Permanent draft genome sequence of Acidiphilium sp. JA12-A1

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Abstract
The tenacious association between strains of the heterotrophic alphaproteobacterial genus Acidiphilium and chemolithotrophic iron oxidizing bacteria has long been known. In this context the genome of the heterotroph Acidiphilium sp. JA12-A1, an isolate from an iron oxidizing mixed culture derived from a pilot plant for bioremediation of acid mine drainage, was determined with the aim to reveal metabolic properties that are fundamental for the syntrophic interaction between Acidiphilium sp. JA12-A1 and the co-occurring chemolithoautotrophic iron oxidizer. The genome sequence consists of 4.18 Mbp on 297 contigs and harbors 4015 protein-coding genes and 50 RNA genes. Additionally, the molecular and functional organization of the Acidiphilium sp. JA12-A1 draft genome was compared to those of the close relatives Acidiphilium cryptum JF-5, Acidiphilium multivorum AIU301 and Acidiphilium sp. PM DSM 24941. The comparative genome analysis underlines the close relationship between these strains and the highly similar metabolic potential supports the idea that other Acidiphilium strains play a similar role in various acid mine drainage communities. Nevertheless, in contrast to other closely related strains Acidiphilium sp. JA12-A1 may be able to take up phosphonates as an additional source of phosphor.

Keywords: Acidiphilium sp. JA12-A1, acid mine drainage, AMD, microbial community, acidophilic bacteria

Introduction
Strains of the alphaproteobacterial genus Acidiphilium have first been isolated from supposed pure cultures of iron oxidizing bacteria such as Acidithiobacillus ferrooxidans [1]. Later on, Acidiphilium spp. have also been identified as characteristic members of the microbial communities in acid mine drainage and mining associated water bodies [2–5]. Although the physiological role of these heterotrophic acidophiles within the microbial community has not yet been completely elucidated, the tenacious association between them and the chemolithoautotrophic iron oxidizers has often been reported to be problematic for the isolation of the iron oxidizing bacteria [1, 6, 7]. Several attempts have been undertaken to investigate the interaction between the iron oxidizing bacterium Acidithiobacillus ferrooxidans and Acidiphilium sp. In a co-culture with Acidiphilium acidophilum the increased growth rate and ferrous iron oxidation rate of Acidithiobacillus ferrooxidans have indicated a stimulating influence of Acidiphilium acidophilus on Acidithiobacillus ferrooxidans [8]. A stable isotope probe based proteome analysis of an Acidithiobacillus ferrooxidans/Acidiphilium cryptum mixed culture has revealed carbon dioxide transfer from the heterotroph to the iron oxidizing bacterium [9]. Based on the absence of organic carbon and energy sources in the cultivation media of iron oxidizing bacteria it has been suggested that Acidiphilium spp. benefit in turn from secreted metabolites and remnants of the biomass from the iron oxidizers by utilizing them as carbon and energy sources [10–12].

Since such an interaction is not only relevant for the isolation and cultivation of iron oxidizing bacteria but also for the general understanding of the ecology of microbial communities in AMD, we were interested in elucidating the potential of Acidiphilium for such a syntrophic interaction. Therefore we sequenced and analyzed the genome of Acidiphilium sp. JA12-A1 with special focus on transport systems for the uptake of nutrients, the pathways of nutrient assimilation and the general energy metabolism. The resulting permanent
draft genome was also compared to the genomes of the close relatives Acidiphilium cryptum JF-5, Acidiphilium multivorum AU1301 and Acidiphilium sp. PM DSM 24941 regarding the genome structure and the functional organization.

**Organism Information**

**Classification and features**

Strain Acidiphilium sp. JA12-A1 was detected as the heterotrophic contamination in the mixed culture JA12 of a novel chemolithoautotrophic iron oxidizing bacterium [13], which is related to “Ferrovum myxofaciens” P3G [7, 14]. The iron oxidizing mixed culture originated from a pilot plant for the biological remediation of AMD close to a lignite mining site in Lusatia, Germany [5, 13, 15]. Acidiphilium sp. JA12-A1 was isolated from the mixed culture by cultivation in SJH medium [16, 17] (Table 1, Additional file 1).

