



Draft Genome Sequences of the Nitrate-Dependent Iron-Oxidizing Proteobacteria *Acidovorax* sp. Strain BoFeN1 and *Paracoccus pantotrophus* Strain KS1

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ABSTRACT The draft genomes of the nitrate-dependent iron-oxidizing bacteria *Acidovorax* sp. strain BoFeN1 and *Paracoccus pantotrophus* strain KS1 are presented. These genomes supply supporting data to investigations of the mechanisms underlying this anaerobic form of microbial biogeochemical iron cycling.

A *Acidovorax* sp. strain BoFeN1 and *Paracoccus pantotrophus* strain KS1 have both demonstrated the capability to perform nitrate-dependent Fe²⁺ oxidation (NDFO), whereby Fe³⁺ precipitates are formed during microbial nitrate reduction (1, 2). NDFO is a geomicrobiological process which has been recognized for the past 2 decades (3) and is responsible for the production of Fe³⁺-bearing minerals in anaerobic, circum-neutral, reducing environments under conditions similar to those that were prevalent on the early Earth and ancient Mars (1, 4–6). Despite this potential importance in the early history of life, the putative underlying mechanisms are largely unconfirmed experimentally (7), despite some advances (8, 9).

Acidovorax sp. strain BoFeN1 is a Gram-negative, rod-shaped bacterium belonging to the family *Comamonadaceae* in the order *Burkholderiales* of the class *Betaproteobacteria*. *Acidovorax* sp. strain BoFeN1 was isolated from littoral sediments of Lake Constance on the Germany–Switzerland border and assigned to the genus *Acidovorax* based on 16S rRNA gene sequence analysis (1). This isolate was donated by Jennyfer Miot of the Mineralogy, Material Physics and Cosmochemistry Institute (IMPMC) in Paris, France.

Paracoccus pantotrophus strain KS1 is a Gram-negative, motile coccoid bacterium belonging to the family *Rhodobacteraceae* in the order *Rhodobacterales*, in the class *Alphaproteobacteria*. *Paracoccus pantotrophus* strain KS1 was isolated from soil at Kew Gardens in the United Kingdom and was originally reported as a member of the genus *Thiobacillus* but was later reclassified to the genus *Paracoccus* based on the 16S rRNA gene sequence (10, 11). This strain was purchased as a live culture (DSM 11072) from the German Collection of Microorganisms and Cell Cultures (DSMZ) in Leibniz, Germany.

The two strains were maintained in pure culture in aerobic nutrient medium (5.0 g liter⁻¹ peptone and 3.0 g liter⁻¹ meat extract) at 30°C prior to DNA extraction and genome sequencing, which was performed by MicrobesNG (<https://microbesng.uk/>) using the Illumina MiSeq platform with 2 × 250-bp paired-end reads. Trimmed reads were produced using Trimmomatic version 0.30 (<http://www.usadellab.org/cms/?page=trimmomatic>) with a sliding window quality cutoff of Q15, and *de novo* assembly was performed using SPAdes version 3.7 (<http://cab.spbu.ru/software/spades/>) (12, 13). Coverage of 30× was achieved during sequencing, and genome annotation was

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performed using the RAST annotation server version 2.0 (<http://rast.nmpdr.org/rast.cgi>) via the classic RAST pipeline (14). The draft genome of strain *Acidovorax* sp. strain BoFeN1 consisted of 4.06 Mb in 184 contigs ($N_{50} = 37,384$), with a GC content of 63.77%. A total of 3,794 protein-coding sequences were predicted from the annotated genome, with 50 tRNAs identified using the ARAGORN version 1.1 tRNA detection program (<http://mbio-serv2.mbioekol.lu.se/ARAGORN/>) (15). The closest match for the 16S rRNA gene was identified in the GenBank database, by using the BLASTN program (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), as *Acidovorax defluvi* strain BSB411 (99% similarity; GenBank accession number [NR_026506](https://pubmed.ncbi.nlm.nih.gov/2026506/)). The draft genome of *Paracoccus pantotrophus* strain KS1 consisted of 4.16 Mb in 227 contigs ($N_{50} = 36,889$), with a GC content of 67.69%. A total of 3,941 protein-coding sequences and 54 tRNAs were predicted from the annotated genome. The nearest 16S rRNA gene sequence was identified using BLASTN, with a best match as *Paracoccus pantotrophus* (100%; accession number [AB098590](https://pubmed.ncbi.nlm.nih.gov/1098590/)).

Neither genome contained a dedicated ferroxidase, suggesting that NDFO in these strains is not a direct enzymatic process to acquire electrons. Full denitrification pathways were confirmed in both strains by the presence of nitrogen species reductase genes (*nar*, *nir*, *nor*, and *nos*), with additional genes for a periplasmic nitrate reductase (Nap) in the *Paracoccus pantotrophus* strain KS1 genome.

Data availability. DDBJ/ENA/GenBank accession numbers have been assigned for *Acidovorax* sp. strain BoFeN1 ([QOZT00000000](https://pubmed.ncbi.nlm.nih.gov/30000000/)) and *Paracoccus pantotrophus* strain KS1 ([QOZU00000000](https://pubmed.ncbi.nlm.nih.gov/30000000/)). Raw sequencing reads for *Acidovorax* sp. strain BoFeN1 ([SRP157586](https://pubmed.ncbi.nlm.nih.gov/157586/)) and *Paracoccus pantotrophus* strain KS1 ([SRP157588](https://pubmed.ncbi.nlm.nih.gov/157588/)) are available in the NCBI Sequence Read Archive.

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