

# Coexistence of Two Different Photosynthetic Operons in *Citromicrobium bathyomarimum* JL354 As Revealed by Whole-Genome Sequencing<sup>∇</sup>

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***Citromicrobium bathyomarimum* is a bacteriochlorophyll *a*-containing aerobic anoxygenic phototrophic bacterium. Here, we report the draft genome sequence of *C. bathyomarimum* JL354, which was the first *C. bathyomarimum* strain isolated from a euphotic marine environment. The JL354 genome sequence reveals, for the first time, the coexistence of two different photosynthetic operons in a single strain.**

Knowledge of aerobic anoxygenic phototrophic bacteria (AAPB) is critical for understanding carbon cycling in the ocean (4, 7), and they have been studied extensively with regard to their abundance and diversity in different marine environments (4, 6, 7, 9, 13, 16, 18, 19). The known marine AAPB species are mainly affiliated with the *Alphaproteobacteria* (including the alpha-3 and alpha-4 subclusters) and *Gammaproteobacteria* (3, 14). The genus *Citromicrobium* is one clade of the alpha-4 AAPB subcluster, and it contains only one species, *Citromicrobium bathyomarimum*. The type strain of *C. bathyomarimum*, strain JF-1, was isolated from deep-sea hydrothermal vent plume waters (17). Other strains of *C. bathyomarimum* were isolated at depths from 500 m to 2,379 m (12). All of these habitats are aphotic environments, and the known *C. bathyomarimum* strains may not play the same ecological role as those AAPB which are in the euphotic zone. Here, we report on the first epipelagic strain of *C. bathyomarimum*, strain JL354, which was isolated from the surface water of the South China Sea.

The *C. bathyomarimum* JL354 16S rRNA gene shares 99.6% sequence similarity with that of the type strain JF-1. Whole-genome shotgun sequencing was performed on JL354 using 454 pyrosequencing technologies, which produced 207,125 reads and 85,861,877 bp sequences. A total of 201,805 high-quality reads were used in assembling the genome to give 26.2-fold coverage of the genome. The complete sequence was analyzed using Glimmer 3.02 (2) for the protein-coding gene, tRNAscan-SE (10) for the tRNA, and RNAmmer (8) for the rRNA. The functions of predicted protein-coding genes were then annotated through comparisons with the databases of NCBI-NR (1), COG (15), and KEGG (5).

The *C. bathyomarimum* JL354 draft genome sequence has a total of 3,273,334 bp (3,401 open reading frames) distributed in 68 contigs with an average GC content of 65.0%. One 16S-23S-5S operon and 45 tRNAs on the draft assembly were

identified, as were complete sets of genes for the synthesis of amino acids, nucleotides, and prosthetic groups. In particular, this strain has two different photosynthetic (PS) operons; one is complete, and the other is incomplete. The complete one consists of the typical subclusters *puhCBA-lhaA-bchMLHBNF* and *pufMLAB-bchZYXC-crtFDC*, and the incomplete one only has *pufLMC-puhCBA*. The similarity of the two *pufLM* gene sequences is less than 70%, and the *pufLM* gene in the incomplete operon is affiliated with the *Gammaproteobacteria* group by phylogenetic analysis (3). This is the first report about two different PS operons coexisting in a single strain.

A detailed inspection of the genome sequence revealed the presence of complete sets of genes encoding flagellum formation and the complete tricarboxylic acid (TCA) cycle. Genes for ammonia uptake were predicted, but no genes for assimilating nitrate and nitrite were found. In addition, genes for type IV secretion systems (T4SS) were identified, including seven genes encoding the secretion systems T4SS (*virB2B3B4-virB6-virB9B10B11*) but no *virD4* gene. Interestingly, prophage sequences were also found in the genome coincident with the two PS operons, suggesting the possibility of lateral gene transfer in AAPB (11).

The draft genome sequence of *C. bathyomarimum* JL354 reported here reveals, for the first time, the coexistence of two different PS operons in a single strain. Together with the presence of the prophage sequences, this characteristic of JL354 provides rich information for further studies on the origin of the photosynthesis gene of AAPB. The genome sequence will facilitate additional bioinformatic and experimental investigations to elucidate the role of AAPB in carbon cycling in the ocean.

**Nucleotide sequence accession numbers.** The data from this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under accession number ADAE00000000. The version described in this paper is the first version, with accession number ADAE01000000.

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