

## Draft Genome Sequence of the Electricigen *Acidiphilium* sp. Strain PM (DSM 24941)

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***Acidiphilium* sp. strain PM (DSM 24941) was isolated from Rio Tinto's acidic, heavy metal-rich waters. Voltammetry experiments revealed that this strain is capable of electricity production even under aerobic conditions. Here we report the draft genome sequence of *Acidiphilium* sp. PM and a preliminary genome analysis that reveals a versatile respiratory metabolism.**

*Acidiphilium* sp. strain PM (DSM 24941) was isolated from Rio Tinto, a naturally acidic, heavy metal-rich river located in southwestern Spain (3). Bacteria of the genus *Acidiphilium* are facultatively aerobic, acidophilic, Gram-negative *Alphaproteobacteria* capable of synthesizing Zn-chelated bacteriochlorophyll *a* (Zn-BChl *a*) (4, 6). All known *Acidiphilium* species can grow chemoorganotrophically, but only *A. acidophilum* has been described to be capable of obtaining energy from reduced inorganic sulfur compounds. The decision to sequence the genome of *Acidiphilium* sp. PM followed the discovery of several biotechnologically relevant properties, especially its capacity to transfer electrons to electrodes under aerobic conditions (8).

A draft genome sequence was determined using a 454 pyrosequencing strategy. Using the GS *de novo* assembler 2.3 (Roche), 252,837 reads were assembled into 814 contigs (15-fold coverage), totaling 3.98 Mbp (average GC content, 68%). A total of 627 contigs longer than 500 bp were annotated by means of an automatic pipeline that used tRNAscan (7) to predict tRNA genes, Glimmer (2) to predict coding sequences, and BLAST and RPSblast (1) comparisons against several protein sequence and protein family databases to generate functional annotations. An automatic metabolic reconstruction was generated with Pathway Tools (5).

On the basis of sequence comparison, contigs were ascribed to the chromosome or to one of nine plasmids, including one that is 91% identical to the *Acidithiobacillus ferrooxidans* pTF4.1 plasmid. A total of 48 tRNA genes were identified, 6 of which are part of two nearly identical rRNA operons with the following structure: 16S-tRNA(Ile)-tRNA(Ala)-23S-5S-tRNA(Met). These operons are 99.7% identical to the two described for *Acidiphilium cryptum* JF-5 (accession number NC\_009484).

Metabolic reconstruction revealed the presence of a complete Entner-Doudoroff pathway, instead of the classical Embden-Meyerhof glycolysis pathway (no gene could be found for 6-phosphofructokinase). The pentose phosphate pathway was also found to be complete. These results are in agreement with previous experimental evidence in other members of the genus (9). A complete tricarboxylic acid cycle was detected, which allows the complete oxidation of glucose to CO<sub>2</sub>. The prediction of three enzymes unique to the Calvin-Benson-Bassham cycle (RuBisCO, phosphoribulokinase, and sedoheptulose biphosphatase) suggests that *Acidiphilium* sp. PM is a facultative autotroph capable of CO<sub>2</sub> fixation under organic carbon limitation.

Our analysis showed no genes related to atmospheric nitrogen fixation. Instead, two distinct pathways were predicted for ammonium assimilation into glutamate. Besides, a gene cluster involved in assimilative nitrate reduction, similar to that found in *Acidiphilium multivorum* AIU301 plasmid pACMV1, was identified in one of the nine predicted plasmids (pAPM\_01).

A cytochrome *bo* oxidase (*cyoABCD*) and two cytochrome *bd* oxidases (*cydAB*) were predicted that could be responsible for the ability of *Acidiphilium* sp. PM to respire oxygen. However, no genes involved in iron respiration were predicted in the genome, even though this ability has been well documented (8).

On the other hand, the prediction of a complete *narGYZ* cluster involved in nitrate respiration and a polysulfide reductase operon (*psrABC*) leads us to propose that *Acidiphilium* sp. PM could respire anaerobically using nitrate or polysulfides as electron acceptors.

*Acidiphilium* sp. strain PM has been deposited in the German Collection of Microorganisms and Cell Cultures (DSM 24941).

**Nucleotide sequence accession number.** The *Acidiphilium* sp. PM whole-genome shotgun project data have been deposited in the GenBank database under project accession number AFPR00000000.

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