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Pingsha Hu, Juan Lang, Karen Wawrousek, Jianping Yu, Pin-Ching Maness and Jin Chen

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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Rubrivivax gelatinosus* CBS

Pingsha Hu,[a] Juan Lang,[b] Karen Wawrousek,[c] Jianping Yu,[c] Pin-Ching Maness,[c] and Jin Chen[a]

MSU-DOE Plant Research Laboratory[a] and Department of Statistics and Probability,[b] Michigan State University, East Lansing, Michigan, USA, and National Renewable Energy Laboratory, Golden, Colorado, USA[c]

***Rubrivivax gelatinosus* CBS, a purple nonsulfur photosynthetic bacterium, can grow photosynthetically using CO and N_2 as the sole carbon and nitrogen nutrients, respectively. *R. gelatinosus* CBS is of particular interest due to its ability to metabolize CO and yield H_2. We present the 5-Mb draft genome sequence of *R. gelatinosus* CBS with the goal of providing genetic insight into the metabolic properties of this bacterium.**

Rubrivivax gelatinosus CBS is a purple nonsulfur photosynthetic bacterium that was isolated from soil in Denver, CO. *R. gelatinosus* CBS can grow in a variety of environments, including the photoheterotrophic or the dark respiratory growth mode, both utilizing diverse organic acids, and photoautotrophic growth using CO_2 (with H_2) or CO alone as the sole carbon substrate (6, 7). The oxidation of CO in *R. gelatinosus* CBS generates energy in the form of ATP, hence allowing anaerobic dark growth using CO as the sole source of carbon and energy (5). *R. gelatinosus* CBS also can fix N_2, a feature common to many photosynthetic bacteria. Coupling this growth on minimal nutrients with its ability to accumulate large amounts of polyhydroxyalkanoates, which are used in bioplastics, makes this organism an attractive microbe to study. These premises form the basis of this genome sequencing effort, which will reveal the underlying mechanisms and pathways affording metabolic flexibility.

Rubrivivax gelatinosus CBS was grown photoheterotrophically on RCVBN medium, and DNA was isolated using the Qiagen DNeasy blood and tissue kit (1). The authenticity of the genome was confirmed by 16S rRNA gene sequencing. The genome of *R. gelatinosus* CBS was sequenced using an Illumina Genome Analyzer II. A total of 22.6 million high-quality-read pairs (2× 75 bp) were used for *de novo* assembly by the CLC Genomics Workbench (v4.7.1), resulting in 1,324 assembled contigs. Two or more contigs were merged into a scaffold if the same paired reads were mapped to these contigs by SSPACE (v1.1) software. SSPACE created 1,240 scaffolds with a total scaffold length of 5,024,473 bp (N_{50}, 8,637 bp), with a G+C content of 70.65%.

The assembled scaffolds were used for functional annotation. Protein coding sequences were initially identified using Glimmer 3.02 (1). Noncoding RNA genes were predicted using RNAmmer (3) and tRNA-scanSE (4). Based on the IGS Annotation Engine (2), the scaffolds are comprised of 5,602 predicted open reading frames (ORFs), where 3,582 (63.9%) are annotated as genes of predicted function, 1,245 (22.2%) as hypothetical proteins, and 761 (13.6%) have no associated functions. The draft genome contains a single predicted copy of a 16S-23S-5S rRNA operon and 45 predicted tRNAs. Based on 16S rRNA similarity, *R. gelatinosus* CBS was closely related to *R. gelatinosus* ATCC 17011.

One unique feature of *R. gelatinosus* CBS is its ability to metabolize CO, yielding H_2. Consequently genes related to CO and H_2 metabolism were identified. Only one set of CO dehydrogenase-encoding genes was identified, responsible for the oxidation of CO to CO_2. Previous work revealed the presence of a hydrogenase enzyme coupled to CO oxidation in *R. gelatinosus* CBS (8). Upon analysis of the CBS genome, genes encoding two hydrogenase enzymes were identified, with the second one likely responsible for H_2 uptake in support of cell growth. Genes involved in metal insertion and active site assembly/maturation for both CO dehydrogenase and hydrogenases were also identified. Additionally, genes involved in chlorophyll, carotenoid, and porphyrin biosynthesis, photosynthesis, and nitrogen fixation are also predicted to be in the genome.

Nucleotide sequence accession number. The draft genome sequence was deposited in GenBank under accession no. AJFF00000000.

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Address correspondence to Jin Chen, jinchen@msu.edu.

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