loss of PGC in *Citromicrobium* sp. JLT1363 may give us some clues for further studies on the evolution of the photosynthesis gene of AAPB.

Nucleotide sequence accession number. The data from this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under accession number AEUE01000000.

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