



Draft Genome Sequence of the Halophilic *Pararhodobacter*-Like Strain CCB-MM2, Which Has Polyhydroxyalkanoate-Synthesizing Potential

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ABSTRACT *Pararhodobacter*-like strain CCB-MM2 is a halophilic alphaproteobacterium isolated from estuarine sediment collected from Matang Mangrove Forest in Malaysia. Here, we present the draft genome sequence of CCB-MM2 and provide insights into its physiological roles and metabolic potential.

Pararhodobacter is a genus within the family *Rhodobacteraceae* that is incapable of photosynthesis, separating it from the genus *Rhodobacter* (1). Thus far, only three isolates from the genus have been classified to the species level, namely, *Pararhodobacter aggregans* DSM 18938^T (1), *Pararhodobacter marinus* CIC4N-9^T (2), and *Pararhodobacter oceanensis* AM505^T (3). *Pararhodobacter*-like strain CCB-MM2 was isolated from Matang Mangrove Forest in Malaysia (4°12'48.06"N, 100°38'49.5204"E) and was part of a study aimed at characterizing the mangrove microbiota (4). Subsequent 16S rRNA gene sequence analysis using the EzTaxon server (5) revealed that CCB-MM2 exhibited 97.98% similarity with *P. aggregans* DSM 18938^T. Phylogenetic analysis based on the 16S rRNA gene sequence constructed using MEGA7 (6) also placed CCB-MM2 in the same cluster as *P. aggregans* DSM 18938^T. Average nucleotide identity (ANI) values between *P. aggregans* DSM 18938^T, *P. marinus* CIC4N-9^T, and *P. oceanensis* AM505^T and strain CCB-MM2, estimated using the ANI calculator (<http://enve-omics.ce.gatech.edu/ani/>), were 81.78%, 81.49%, and 77.42%, respectively.

CCB-MM2 was revived from frozen glycerol stock; a single colony from an artificial seawater medium (ASWM) plate was inoculated into ASWM broth and grown with shaking at 30°C (7). Genomic DNA was extracted from the late logarithmic phase culture using the DNeasy blood and tissue kit (Qiagen, USA). A sequencing library was prepared using a Nextera XT DNA sample preparation kit (Illumina, USA), and the constructed library was sequenced on a MiSeq instrument using 250-bp paired-end chemistry. In sum, 3,658,868 raw reads, totaling 835.05 Mb bases (~100-fold coverage), were generated by the sequencing run. The quality of the raw reads was assessed using FastQC v0.11.5 (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). Default parameters were used for all software unless otherwise noted. SPAdes v3.6.1 (8) was used for the *de novo* assembly of the sequencing data. The draft genome of CCB-MM2 has a length of 5,149,122 bp with a scaffold N_{50} value of 132,033 bp and a G+C content of 65.96% (Table 1). The genome of CCB-MM2 was annotated with Rapid Annotations using Subsystems Technology (9) and NCBI Prokaryotic Genome Annotation Pipeline (10). A total of 4,861 genes were annotated from the draft genome, consisting of 4,804 protein coding and 57 non-protein coding genes (48 tRNAs, 3 16S rRNAs, 2 23S rRNAs, and 4 5S rRNAs).

The gene transfer agent (GTA) system is important for genetic exchange in prokaryotes, and the gene cluster has been described in many other species of *Alphaproteobacteria*, including *Rhodobacter capsulatus*, the best-studied example (11). Genome

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TABLE 1 Genome statistics of *Pararhodobacter*-like strain CCB-MM2

Genome statistic	Value
Genome assembly size (bp)	5,149,122
No. of scaffolds	136
Scaffold N_{50} (bp)	132,033
G+C content (%)	65.96
Total no. of genes	4,861
No. of protein coding genes	4,804
No. of RNA genes	57

annotation revealed the presence of an ~12-kb head-tail gene cluster in CCB-MM2 that is homologous to the *R. capsulatus* GTA (RcGTA) gene cluster (12). The partial RcGTA-like cluster of CCB-MM2 consists of 13 open reading frames (*orf2* to *orf4* and *orf6* to *orf15*) that are homologs of the RcGTA structural genes. Additionally, annotation of the genome indicated that strain CCB-MM2 possesses genes encoding key enzymes involved in polyhydroxyalkanoate (PHA) biosynthesis. Genes encoding β -ketothiolase (*phaA*), NADPH-dependent acetyl coenzyme A (CoA) reductase (*phaB*), and PHA synthase (*phaC*) were found in CCB-MM2, revealing its ability to biosynthesize PHA. The availability of the genome sequence of *Pararhodobacter*-like strain CCB-MM2 improves our understanding of the strain's metabolic pathways and will inevitably facilitate discovery of its potential in synthesizing industrially useful compounds.

Data availability. This whole-genome shotgun (WGS) project can be accessed at GenBank under accession no. [LRRR00000000](https://www.ncbi.nlm.nih.gov/nuccore/LRRR00000000). The raw sequence reads are available at the NCBI Sequence Read Archive under accession no. [SRR9593062](https://www.ncbi.nlm.nih.gov/sra/SRR9593062).

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