Genome Sequence of the Acidophilic Bacterium Acidocella sp. Strain MX-AZ02

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Acidocella sp. strain MX-AZ02 was isolated from a naturally acidic (pH 2.3) and heavy metal-containing shallow lake in the Los Azufres National Park in western Mexico. The Acidocella genus comprises aerobic, acidiphilic, Gram-negative bacteria belonging to the class Alphaproteobacteria (1). Acidocella relatives have been identified both in natural and acid mine drainage environments exhibiting high heavy-metal levels (2–6). Acidocella has also been detected among Sphagnum moss microbiota growing under varying acidic conditions (7, 8). Currently, the genus contains three reference strains isolated from acidic environments (9–11).

DNA was isolated from Acidocella sp. MX-AZ02, which yields smooth, round, and translucent colonies on DSMZ medium 35a. The organism is maintained at the Center of Genomic Sciences in the culture collection of the Ecological Genomics Department, National University of Mexico (UNAM). The sequencing was performed with the Roche 454 GS-FLX titanium technology generating 58.04 Mbp (~16-fold coverage) from a mate-paired library with 3-kb inserts. The reads were assembled de novo using Newbler assembler 2.3 (454 Life Sciences). The assembly produced 303 contigs of >500 bp each with an N50 size of 22.12 kb. Nine scaffolds were generated containing 250 contigs. Genome annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

The genome of Acidocella sp. MX-AZ02 was estimated to be 3.6 Mbp with a G+C content of 64.1% and it carried 3,553 open reading frames (ORFs). The 16S rRNA gene phylogeny indicated that the strain is closely related to type strains Acidocella facilis PW2, Acidocella aluminidurans AL46, and Acidocella aminolytica 101, sharing 99.86%, 99.50%, and 97.93% sequence identities, respectively, over 1,407 bp.

Metal resistance determinants have been identified for Acidocella strains (12, 13, 14). The Acidocella sp. MX-AZ02 genome codes for arsenic, chromium, copper, and cobalt-zinc-cadmium transporters, as well as heavy-metal sensor signal transduction histidine kinases and chaperones. Carbonic anhydrases were also encoded, which may provide a means to cope with the low CO₂ levels in acidic waters.

One Acidocella strain was shown to metabolize fructose from medium containing cell-free algal exudates, but it was unable to metabolize mannitol or glucose (15). Acidocella sp. MX-AZ02 may use glucose in the isolation medium as a carbon source. An acidophilic and abundant unicellular green alga was recently characterized from the same lake from which Acidocella sp. MX-AZ02 was isolated (16). Possibly, Acidocella sp. MX-AZ02 utilizes organic compounds from the alga, as was proposed previously for acidiphilic microalgae and acidiphilic heterotrophic bacteria (15).

The draft genome of Acidocella sp. MX-AZ02 will facilitate the identification of metal resistance determinants and may help us understand bacterial–algal interactions. This is the first isolated bacterial genome for an Acidocella strain and is the first sequenced bacterial genome from the Los Azufres National Park.

**Nucleotide sequence accession number.** The draft of the genome sequence is deposited at DDBJ/EMBL/GenBank under the accession no. AMPS00000000.

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**REFERENCES**