The complete 16S rRNA gene sequence of Acidiphilium sp. JA12-A1 was compared to the non-redundant nucleotide collection of the NCBI using NCBI MegaBLAST [18, 19]. The analysis of the 100 best hits revealed a sequence similarity of 99 % to 16S rRNA gene fragments of Acidiphilium multivorum AU1301, Acidiphilium cryptum JF-5, Acidiphilium organovorum TFC, Acidiphilium sp. SJH, and “Acidiphilium symbioticum” and others, and a sequence similarity of 95 % to Acidiphilium acidophilum MS Silver, Acidiphilium angustum ATCC 35903 and Acidiphilium rubrum. These gene fragments also formed the basis for the calculation of a dendrogram illustrating the phylogenetic neighborhood of Acidiphilium sp. JA12-A1 (Fig. 1).

The 16S rRNA gene sequences cluster into two distinct subgroups within the genus Acidiphilium. The novel strain Acidiphilium sp. JA12-A1 belongs to

| MIGS ID | Property             | Term                                                                 | Evidence code* |
|--------|----------------------|----------------------------------------------------------------------|----------------|
|        | **Classification**   | **Domain Bacteria**                                                  | TAS [32]       |
|        |                      | Phylum Proteobacteria                                                | TAS [33–35]    |
|        |                      | Class Alphaproteobacteria                                            | TAS [34, 36]   |
|        |                      | Order Rhodospirillales                                              | TAS [37, 38]   |
|        |                      | Family Acetobacteraceae                                             | TAS [39, 40]   |
|        |                      | Genus Acidiphilium                                                  | TAS [2, 41, 42]|
|        |                      | Species Acidiphilium sp.                                            | TAS [2]        |
|        | Strain: JA12-A1      | **Gram stain** Negative                                              | TAS [2]        |
|        |                      | **Cell shape** Rod                                                   | IDA            |
|        |                      | **Motility** Motile                                                  | IDA            |
|        |                      | **Sporulation** Not reported                                         | NAS            |
|        |                      | **Temperature range** Mesophile                                     | NAS            |
|        |                      | **Optimum temperature** 30 °C                                       | NAS            |
|        |                      | **pH range; Optimum** Not reported                                   | NAS            |
|        |                      | **Carbon source** Heterotroph (galactose, glucose, tryptic soy broth,| NAS            |
|        |                      | fructose, yeast extract)                                             |                |
| MIGS-6 | Habitat              | Acid mine drainage                                                   | NAS            |
| MIGS-63| Salinity             | Not reported                                                        | NAS            |
| MIGS-22| Oxygen requirement    | Aerobic, anaerobic                                                   | NAS            |
| MIGS-15| Biotic relationship   | Free-living                                                         | NAS            |
| MIGS-14| Pathogenicity        | Non-pathogen                                                        | NAS            |
| MIGS-4 | Geographic location  | Lignite mining site, Lusatia, Germany                                | NAS            |
| MIGS-5 | Sample collection     | 2011                                                                | NAS            |
| MIGS-4.1| Latitude            | 51° 28’ 10.38” N                                                    | NAS            |
| MIGS-4.2| Longitude           | 14° 28’ 22.19” E                                                   | NAS            |
| MIGS-4.4| Altitude            | 125.45 m                                                           | NAS            |

*Evidence codes - IDA: Inferred from Direct Assay; TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). These evidence codes are from the Gene Ontology project [43]
the same subgroup as *Acidiphilium cryptum* JF-5, *Acidiphilium multivorum* AIU301 and *Acidiphilium* sp. PM DSM 24941.

In terms of physiological features *Acidiphilium* sp. JA12-A1 appears to be closely related to the type strain *Acidiphilium cryptum* Lhet2 [2]: *Acidiphilium* sp. JA12-A1 is a Gram-negative, rod-shaped (ca. 1.9 μm × 0.7 μm), motile alphaproteobacterium, which lives under acidophilic conditions. It has a chemoorganotrophic lifestyle growing with galactose, fructose, yeast extract and soy broth as growth substrates. In the mixed culture with the iron oxidizer “*Ferrovum*” sp. JA12 [31] the proportion of *Acidiphilium* sp. JA12-A1 was estimated by terminal restriction fragment length polymorphism (T-RFLP) analysis to vary between 1% and 50% depending on the ferrous iron concentration and growth phase (unpublished results). An electron micrograph of *Acidiphilium* sp. JA12 is provided in Fig. 2.

