Draft Genome Sequences of Acidithrix sp. Strain C25 and Acidocella sp. Strain C78, Acidophiles Isolated from Iron-Rich Pelagic Aggregates (Iron Snow)

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ABSTRACT We report the draft genome sequences of two acidophiles, the Fe-oxidizing bacterium Acidithrix sp. strain C25 and the putative Fe-reducing Acidocella sp. strain C78. Both strains were isolated from iron-rich pelagic aggregates (iron snow) collected below the redoxcline at a 5-m depth in an acidic pit lake located in Germany (51°31’9.2” N, 13°41’9.34.7” E).

Fe-cycling bacteria represent a large fraction of iron snow microbial communities in acidic pit lakes (1). Acidithrix sp. strain C25, a heterotrophic Fe(II)-oxidizing bacterium within the Acidimicrobiaceae family of the Actinobacteria phylum, is the second isolated and sequenced strain within the Acidithrix genus (2, 3). Acidocella sp. strain C78, a putative heterotrophic Fe(III)-reducing bacterium, belongs to the Acetobacteraceae family of the Proteobacteria phylum. Acidocella sp. strain YE4-N1-5-CH, isolated from this pit lake, and other Acidocella isolates have the capacity for dissimilatory Fe(III) reduction (4, 5). To further understand the metabolic potential and the contribution of these microbes to iron snow formation, we sequenced a n d a n a l y z e d t h e s e t w o genomes.

Both strains were isolated from 100 μl of diluted lake water (10^{-1} to 10^{-3}) transferred to two types of overlay plates containing 25 mM FeSO₄—Feo (without a carbon source) for Acidithrix sp. C25 and YEo (0.2% yeast extract) for Acidocella sp. C78 (6, 7). Single colonies, transferred at least five times to establish pure cultures, were lysed and used for 16S rRNA gene PCR and phylogenetic analysis (7). To obtain sufficient biomass for DNA extraction, cultures were incubated in artificial pilot-plant water medium (APPW) amended with yeast extract (0.2 g liter^{-1}). Acidithrix sp. C25 incubations were additionally amended with 25 mM FeSO₄ (8). Genomic DNA was extracted using a phenol-chloroform-based protocol (9). Whole-genome sequencing was performed by RTL Genomics (Lubbock, TX, USA). Needle-sheared DNA was used to prepare 10- to 20-kb sequencing libraries using the PacBio SMRTbell template prep kit v1.0 without further size selection and was subsequently sequenced using P6-C4 chemistry with an 180-min collection protocol using a PacBio RS II platform (Pacific Biosciences, Menlo Park, CA) according to the standard manufacturer’s protocols. The raw reads were filtered and assembled de novo with the Hierarchical Genome Assembly Process v3 (HGAP3) (10) using default settings (https://github.com/ben-lerch/HGAP-3.0). Genome completeness and contamination were assessed with CheckM v1.0.13 using default parameters (11). Genome annotation was performed with RASTtk v2.0 using default parameters (12). The genome characteristics of both strains are listed in Table 1.

Analysis of the Acidithrix sp. C25 genome revealed genes encoding the complete Calvin-Benson-Bassham cycle, which indicates that the heterotrophic Acidithrix sp. C25 has the genetic potential for CO₂ fixation. We could not identify homologs linked to Fe(II) oxidation under acidic conditions, such as cyc2, cyt572, cyt579, sulfocyanin, and foxCD. We found a gene...
<table>
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<th>Strain name</th>
<th>Genome size (bp)</th>
<th>Total PacBio sequences (bp)</th>
<th>PacBio sequence ( N_{50}) (bp)</th>
<th>Coverage (X)</th>
<th>No. of contigs</th>
<th>G+C content (%)</th>
<th>( N_{50}) (bp)</th>
<th>Completeness (%)</th>
<th>Redundancy (%)</th>
<th>No. of genes</th>
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<td>5</td>
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</table>
encoding aromatic L-amino-acid decarboxylase, which converts phenylalanine to phenethylamine, an aggregation-mediating infochemical within iron snow (7, 13).

The Acidocella sp. C78 genome encodes the complete Calvin-Benson-Bassham cycle, indicating the genetic capacity for CO2 fixation. Multiple genes encoding polysaccharide-degrading enzymes (e.g., glycosidase) and a gene encoding the methionine sulfoxide reductase heme-binding subunit, previously linked to Fe(III) reduction (14), were detected. These draft genome sequences are a valuable resource to understand iron snow functioning.

Data availability. The sequencing reads and assemblies of Acidithrix sp. C25 and Acidocella sp. C78 for this whole-genome sequencing project are available in ENA under the BioProject accession numbers PRJEB40539 and PRJEB40546, respectively, and the assembly accession numbers are listed in Table 1. The versions described in this paper are the first versions.

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REFERENCES


