

Draft Genome Sequence of *Pseudomonas* sp. Strain 10-1B, a Polycyclic Aromatic Hydrocarbon Degradator in Contaminated Soil

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***Pseudomonas* sp. strain 10-1B was isolated from artificially polluted soil after selective enrichment. Its draft genome consists of several predicted genes that are involved in the hydroxylation of the aromatic ring, which is the rate-limiting step in the biodegradation of polycyclic aromatic hydrocarbons.**

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Pollution of soil with persistent organic pollutants, especially polycyclic aromatic hydrocarbons (PAHs), is a global problem. Such organic pollutants have been a consequence of various industrial processes that have spared no part of the ecosystem (1). Bioremediation is a promising solution for remediating these pollutants in soils in a cost-effective and environmentally safe manner (2). Bacteria are known to play an active role in degradation and eventual remediation of organic pollutants in soil during this process (3).

Agricultural soil with no history of pollution was collected from the research farm of the Agricultural Research Council, Vegetable and Ornamental Plant Institute, Pretoria, South Africa. The soil is of alluvial origin classified as an Oakleaf soil form (South African classification). It was artificially contaminated in the laboratory with used car engine oil containing a high PAH content. *Pseudomonas* sp. strain 10-1B was isolated from a bacterial community that endured this artificial contamination. *Pseudomonas* spp. are particularly known for their highly versatile metabolic activities in various ecosystems, including soil (4). The strain investigated here was identified as a *Pseudomonas* sp. on the basis of its 16S rRNA gene sequence analyses. *Pseudomonas* sp. strain 10-1B was confirmed to be PAH-degrading through culture characterization after selective enrichment using PAH as the sole carbon source (5), followed by identification and molecular characterization of the Gram-negative PAH-degrading gene in the draft genome presented here.

Genomic DNA of strain 10-1B was isolated using a Macherey-Nagel NucleoSpin soil kit and sequenced on a MiSeq sequencer (Illumina) at the ARC's Biotechnology Platform, using the Nextera sample preparation kit and the 300-bp paired-end V3 Illumina chemistry. The reads were trimmed on quality, ambiguous bases, and adapters before being merged and *de novo* assembled using CLC Genomics Workbench version 7.5 (CLC bio, USA). Default assembly settings were used but with a maximum word size of 64 bp and contig cutoff of <1 kb. A total of 102 contigs were obtained, with an N_{50} of 125,760

nucleotides and a total genome size of 6,346,514 nucleotides, for the draft genome of *Pseudomonas* sp. strain 10-1B. The mean G+C content of the draft genome was 62.5%. The genome was annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; http://www.ncbi.nlm.nih.gov/genome/annotation_prok). The draft genome annotation predicted 5,584 protein-encoding genes and 5,361 coding sequences (CDSs), in addition to 71 RNAs, of which 65 were tRNAs. In addition, several dioxygenases, reductases, ferredoxin, and Rieske proteins, all known to play an active role in biodegradation processes (6), were identified. Other genes, such as dehydrogenases, identified as being involved in hydrocarbon degradation, were also predicted within the draft genome.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JYKS000000000](https://www.ncbi.nlm.nih.gov/nuccore/JYKS000000000). The version described in this paper is version JYKS01000000.

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