**Genome sequencing information**

**Genome project history**

The genome of *Acidiphilium* sp. JA12-A1 was sequenced to obtain genetic information on physiological properties that may play a fundamental role in its tenacious association with the co-occurring iron oxidizing bacterium in the mixed culture JA12. The permanent draft genome
sequence is available at the NCBI with the accession number JFHO00000000 (genome project number 238988). The cultivation and genome sequence analysis was undertaken at the TU Bergakademie Freiberg while the genome sequencing and annotation was performed at Göttingen Genomics Laboratory (G2L). Table 2 provides a summary of the project information according to MIGS compliance [32].

**Growth conditions and genomic DNA preparation**

*Acidiphilium* sp. JA12-A1 was cultivated in liquid SJH medium [16, 17] at 30 °C. It was continuously shaken on a rotary shaker at 120 rpm. The cells were harvested by centrifugation at 10,000 × g. The DNA was isolated using the Ultra Clean™ Microbial DNA Isolation Kit (MoBio, Carlsbad, CA) according to the manufacturer's instructions.

**Genome sequencing and assembly**

Genome sequencing of *Acidiphilium* sp. JA12-A1 was performed via a hybrid approach using the 454 GS-FLX TitaniumXL system (Titanium GS70 chemistry, Roche Life Science, Mannheim, Germany) and the Genome Analyzer II (Illumina, San Diego, CA). Shotgun libraries were prepared according to the manufacturer's protocols, resulting in 126,343 reads for 454 shotgun and 10,136,209 112-bp paired-end Illumina reads. We used all 126,343 454 shotgun reads and 3,000,000 of the 112-bp paired-end Illumina reads for the initial hybrid de novo assembly, which was calculated using the MIRA 3.4 [44] and Newbler 2.8 (Roche Life Science, Mannheim, Germany) software. The final assembly contained 297 contigs with a 73.5-times coverage on average.

**Genome annotation**

The software tools YACOP and Glimmer [45] were used for automatic gene prediction, while identification of rRNA and tRNA genes was performed using RNAmmer and tRNAscan, respectively [46, 47]. An automatic annotation was performed within the integrated microbial genomes-expert review (IMG-ER) system [48, 49] and subsequently curated manually by using the Swiss-Prot, TrEMBL, and InterPro databases [50].

**Genome Properties**

The draft genome of *Acidiphilium* sp. JA12-A1 consists of 4.18 Mbp on 298 contigs, of which 99 have a length of at least 10 kbp. Genome features are summarized in Table 3. The average G + C content is 66.9 %. The draft genome encodes 4065 genes in total, of which 4015 (98.8 %) are predicted protein coding genes and 50 (1.2 %) are RNA genes. 2663 (65.5 %) genes are assigned to COG groups (Table 4), 1238 (30.5 %) are connected to KEGG pathways and 520 (12.8 %) are assigned to the transporter classification. A comparison of genome features of *Acidiphilium* sp. JA12-A1 to the genomes of *Acidiphilium cryptum* JF-5, *Acidiphilium multivorum* AUI301 and *Acidiphilium* sp. DSM 24941 is provided in Table 5.

**Insights from the genome sequence**

In order to understand the potential interaction between *Acidiphilium* sp. JA12-A1 and the iron oxidizer “Ferrovum” sp. JA12 in the mixed culture we analyzed the genome of *Acidiphilium* sp. JA12-A1 with special focus on genes that may be involved in the utilization of “Ferrovum” derived organic substances as an energy source and as growth substrates.

The genome analysis revealed six genes that encode for putative oligo- and polysaccharide hydrolyzing enzymes, among which we identified α-amylases or amylase-related enzymes, β-glucosidase, endoglucanase, a trehalase and a glycogen-debranching enzyme. *Acidiphilium* sp. JA12-A1 may use these enzymes to break down polysaccharides that are part of the cell envelope of the iron oxidizer “Ferrovum” or that are excreted as slimes. Applying the EBI InterProScan to the sequences of these enzymes resulted in predicted N-terminal signal peptides in the β-glucosidase and endoglucanase which indicates a potential excretion of these enzymes.

