Sulfurihydrogenibium azorense, sp. nov., a thermophilic hydrogen-oxidizing microaerophile from terrestrial hot springs in the Azores

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Five hydrogen-oxidizing, thermophilic, strictly chemolithoautotrophic, microaerophilic strains, with similar (99–100 %) 16S rRNA gene sequences were isolated from terrestrial hot springs at Furnas, São Miguel Island, Azores, Portugal. The strain, designated Az-Fu1^T, was characterized. The motile, 0.9–2.0 µm rods were Gram-negative and non-sporulating. The temperature growth range was from 50 to 73 °C (optimum at 68 °C). The strains grew fastest in 0.1 % (w/v) NaCl and at pH 6, although growth was observed from pH 5.5 to 7.0. Az-Fu1^T can use elemental sulfur, sulfite, thiosulfate, ferrous iron or hydrogen as electron donors, and oxygen (0.2–9.0 %, v/v) as electron acceptor. Az-Fu1^T is also able to grow anaerobically, with elemental sulfur, arsenate and ferric iron as electron acceptors. The Az-Fu1^T G + C content was 33.6 mol%. Maximum-likelihood analysis of the 16S rRNA phylogeny placed the isolate in a distinct lineage within the *Aquificales*, closely related to *Sulfurihydrogenibium subterraneum* (2.0 % distant). The 16S rRNA gene of Az-Fu1^T is 7.7 % different from that of *Persephonella marina* and 6.8 % different from *Hydrogenothermus marinus*. Based on the phenotypic and phylogenetic characteristics presented here, it is proposed that Az-Fu1^T belongs to the recently described genus *Sulfurihydrogenibium*. It is further proposed that Az-Fu1^T represents a new species, *Sulfurihydrogenibium azorense*.

Based on phylogenetic analysis of the small-subunit rRNA (16S rRNA) gene sequences, the order *Aquificales* is the deepest lineage within the domain *Bacteria* (Burggraf *et al.*, 1992; Pitulle *et al.*, 1994). All members of the *Aquificales*, with the exception of '*Hydrogenobacter subterraneus*', are chemolithoautotrophic, microaerophilic, thermophilic to hyperthermophilic, hydrogen-oxidizing ('Knallgas') bacteria (Aragno, 1992). Currently, the order *Aquificales* harbours seven genera: *Aquifex* (Huber *et al.*, 1992), *Hydrogenobacter* (Saveleva *et al.*, 1982; Kawasumi *et al.*, 1984; Stöhr *et al.*, 2001), *Hydrogenobaculum* (Shima & Suzuki, 1993; Stöhr *et al.*, 2001), *Thermocrinis* (Huber *et al.*, 1998; Eder & Huber, 2002), *Hydrogenothermus* (Stöhr *et al.*, 2001), *Persephonella* (Götz *et al.*, 2002) and the recently described *Sulfurihydrogenibium* (Takai *et al.*, 2003). Members of the order are widespread in both terrestrial and deep-sea hydrothermal systems and have been isolated from shallow marine (Huber *et al.*, 1992; Nishihara *et al.*, 1990; Stöhr *et al.*, 2001) and terrestrial hydrothermal systems (Kryukov *et al.*, 1983; Kawasumi *et al.*, 1984; Shima & Suzuki, 1993; Huber *et al.*, 1998; Kristjansson *et al.*, 1985),

from heated compost (Beffa *et al.*, 1996), from deep-sea hydrothermal vents (Reysenbach *et al.*, 2000a) and recently from a subsurface gold mine (Takai *et al.*, 2002, 2003).

