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GENOME SEQUENCES

Draft Genome Sequence of the Cyanotroph *Pseudomonas monteilii* BCN3

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ABSTRACT We report here the first draft genome of *Pseudomonas monteilii* BCN3, a cyanotroph isolated from sewage sludge. The genome consists of approximately 6,029,517 bp with a G+C content of 61.89% and 5,369 annotated protein-coding genes.

Pseudomonas monteilii (formerly *Pseudomonas putida*) BCN3, isolated as previously described (1), exhibits the ability to grow in minimal medium (2) with cyanide as the sole nitrogen source (cyanotrophy). Of 10 separate bacteria previously isolated, *P. monteilii* BCN3 exhibited the fastest growth rate (generation time [t_{gen}], 2 h) and was therefore chosen for genome sequencing for the purpose of uncovering unique genes linked to cyanide growth. Here, we report the draft genome sequence of the first representative *P. monteilii* strain able to grow cyanotrophically.

Genomic DNA was isolated employing an UltraClean microbial DNA isolation kit (Mo Bio, Qiagen) according to the manufacturer's instructions. Cells of *P. monteilii* BCN3 were inoculated from a single colony and grown overnight at 30°C in complete medium (Lennox broth [LB]) (3). Genomic DNA was prepared using the Illumina Nextera DNA Flex library preparation kit, and a 76-bp insert library was sequenced at the University of North Texas BioDiscovery Institute Genomics Center using Illumina NextSeq system technology. This produced 6,451,536 paired-end reads with an average read length of 76 bp (81.4× coverage) that were quality checked using FastQC version 1.0.0 with default parameters (BaseSpace Labs, Illumina). The genome was *de novo* assembled using the SPAdes genome assembler version 3.9.0 (4) and improved through closing gaps with Rescaf version 1.0.1 (BaseSpace Labs, Illumina), in each case employing default parameters. A BLASTn search (5) using full-length *P. monteilii* BCN3 16S rRNA as a query (identified from a preliminary annotation by Rapid Annotations using Subsystems Technology [RAST]) (6) returned closely related *P. monteilii* and *P. putida* strains. The strain most similar to *P. monteilii* BCN3 for which the complete genome sequence is available, *Pseudomonas* sp. strain XWY1 (NCBI accession no. CP026332), was used as a reference to reorder the scaffolds of *P. monteilii* BCN3 DNA employing progressiveMauve version 2.3.1 (7) set to default parameters. The *P. monteilii* BCN3 genome was assembled into 96 scaffolds of 105 contigs (N_{50} value, 95,637 bp) with a total length of 6,029,517 bp and a G+C content of 61.9%. The NCBI Prokaryotic Genome Annotation Pipeline version 4.6 (8) was then used to predict and annotate *P. monteilii* BCN3 open reading frames, consisting of 5,369 protein and 81 RNA coding genes.

Sequencing the genome of *P. monteilii* BCN3 enabled genome comparisons for identifying genes linked to cyanotrophy. One such set of genes found conserved in other cyanotrophs (2, 9) is a seven-gene cluster known as Nit1C, shown here also to be present in *P. monteilii* BCN3 as identified from the annotation of the Nit1C genes (locus tags D0894_12380 to D0894_12410). A search of available bacterial genomes for Nit1C reveals its presence in 270 different bacteria, suggesting that additional cyanotrophs

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remain to be uncovered (2). Further identification of gene functions related to cyanotrophy are currently in progress.

Data availability. The draft *P. monteilii* BCN3 genome sequence has been deposited in DDBJ/ENA/GenBank under the accession no. QWLL00000000. The version described here is the first version of the draft genome. The Sequence Read Archive (SRA) accession no. is SRX4980437.

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