The genome of *Acidiphilium* sp. JA12-A1 encodes a variety of transport systems to take up secreted organic compounds or the products of the hydrolysis of polysaccharides. These transport systems comprise annotated

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**Table 2** Project information

| MIGS ID | Property            | Term                                         |
|--------|---------------------|----------------------------------------------|
| MIGS 31| Finishing quality   | Improved high-quality draft                  |
| MIGS-28| Libraries used      | Two genomic libraries: 454 pyrosequencing    |
|        |                     | shotgun library, Illumina paired-end        |
|        |                     | library (1 kb insert size)                   |
| MIGS 29| Sequencing platforms| 454 GS FLX Titanium, Illumina GAII          |
| MIGS 31.2| Fold coverage      | 18.7 × 454, 54.8 × Illumina                 |
| MIGS 30| Assemblers          | Newbler 2.8, MIRA 3.4                       |
| MIGS 32| Gene calling method | YACOP, Glimmer                             |
|        | Locus Tag           | ACIDI                                       |
|        | Genbank ID          | JFHO01000000                               |
|        | GenBank Date of     | 2014-05-20                                  |
|        | Release             |                                              |
|        | GOLD ID             | GI0008223                                   |
|        | BIOPROJECT           | PRJNA238588                                 |
| MIGS 13| Source Material     | TU BAF Acidii                               |
|        | Identifier          |                                              |
|        | Project relevance   | Environmental and biotechnological          |
sugar transporters or sugar phosphate permeases of the major facilitator family, 15 ABC-transport systems for mono- and disaccharides and a phosphotransferase system (PTS) of the fructose type. The ABC-transporters are predicted to take up ribose, xylose, galactose or similar monosaccharides. The PTS in *Acidiphilium* sp. JA12-A1 consists, similar to the PTS of other *Acidiphilium* strains, of two fusion proteins (HPr/EI/EIIA and EIIB/EIIC).

Based on the genome sequence we reconstructed the metabolic pathways that may enable *Acidiphilium* sp. JA12-A1 to gain energy by the complete aerobic oxidation of organic compounds, preferably of monosaccharides. Although we did not identify the fructose-6-phosphate kinase, one of the key enzymes of the glycolysis, *Acidiphilium* sp. JA12-A1 may bypass the reaction via the activity of enzymes of the pentosephosphate pathway, thus still being able to convert glucose to acetyl-CoA. Acetyl-CoA is further oxidized to carbon dioxide by the citrate cycle and the electrons are transferred to oxygen by the protein complexes of the aerobic respiratory chain. We also identified gene clusters encoding the subunits of a photosynthetic reaction center, associated cytochromes and proteins involved in the biogenesis of the reaction center proteins that may enable *Acidiphilium* sp. JA12-A1 to use light as additional energy source.

In addition to the aerobic respiration *Acidiphilium* sp. JA12-A1 may also be able to reduce ferric iron under microaerobic or anaerobic conditions as it has been described for other *Acidiphilium* strains [51, 52]. Despite of the experimental evidence for the ferric iron reduction, the proteins that are involved in the direct reduction of ferric iron in acidophiles have still not been identified [53]. The genome analysis of *Acidiphilium* sp. JA12-A1 also failed to reveal any further details of the electron transfer processes to ferric iron.

Apart from providing the source of energy the sugar compounds also appear to be the preferred carbon source for the biomass production in *Acidiphilium* sp. JA12-A1. We inferred the pathways that are necessary for the conversion of the monosaccharides to the precursors of the biomass production, such as the amino and nucleotide sugar metabolism, the citrate cycle, the fatty acid synthesis and the purine and pyrimidine metabolism. Besides the synthesis of biomass there is genetic evidence for the storage of carbon compounds as polyhydroxybutyrate (PHB) which is further supported by transmission electron microscopic analysis of representative cells showing PHB granula (Fig. 2). *Acidiphilium* sp. JA12-A1 also appears to be able to fix carbon dioxide heterotrophically, since its genome encodes a pyruvate carboxylase and a pyruvate carboxykinase.

