



High-Quality Draft Genome Sequence of *Pseudomonas wadenswilerensis* CCOS 864^T

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ABSTRACT *Pseudomonas wadenswilerensis* CCOS 864^T was isolated in 2014 from forest soil. The organism belongs taxonomically to the *Pseudomonas putida* group, members of which have been well studied for their potential in biotechnological applications. We present here the draft genome sequence of *P. wadenswilerensis* CCOS 864^T.

The genus *Pseudomonas* belongs to the gamma subclass of *Proteobacteria* and forms a large taxonomic grouping of species (1, 2). Members of this genus appear as Gram negative and are involved in a highly diverse range of activities (2). Pseudomonads can be isolated from many different environmental sources, including soil, water, plants, animals, and air (3). Over the years, members of the *Pseudomonas putida* group were studied because of their usage as an efficient cell factory in industrial biotechnological applications (4). Nowadays, *Pseudomonas* spp. are used for the production of bio-based polymers, small-molecular-weight chiral compounds, heterologous proteins, biosurfactants, and several biotechnologically important enzymes (lipases, proteases, and amylases) (3–5). In 2014, a new species of *Pseudomonas* was isolated during the search for novel biocatalysts. The isolate, identified as *Pseudomonas wadenswilerensis* CCOS 864^T, was obtained from soil samples collected in the Riedholz Forest in Richterswil, Switzerland (6).

Genomic DNA of *P. wadenswilerensis* CCOS 864^T, grown overnight at 28°C in LB medium, was isolated using the NucleoSpin tissue kit (Macherey-Nagel, Düren, Germany) and fragmented using the Covaris E220 ultrasonicator (average target size, 550 bp). Library preparation was done using the Illumina NeoPrep library system according to the manufacturer's instructions. Genome sequencing was done at Zurich University of Applied Sciences (ZHAW) using an Illumina MiSeq instrument (2 × 300-bp reads) with a total output of 1,960,890 reads (6). For *de novo* assembly, the SeqMan NGen software version 12.1.0 (DNASTAR, Madison, WI) with standard settings was used. After several assembly steps, a final 18 contigs and an N_{50} value of 532,738 bp were obtained. The final assembly had a total length of 5,966,942 bp and a G+C content of 63.39%. After annotation in GenDB (7), comparative genomics to related pseudomonads was performed in EDGAR version 2.3 (8).

By determination of the genome-to-genome distances values (GGDC) based on *in silico* DNA-DNA hybridization (DDH) (9) and calculation of average nucleotide identities (ANIb) with JSpeciesWS version 3.0.20 (10), we confirmed the species delineation against other species of the *P. putida* group. An average ANIb result of 92.39% ± 0.03% and GGDC of 51.2% ± 0.1% DDH were obtained with three genomes from the species *Pseudomonas donghuensis* (11, 12), while all other members of the *P. putida* group had lower ANIb and GGDC values. Therefore, the genome sequence confirms that *P.*

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wadenswilerensis CCOS 864^T constitutes a separate species distinguishable from other members of the *P. putida* group. The analysis of the genome content will still show the unique properties of this strain.

Data availability. The draft genome sequence of *P. wadenswilerensis* CCOS 864^T has been deposited in DDBJ/EMBL/GenBank under the BioProject number [PRJEB27830](https://www.ncbi.nlm.nih.gov/bioproject/PRJEB27830) and the sequence accession number [UIDD00000000](https://www.ncbi.nlm.nih.gov/nuclseq/UIDD00000000). The version described in this paper is version UIDD01000000. Raw sequence reads (Illumina) have been deposited in the Sequence Read Archive under the accession number [ERR2814815](https://www.ncbi.nlm.nih.gov/sra/ERR2814815).

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