Using molecular phylogenetic techniques it has been shown that near neutral terrestrial thermal springs (above 65 °C) are often dominated by members of the *Aquificales* (Yamamoto *et al.*, 1998; Reysenbach *et al.*, 2000b; Skirnisdottir *et al.*, 2000) and referred to as 'black filaments' (Reysenbach *et al.*, 2000b) or 'sulfur-turf' (Yamamoto *et al.*, 1998; Hjörleifsdottir *et al.*, 2001) due to their tendency to form extensive microbial mats that appear black or yellow from iron or sulfur mineral deposits. Using a combination of culture-dependent techniques and molecular analyses, we isolated the first terrestrial representative of these *Aquificales* from a terrestrial hot spring in the Azores, Portugal (Reysenbach *et al.*, 2002a), and we propose a new species, *Sulfurihydrogenibium azorense* sp. nov.

Water and filamentous biomass samples were collected in Bellco serum bottles (Bellco Glass) in the area of Água do Caldeirão, Furnas, on São Miguel Island, Azores, in January of 2001. The temperature measured at the sampling sites varied between 65 and 70 °C and the pH varied between 5.9 and 7.0. A sample (0.5 ml) was inoculated into 5 ml

The GenBank accession number for the 16S rRNA sequence of strain Az-Fu1^T is AF528192.

modified MSH medium with a final gas phase of CO₂/O₂/H₂ (41.6:1.8:56.6, by vol., 242.5 kPa). Modified MSH medium (Boone *et al.*, 1989) was prepared with anoxic distilled water under a CO₂ atmosphere and contained (l⁻¹): 2 g NaOH, 0.5 g KCl, 1.36 g MgCl₂·6H₂O, 7 g MgSO₄·7H₂O, 2 g Na₂S₂O₃·5H₂O, 0.4 g CaCl₂·2H₂O, 0.2 g NH₄Cl, 0.3 g K₂HPO₄·3H₂O and 10 ml of a trace element stock solution (adapted from Ferguson & Mah, 1983). Prior to autoclaving, the pH of the medium was adjusted to 6.0 with 10 M NaOH. O₂ was added after autoclaving and the tubes were pressurized with H₂ after inoculation.

Enrichments were incubated for 1 day at 70 °C, without agitation, and immediately transferred. The cultures were purified by four consecutive end-point dilutions on modified MSH medium. Colonies were isolated on 2% (w/v) gelrite roll tubes (Jones *et al.*, 1983). The gelrite medium (iron-reducing or H₂-oxidizing) was supplemented with 0.001% (w/v) CuSO₄·5H₂O, according to Masaharu *et al.* (1987). Pure cultures were stored in modified MSH medium containing 15% (v/v) glycerol both at -80 °C and in liquid nitrogen.

Growth was determined either by measuring changes in OD₆₀₀, by total protein content (Coomassie protein assay) or by direct cell counts using a Petroff-Hauser counting chamber. Unless otherwise stated, all growth experiments were done at 68 °C, under the microaerophilic conditions described above, and conducted in triplicate. Az-Fu1^T growth with and without agitation was compared. The effect of pH on growth was determined from pH 4.0 to 8.5 using acetate/acetic acid buffer, MES, PIPES, HEPES and Tris/HCl. The pH of the medium was adjusted prior to autoclaving, checked after 1 h incubation at 68 °C and checked again at the end of growth. NaCl requirements were determined at 0–4% (w/v) NaCl. Oxygen requirements and tolerance were determined by injecting defined volumes of pure O₂ into culture tubes. O₂ final concentrations from 0 to 12% (v/v) were tested. The optimal temperature for growth was determined by calculating specific growth rates of cultures incubated at various temperatures. The relationship of specific growth rate to temperature was then fitted with TableCurve (2D Windows, v4.07; AISN Software) to the square-root equation Ratkowsky *et al.* (1982).

