



Draft Genome Sequence of *Pseudomonas chlororaphis* ATCC 9446, a Nonpathogenic Bacterium with Bioremediation and Industrial Potential

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ABSTRACT *Pseudomonas chlororaphis* strain ATCC 9446 is a biocontrol-related organism. We report here its draft genome sequence assembled into 35 contigs consisting of 6,783,030 bp. Genome annotation predicted a total of 6,200 genes, 6,128 coding sequences, 81 pseudogenes, 58 tRNAs, 4 noncoding RNAs (ncRNAs), and 41 frameshifted genes.

Different strains of *Pseudomonas chlororaphis* have been reported as biocontrol agents over a wide variety of organisms (1–6). *P. chlororaphis* strain ATCC 9446 is a member of a genus which has features that are interesting for different applications. Its potential capability to degrade triphenyltin, an organotin compound known to cause harmful effects on a variety of aquatic organisms, has been studied (7, 8). Furthermore, this strain was reported to produce 2-keto-L-gulonic acid, L-carnitine, and 6-aminopenicillanic acid (9–11).

The genome of strain ATCC 9446v was sequenced at the Sequencing and Polymorphism Identification Unit of the Instituto Nacional de Medicina Genómica in a NextSeq 500 Illumina sequencer with a 2 × 150 paired-end indexed configuration, achieving a genome coverage of 120-fold. Assembly was performed with SPAdes version 3.9.0 and IDBA_UD version 1.1.1 parallel, and the contigs obtained were merged and optimized using METASSEMBLER version 1.5 (12–14). Contigs were reordered using MAUVE version snapshot_2015_02_13 using the genome of *P. chlororaphis* 189 as a reference (15).

The draft genome of *P. chlororaphis* strain ATCC 9446 consists of 6,783,030 bp assembled in 35 contigs, with an average G+C content of 63%; the contigs length average was 15,918 bp (*N*50, 843,135 bp). The draft genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline, which predicted a total of 6,200 genes, 6,128 coding sequences, 81 pseudogenes, 58 tRNAs, 4 noncoding RNAs (ncRNAs), and 41 frameshifted genes (16). Annotation revealed genes related to toluene tolerance, alkanolates, alginate, phenazines, nonribosomal peptides, and polyketide synthesis, among many other genes involved in diverse metabolic pathways with biotechnological applications.

Accession number(s). This whole-genome shotgun project was deposited at DDBJ/EMBL/GenBank under the accession number [NBATO0000000](https://www.ncbi.nlm.nih.gov/nuccore/NBATO0000000). The version described in this report is BioProject [PRJNA380114](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA380114) and BioSample [SAMN06627644](https://www.ncbi.nlm.nih.gov/biosample/SAMN06627644).

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