



First Insights into the Genome Sequence of *Pseudomonas oleovorans* DSM 1045

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ABSTRACT The Gram-negative proteobacterium *Pseudomonas oleovorans* DSM 1045 is considered a promising source for enzymes of biotechnological interest, e.g., hydrolases and transaminases. Here, we present a draft sequence of its 4.86-Mb genome, enabling the identification of novel biocatalysts.

Hydrocarbon-degrading bacteria, including members of the genus *Pseudomonas*, represent a promising source for novel biocatalysts of biotechnological relevance (1, 2). Belonging to this group, the *Pseudomonas oleovorans* type strain DSM 1045 was isolated as a contaminant of industrial cutting fluids and shown to utilize cyclic aliphatic hydrocarbons, like naphthenic acids (2). Its biotechnological potential was indicated by the observation that cell extracts could catalyze ω -transamination reactions (3).

Chromosomal DNA of *Pseudomonas oleovorans* DSM 1045 was isolated from 2 ml of overnight-grown culture (growth medium LB, 30°C; Carl-Roth-Karlsruhe) using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. The extracted DNA was used to generate Illumina shotgun paired-end sequencing libraries, which were sequenced with a MiSeq instrument and the MiSeq reagent kit version 3 (600 cycles), as recommended by the manufacturer (Illumina, San Diego, CA, USA). Quality filtering using Trimmomatic version 0.32 (4) resulted in 2,602,096 paired-end reads. The assembly was performed with the SPAdes genome assembler software version 3.8.0 (5) and resulted in 108 contigs (>500 bp), with an average coverage of 112-fold. The assembly was validated and the read coverage determined with QualiMap version 2.1 (6). The draft genome of *P. oleovorans* DSM 1045 consisted of a single chromosome (4.86 Mb) with an overall G+C content of 62.07%. Automatic gene prediction and identification of rRNA and tRNA genes were performed using the software tool Prokka (7). The draft genome contained 7 rRNA genes, 62 tRNA genes, 3,398 protein-coding genes with predicted functions, and 1,243 genes coding for hypothetical proteins.

A homology search for biocatalysts of potential biotechnological relevance with all *in silico*-translated coding sequences (CDSs) using BLASTP (8) led to the detection of 15 putative enzymes predicted to be lipases, esterases, or phospholipases. Furthermore, three putative ω -transaminases were identified, and one imine reductase was identified according to sequence motifs described in Fadernrecht et al. (9). Genes encoding a Sec and Tat secretion pathway, as well as genes encoding a type II secretion machinery, were identified, indicating the potential to produce extracellular enzymes. Furthermore, biosynthetic capabilities are predicted for antimicrobial bacteriocins and polyhydroxy-alkanoate biopolymers, as identified with antiSMASH 4.0.0rc1 (10). An aliphatic alkane degradation pathway could not be detected, coinciding with the observation that this strain does not grow on long-chain alkanes (11). Genes encoding homologs to aliphatic alcohol dehydrogenase AlkJ (of *Pseudomonas putida* GPo1) and rhamnosyltransferase

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RhIA (of *Pseudomonas aeruginosa*) further suggest capabilities for the synthesis of aliphatic alcohols and of 3-(hydroxyalkanoyloxy)alkanoic acid type biosurfactants.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [NIUB00000000](https://doi.org/10.1093/bioinformatics/btv566). The version described in this paper is version NIUB01000000.

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