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Draft Genome Sequence of *Rhodococcus* sp. Strain ATCC 49988, a Quinoline-Degrading Bacterium

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ABSTRACT We report here the 4.9-Mb genome sequence of a quinoline-degrading bacterium, *Rhodococcus* sp. strain ATCC 49988. The draft genome data will enable the identification of genes and future genetic modification to enhance traits relevant to heteroaromatic compound degradation.

Quinoline is a nitrogen-containing heterocyclic compound that is used as a solvent in the chemical industry and occurs widely in coal tar, oil shale, and plant alkaloids. It is known to be a mutagenic and carcinogenic compound (1). Due to its widespread use and toxic properties, the degradation of quinoline by microorganisms has been studied extensively. *Rhodococcus* sp. strain ATCC 49988 was isolated from soil by enrichment culture using quinoline as a dominant carbon, nitrogen, and energy source (2). In order to understand the genetic basis of quinoline degradation and other abilities of this strain, genome sequence analysis of *Rhodococcus* sp. strain ATCC 49988 was carried out.

Rhodococcus sp. strain ATCC 49988 was obtained from the ATCC. It was grown in tryptic soy broth at 30°C with shaking at 200 rpm for 16 h, after which DNA for whole-genome sequencing was isolated using a DNeasy PowerSoil kit (catalog number 12888-50; Qiagen), followed by preparation of an Illumina Nextera XT paired-end library. Whole-genome sequencing was performed using a MiSeq system (Illumina) and produced 13,615,724 (average length, 160 bp) paired-end reads. The raw sequence was processed using the KBase (3) platform (https://narrative.kbase.us/narrative/ws.39490.obj.1), and the sequence was uploaded in FASTQ format. During analysis, default parameters were used for all software, unless otherwise specified. The read quality was assessed using FastQC v 0.11.5 (4), and the adaptor sequences specific to the Nextera DNA library were trimmed using Trimmomatic v 0.36 (5). *De novo* assembly conducted using SPAdes v 3.12.0 (6) yielded 27 contigs. The draft genome sequence has a total length of 4,970,306 bp (N_{50}, 792,857 bp) and a GC content of 67.87%. The genome coverage was 155.0×. Genome assembly statistics were computed using QUAST v 0.0.4 (7). The assembled contigs ranged in size from 805 bp to 1,052,617 bp. The assembly was evaluated for completeness and contamination using CheckM v 1.0.8 (8), which characterized the assembly as 99.4% complete with 0% contamination.

The genome sequence of this *Rhodococcus* sp. strain was first annotated using Prokka v 1.12 (9), which predicted a total of 4,508 protein-coding genes in the genome (https://narrative.kbase.us/#dataview/39490/15/1). Next, the genome was functionally annotated using Rapid Annotations using Subsystems Technology (RAST) v 0.1.1 (10; https://narrative.kbase.us/#dataview/39490/17/1), which assigned 1,406 (31%) of the genes to SEED subsystems. Several putative polycyclic aromatic hydrocarbon (PAH)

catabolic enzymes (11), such as monooxygenase, dioxygenases, dehydrogenases, and cytochrome P450, were found in the *Rhodococcus* genome. However, genes for quinoline 2-oxidoreductase were not annotated in the genome, indicating that this species uses a different enzyme to convert quinoline to 2-hydroxyquinoline. The genomic information of this *Rhodococcus* sp. strain will not only facilitate our understanding of the metabolism for recalcitrant heteroaromatic compounds but will also expand our knowledge of the physiology of the *Rhodococcus* genus.

Data availability. The draft genome sequence of this *Rhodococcus* sp. strain has been deposited in GenBank under the accession numbers SDMJ01000001 to SDMJ01000026, and the raw sequencing reads are available in the Sequence Read Archive under accession number SRP179964.

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