

# Draft Genome Sequence of *Methylobacterium* sp. ME121, Isolated from Soil as a Mixed Single Colony with *Kaistia* sp. 32K

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***Methylobacterium* sp. ME121 was isolated from soil as a mixed single colony with *Kaistia* sp. 32K, and its growth was enhanced by coculture. Here, we report the draft genome sequence of *Methylobacterium* sp. ME121, which may contribute to the study of the molecular mechanisms underlying this phenomenon.**

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It has been suggested that a majority of environmental microorganisms are still uncultured, and some of them form symbiotic relationships with other organisms. For example, *Symbiobacterium thermophilum* was reported as a symbiotic bacterium requiring support of the associated *Geobacillus stearothermophilus* for growth (1). The genomic information of such symbiotic bacteria could be of use for studying the molecular mechanisms underlying microbial symbiosis (2).

*Methylobacterium* sp. ME121 was isolated from soil as a mixed single colony with *Kaistia* sp. 32K during our screening of L-glucose-utilizing microorganisms (3), and its growth was enhanced by coculture. It was expected that genomic analysis of this bacterium would provide novel information on coculture-dependent growth enhancement. *Methylobacterium* sp. ME121 appeared to be most closely related to *M. radiotolerans* based on the 16S rRNA gene sequence identity.

The draft genome sequence of *Methylobacterium* sp. ME121 is 7,096,979 bp in total length and comprises 197 large contigs (>500 bp) and was obtained with the Roche GS Junior and assembled using the GS *de novo* assembler version 2.7. Automatic annotation was performed using the Microbial Genome Annotation Pipeline (4), which predicted a total of 6,676 protein-coding genes. The product names of the predicted protein-coding genes were revised manually. tRNA detection was performed using the tRNA scan software (5), which predicted a total of 56 tRNAs.

*Methylobacterium* species generally live on plant surfaces and assimilate methanol emitted by plants. The genome sequences of *M. aquaticum* and *M. radiotolerans* were analyzed, and the genes involved in methylotrophy were identified (6, 7). The annotation of the draft genome sequence shows that *Methylobacterium* sp. ME121 has some genes that encode pu-

tative methanol/ethanol family PQQ-dependent dehydrogenases involved in methylotrophy. Some unknown factor (e.g., methanol) provided by the coculture may contribute to increase the growth of *Methylobacterium* sp. ME121. Future study will identify such a factor, and it would serve to clarify the molecular mechanisms of coculture-dependent growth enhancement.

**Nucleotide sequence accession numbers.** The draft genome sequence of *Methylobacterium* sp. ME121 was deposited at DDBJ/EMBL/GenBank under the accession number [BBUX00000000](https://www.ncbi.nlm.nih.gov/nuccore/BBUX00000000). The version described in this paper is the first version, [BBUX00000000.1](https://www.ncbi.nlm.nih.gov/nuccore/BBUX00000000.1).

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