### Table 3: Genome statistics *Acidiphilium* sp. JA12-A1

| Attribute                     | Value     | % of Total |
|-------------------------------|-----------|------------|
| Genome size (bp)              | 4,184,331 | 100.0      |
| DNA coding (bp)               | 3,699,946 | 88.4       |
| DNA G + C (bp)                | 2,801,106 | 66.9       |
| DNA scaffolds                 | 298       |            |
| Total genes                   | 4,065     | 100.0      |
| Protein coding genes          | 4,015     | 98.8       |
| RNA genes                     | 50        | 1.2        |
| Pseudo genes                  | 293       | 7.2        |
| Genes in internal clusters    | 3,092     | 76.1       |
| Genes with function prediction| 3,193     | 78.6       |
| Genes assigned to COGs        | 2,663     | 65.5       |
| Genes with Pfam domains       | 3,191     | 78.5       |
| Genes with signal peptides    | 268       | 6.6        |
| Genes with transmembrane helices | 857 | 21.1       |
| CRISPR repeats                | Not reported |          |

### Table 4: Number of genes associated with general COG functional categories

| Code | Value | % age | Description                                      |
|------|-------|-------|-------------------------------------------------|
| J    | 147   | 5.0   | Translation, ribosomal structure and biogenesis  |
| A    | 0     | 0.0   | RNA processing and modification                 |
| K    | 180   | 6.1   | Transcription                                   |
| L    | 157   | 5.3   | Replication, recombination and repair           |
| B    | 2     | 0.1   | Chromatin structure and dynamics                |
| D    | 167   | 5.7   | Cell cycle control, Cell division, chromosome partitioning |
| V    | 35    | 1.2   | Defense mechanisms                              |
| T    | 77    | 2.6   | Signal transduction mechanisms                  |
| M    | 167   | 5.7   | Cell wall/membrane biogenesis                   |
| N    | 44    | 1.5   | Cell motility                                   |
| U    | 77    | 2.6   | Intracellular trafficking and secretion         |
| O    | 107   | 3.6   | Posttranslational modification, protein turnover, chaperones |
| C    | 260   | 8.8   | Energy production and conversion                |
| G    | 247   | 8.3   | Carbohydrate transport and metabolism           |
| E    | 294   | 10.0  | Amino acid transport and metabolism             |
| F    | 66    | 2.2   | Nucleotide transport and metabolism             |
| H    | 125   | 4.2   | Coenzyme transport and metabolism               |
| I    | 164   | 5.6   | Lipid transport and metabolism                  |
| P    | 124   | 4.2   | Inorganic ion transport and metabolism          |
| Q    | 89    | 3.0   | Secondary metabolites biosynthesis, transport and catabolism |
| R    | 320   | 10.8  | General function prediction only                |
| S    | 241   | 8.2   | Function unknown                                |
| -    | 1,400 | 34.4  | Not in COGs                                    |

The total is based on the total number of protein coding genes in the genome.
Although there are four genome sequences of species belonging to the genus *Acidiphilium* to compare the genome of strain JA12-A1 with, we focused our comparative genomics approach on *Acidiphilium cryptum* JF-5, *Acidiphilium multivorum* AUI301, *Acidiphilium* sp. PM DSM 24941 and *Acidiphilium* sp. JA12-A1. A comparison of the genomes of *Acidiphilium* sp. JA12-A1 and *Acidiphilium angustum* ATCC 35903 confirmed the phylogenetic distance and revealed that these genomes cannot be meaningfully aligned (results not shown). Therefore, the circular representation of the genome comparisons (Fig. 3) and the Venn diagram summarizing orthologous genes between the genomes are limited to strains belonging to the same phylogenetic cluster as *Acidiphilium* sp. JA12-A1 (Fig. 4).

The circular representation of genome sequences of four *Acidiphilium* strains revealed a high structural similarity of the genomes (Fig. 3). To identify orthologous genes between all four organisms, we performed a whole genome comparison. To prepare the data for analysis we used the scripts ncbi_ftp_download v0.2, cat_seq v0.1 and cds_extractor v0.6 [54] and Proteinortho v5.04 [55] with a similarity cutoff of 50 % and an E-value of 1e-10. Paralogous genes detected for all genomes were not included into this approach. All four strains have a core genome comprising 2515 genes, which is up to 70 % of the genes present in a single genome (Fig. 4). *Acidiphilium* JA12-A1 has 2943 orthologous genes in common with *Acidiphilium multivorum* AIU301, 2789 with *Acidiphilium cryptum* JF-5 and 2734 with *Acidiphilium* sp. PM DSM 24941. We detected the highest number of orthologous genes (2901) between *Acidiphilium cryptum* JF-5 and *Acidiphilium multivorum* AIU301. *Acidiphilium* sp. PM DSM 24941 and *Acidiphilium multivorum* AIU301 have 2870 in common, while *Acidiphilium cryptum* JF-5 and *Acidiphilium* sp. PM DSM 24941 share 2654 genes. *Acidiphilium* sp. PM DSM 24941 harbors the highest number of singletons (716) followed by *Acidiphilium* JA12-A1 with 475, *Acidiphilium multivorum* AIU301 with 381 and *Acidiphilium cryptum* JF-5 with 350, respectively. This, therefore, confirms the high degree of similarity among the various *Acidiphilium* strains as already concluded from the 16S rRNA gene based phylogeny (Fig. 1). Moreover, the high degree of congruence of the selected genome features provided in Table 5 demonstrates the high similarity among the four genomes with respect to the functional organization, (e.g. number of genes assigned to various COG functional categories (not shown), and pathways of the central metabolism).

