



# Complete Genome Sequence of *Pseudomonas* sp. Strain MM213, an Isolate from a Brookside in Bielefeld, Germany

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**ABSTRACT** Here, we report the genome sequence of *Pseudomonas* sp. strain MM213, isolated from brookside soil in Bielefeld, Germany. The genome is complete and consists of 6,746,355 bp, with a GC content of 59.4% and 6,145 predicted protein-coding sequences. *Pseudomonas* sp. strain MM213 is part of the *Pseudomonas mandelii* group.

The genus *Pseudomonas* is composed of Gram-negative, rod-shaped gammaproteobacteria and is the most diverse bacterial taxon known to date, with 242 validated species (1). Members of the genus *Pseudomonas* inhabit a wide variety of environments, possess great metabolic variety, and have the potential for adaptation to unstable environmental conditions (1).

The soil sample, which was claylike and wet without any vegetation present, was obtained from a brookside in Bielefeld, Germany (52°01'45.5"N, 8°29'11.9"E), suspended in saline solution (0.9% [wt/vol] NaCl), and shaken for 5 min. The sample was taken from 5 cm beneath the ground. The suspension was filtered using a cellulose filter (REF 431015; Macherey-Nagel, Düren, Germany) and centrifuged, and the cell pellet was resuspended in fresh saline solution. Various dilutions were plated on agar medium (1.5% agar, 1% peptone from soy, 0.3% NaCl, 0.1% sucrose, 0.1% cellulose, 0.1% xylan, 0.1% chitin, and 0.05% Tris-HCl) and incubated at 28°C for 1 week. Colonies formed on agar plates were yellow. A single colony was picked for DNA isolation.

The NucleoSpin microbial DNA minikit for DNA from microorganisms (REF 740235; Macherey-Nagel) with optional RNA digestion was used to isolate the genomic DNA. With this DNA, a library was constructed with the native barcoding kit (EXP-NBD104; Oxford Nanopore Technologies, Oxford, UK) according to the manufacturer's specifications and sequenced with an R9.4.1 flow cell (Oxford Nanopore Technologies). All software was used with default parameters unless otherwise specified. DNA sequences were called live using the Super accuracy base-calling model (MinKNOW v1.4.3; Oxford Nanopore Technologies) on a GridION system. Adapters were trimmed using Porechop v0.2.4 (2). In total, 134,282 reads with 1.1 billion bases, with an  $N_{50}$  value of 14,732 bp, were sequenced; 50% of the data was trimmed with FilTlong v0.20 (3). The genome was assembled with Canu v2.1.1 (4) and polished with Racon v1.4.3 (5), followed by a second polishing with Medaka v1.4.3 (Oxford Nanopore Technologies). The genome had a coverage of 89×. The bacterial strain was identified using the BLAST function of the Type (Strain) Genome Server (TYGS) (6). Completeness was examined with BUSCO v5.1.2 (7). Genes were predicted with Prodigal v2.6.2 (8). The metabolic pathways were examined with KAAS (9). Potential secondary metabolite gene clusters were identified using antiSMASH (10).