Despite the high similarity in genome organization and content there are also unique genes in each of the *Acidiphilium* species that were included in this comparative genome analysis. For instance, *Acidiphilium* sp. JA12-A1, *Acidiphilium cryptum* JF-5 and *Acidiphilium multivorum* AIU301 contain a cluster of homologous genes encoding phosphonate C-P-lyases which are required for utilization of organic phosphate compounds. However, of those only *Acidiphilium* sp. JA12-A1 encodes a putative phosphonate specific ABC transporter. ABC transporter encoding genes are usually clustered. In the case of *Acidiphilium* sp. JA12 the genes are

### Table 5 Comparison of genome features of *Acidiphilium* sp. JA12-A1 to close relatives

| Genome features                        | *A. cryptum* JF-5<sup>a</sup> | *A. multivorum* AIU301<sup>b</sup> | *Acidiphilium* sp. PM DSM 24941<sup>c</sup> | *Acidiphilium* sp. JA12-A1<sup>d</sup> |
|----------------------------------------|-------------------------------|----------------------------------|---------------------------------------------|----------------------------------------|
| Sequencing status                      | Finished                      | Finished                         | Draft                                       | Permanent draft                        |
| Genome size (Mbp)                      | 4.0                           | 4.2                             | 3.9                                         | 4.2                                    |
| Number of plasmids                     | 8                             | 8                               | 9                                           | Not reported                           |
| GC (percentage)                        | 67.1 %                        | 67.0 %                          | 66.4 %                                      | 66.9 %                                 |
| Total gene count                       | 3,701                         | 4,004                           | 3,908                                       | 4,065                                  |
| Number of CDS genes (percentage)       | 3,637 (98.3 %)                | 3,948 (98.6 %)                  | 3,859 (98.8 %)                              | 4,015 (98.8 %)                         |
| Number of RNA genes                    | 64 (1.7 %)                    | 56 (1.4 %)                      | 49 (1.3 %)                                  | 50 (1.2 %)                             |
| Number of genes assigned to COGs       | 2,830 (79.1 %)                | 3,188 (76.5 %)                  | 3,116 (79.7 %)                              | 2,663 (65.5 %)                         |
| Number of genes connected to KEGG      | 1,197 (32.3 %)                | 1,283 (32.0 %)                  | 1,133 (29.0 %)                              | 1,238 (30.5 %)                         |
| Number of genes assigned to enzymes    | 1,055 (28.5 %)                | 1,107 (27.7 %)                  | 965 (24.7 %)                                | 1,076 (26.5 %)                         |
| Number of genes assigned to transporter classification (percentage) | 524 (14.1 %) | 562 (14.0 %) | 573 (14.7 %) | 520 (12.8 %) |
| Number of genes coding transmembrane proteins (percentage) | 817 (22.1 %) | 880 (22.0 %) | 839 (21.5 %) | 857 (21.1 %) |
| Number of genes with signal peptides (percentage) | 240 (6.5 %) | 266 (6.6 %) | 232 (5.9 %) | 268 (6.6 %) |

*accession number: NC_009484; NC_015186; AFPR00000000; JFHO00000000

Extended insights

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spread within the genome indicating that these have possibly been acquired via horizontal gene transfer.

**Conclusions**

The microbial communities of AMD and mining associated water bodies have been investigated in some detail over the last decades [3, 5, 10–12, 14, 56–58]. All of these reports agree on the supposed role of heterotrophic microorganisms, including members of the genus *Acidiphilium*, regarding their utilization of organic substances secreted by other community members or derived from microbial cell decay.

Analyzing the genome sequence of the novel strain *Acidiphilium* sp. JA12-A1 we inferred such an interspecies carbon transfer in an iron oxidizing mixed culture derived from a pilot plant for the biological remediation of AMD. The potential carbon transfer involves *Acidiphilium* sp. JA12-A1 excreting polysaccharide hydrolyzing enzymes, such as β-glucosidases or endoglucanases, to break down cell envelope polysaccharides from decaying cells and from the co-occurring iron oxidizer that is
related to *F. myxofaciens* P3G [7]. Monosaccharides originating from polysaccharide hydrolysis or from lysed cells are taken up by *Acidiphilium* sp. JA12-A1 via specific uptake systems to produce bacterial biomass. Alternatively, the monosaccharides or parts thereof are oxidized to gain energy for the cellular metabolism. Under aerobic conditions the electron donor is completely oxidized to carbon dioxide which is the preferred carbon source for the autotrophic iron oxidizer. However, the iron oxidizer may not only profit from the local increase of the carbon dioxide availability but also from the removal of organic compounds by *Acidiphilium* sp. JA12-A1, since chemolithoautotrophic iron oxidizers have long been known to be sensitive to organic compounds [59]. The sum of these potential interactions may account for the tenacious association of both organisms in the mixed culture and provide an explanation for the difficulties encountered when attempting to obtain pure cultures of the iron oxidizing bacteria.

In order to experimentally substantiate such an interspecies carbon transfer we suggest to analyze, similar to the study of Kermer et al. [9], secreted metabolites in combination with a stable isotope approach ($^{13}$C-labelled carbon dioxide) since this may reveal the actual metabolites that are utilized by *Acidiphilium* sp. JA12-A1 in the mixed culture. This approach may not only extend our knowledge of the proposed interspecies carbon transfer [9], but also elucidate whether *Acidiphilium* sp. JA12-A1 incorporates carbon dioxide heterotrophically by carboxylation reactions under the conditions provided within the mixed culture. In *Acidiphilium rubrum* the incorporation of carbon dioxide was described to be enhanced under aerobic-light conditions with the required energy provided by light utilization via a photosynthetic reaction center and phototrophic pigments [60]. We identified gene clusters homologous to those described for *Acidiphilium rubrum* and other *Acidiphilium* strains in the genome of *Acidiphilium* sp. JA12-A1 hinting at a potential photosynthetic activity. However, since none of the described *Acidiphilium* strains seems to be capable of using light as sole source of energy [61], it has been proposed that the photosynthetic activity is used to pump protons across the cytoplasmic membrane in order to stabilize the proton balance between the acidic environment and the neutral cytoplasm [60].

*Acidiphilium* strains are also thought to play a direct role in the iron cycle by regenerating dissolved ferrous iron through the reduction of ferric iron under microaerobic and anoxic conditions [11, 62]. Other studies have shown that ferrous iron is regenerated from the reduction of ferric iron minerals by *Acidiphilium* spp. and other acidophilic ferric iron reducers [52]. The ferrous iron is then available as an energy source for the iron oxidizers again. Details of the pathway of ferric iron reduction could, however, not be deduced from the genome of *Acidiphilium* sp. JA12-A1.

The *Acidiphilium* strains *Acidiphilium cryptum* JF-5, *Acidiphilium multivorans* AUJ301, *Acidiphilium* sp. PM DSM 24941 and *Acidiphilium* sp. JA12-A1, which all belong to the same phylogenetic subgroup within the genus *Acidiphilium*, show high similarities regarding their structural and functional genome organization. Since they also share important metabolic traits with respect to growth conditions and nutrient requirements the proposed interaction between *Acidiphilium* sp. JA12-A1 and the iron oxidizer *Ferrovum* spp. may also be true for other members of the genus *Acidiphilium* in their natural habitats.

**Additional file**

**Additional file 1: Table S1.** Associated MIGS record. (DOC 73 kb)

**Abbreviations**

AMD: acid mine drainage; PHB: polyhydroxybutyrate.
Competing interests
The authors declare that they have no competing interests.

Authors’ contributions
MM and MS designed the study. MM supervised the genome analysis. SRU planned the project GETGEOWEB and the BMBF through the project SURFTRAPII (03G0821B) within the R&D-program GEOTECHNOLOGIEN.

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