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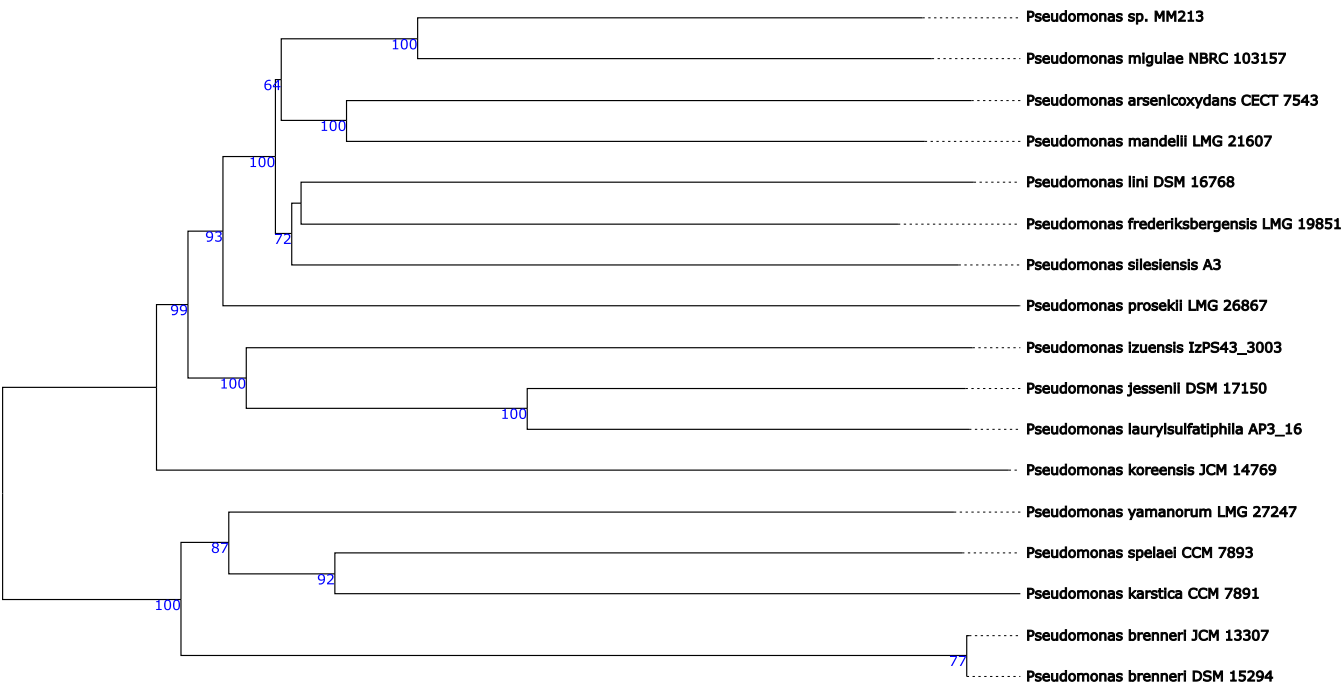
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**FIG 1** Genome BLAST Distance Phylogeny (GBDP) tree (6). A phylogenetic tree was constructed with TYGS (6). The tree represents only the *Pseudomonas* strains most closely related to the described isolate, *Pseudomonas* sp. strain MM213 (6). The bootstrap support values from 100 replications are marked in blue at each branch point. The branch lengths are scaled in terms of GBDP distance formula  $d_s$ . The numbers above the branches are GBDP pseudo-bootstrap support values of >60% from 100 replications. The tree was rooted at the midpoint. The numbers at the end of each branch represent the strain numbers for each species.

*Pseudomonas* sp. strain MM213 phylogenetically groups within the subgroup *Pseudomonas mandelii* and in the major group *Pseudomonas fluorescens* (11) (Fig. 1). The most closely related known organism is *Pseudomonas migulae* NBRC 103157 (GenBank assembly accession number [GCA\\_002091715.1](#)), with a  $d_4$  digital DNA-DNA hybridization (dDDH) similarity of 46.4% (6). A member of the subgroup *P. mandelii* is a cold-adapted, nonhalophilic bacterium that can grow at 4°C but does not grow at 37°C (12). *P. mandelii* strains do occur in mineral waters and agricultural fields (13). The assembly had a completeness of 96% (Table 1).

*Pseudomonas* sp. strain MM213 has the potential to produce secondary metabolites such as vitamins B1 to B5, B7, and B12 (9). The genome suggests the presence of flagella and benzoate degradation (9).

*Pseudomonas* sp. strain MM213 is likely able to produce aryl polyenes, because 45% of the genes within this cluster have a significant BLAST hit to the gene cluster from *Aliivibrio fischeri* ES114 (GenBank assembly accession number [GCA\\_000985635.1](#)) (10, 14). Aryl polyenes are yellow carotenoid-like pigments that have been found to be antioxidants and protection against reactive oxygen species (15).

**Data availability.** The genome sequence of *Pseudomonas* sp. strain MM213 has been deposited in NCBI GenBank under accession number [CP081943](#). The NCBI Sequence Read Archive (SRA) accession number for the raw reads is [SRR15533117](#).

**TABLE 1** BUSCO results for *Pseudomonas* sp. strain MM213

BUSCO parameter	Result (%)
Completeness	96
Single copy	95.7
Duplicated	0.3
Fragmented	0.3
Missing	3.7

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