Electron acceptors and electron donors were added after autoclaving to a minimal medium (modified MSH medium without Na₂S₂O₃ and with only 4 g MgSO₄·7H₂O l⁻¹ to ensure an adequate sulfur source) (Table 1). Soluble (ferric citrate, 10 mM) and insoluble (ferrihydrite) iron (III) (10 mM) was used. Ferrous iron was added at 10 mM, sulfur was added at 1% (w/v) and NH₄⁺ was tested at 10 mM final concentration. SeO₄²⁻, SeO₃²⁻, AsO₄³⁻ and AsO₃³⁻ were added according to Takai *et al.* (2002) and all other electron donors and acceptors were at concentrations reported by Götz *et al.* (2002). Controls contained no electron acceptor and no electron donor. Abiotic controls

Table 1. Observed metabolic differences between strain Az-Fu1^T and *Sulfurihydrogenibium subterraneum*

Both isolates could use H₂+O₂, S⁰+O₂, S₂O₃²⁻+O₂, S⁰+Fe³⁺ and H₂+Fe³⁺, but could not grow with O₂+SeO₃²⁻ or H₂+NO₂⁻. Data for *Sulfurihydrogenibium subterraneum* are taken from Takai *et al.* (2003). ND, Not determined; -, no growth.

Character	Az-Fu1 ^T	<i>Sulfurihydrogenibium subterraneum</i>
Iron metabolism		
S ₂ O ₃ ²⁻ +Fe ³⁺	+*	+
Fe ²⁺ +O ₂	+*	+*†
Fe ²⁺ +NO ₃ ⁻	-	ND
Nitrogen metabolism		
H ₂ /S ⁰ /S ₂ O ₃ ²⁻ +NO ₃ ⁻	-	+
NH ₄ ⁺ +O ₂	-	ND
NH ₄ ⁺ +NO ₂ ⁻	-	ND
Sulfur metabolism		
H ₂ +S ⁰	+*	+*†
H ₂ +S ₂ O ₃ ²⁻ /SO ₄ ²⁻	-	ND
H ₂ +SO ₃ ²⁻	+*	ND
SO ₃ ²⁻ +O ₂	+*	ND
Arsenic metabolism		
H ₂ /S ⁰ /S ₂ O ₃ ²⁻ +AsO ₄ ³⁻	+*	+
AsO ₃ ³⁻ +O ₂	+	+*†
Selenium metabolism		
H ₂ /S ⁰ /S ₂ O ₃ ²⁻ +SeO ₄ ²⁻	+*	+
H ₂ /S ⁰ +SeO ₃ ²⁻	+*	+
S ₂ O ₃ ²⁻ +SeO ₃ ²⁻	-	+

*Low growth yields.

†Data determined in this study.

were also used when necessary to validate the tests. Additionally, growth of *Sulfurihydrogenibium subterraneum* under similar conditions was used as a control.

Organic carbon sources were tested in the presence and in the absence of oxygen. Hydrogen was used as electron donor; however, we also tested whether the isolate can grow fermentatively. Carbon sources were added at 0.1 and 1% (w/v) final concentration (yeast extract, sucrose, fructose, glucose, mannose, maltose, starch, formate, casamino acids, tartaric acid, peptone), 0.1% (v/v) final concentration (methanol, formaldehyde, formamide), or 1 and 10 mM final concentration (lactate, formate, succinate, oxalate, sorbitol, citrate and propionate). Cultures were transferred at least twice on the same substrate combination to ensure that growth was not due to substrate carry-over from the inoculum.

Gram staining was carried out using standard procedures. For electron microscopy, samples were shipped overnight to Department of Microbiology, College of Biological Science, University of Guelph, Canada, in 1% (v/v) glutaraldehyde. The samples were treated as described by Götz

et al. (2002) using standard glutaraldehyde/osmium tetroxide fixation and LR White embedding regimens for thin sectioning (Beveridge *et al.*, 1994).

Genomic DNA was extracted according to Götz *et al.* (2002). For the determination of DNA base composition, DNA was extracted from 1 g wet wt of the culture cell pellet. The cells were disrupted with a French pressure cell and the DNA was purified on hydroxyapatite according to the procedure of Cashion *et al.* (1977). For the DNA base composition the genomic DNA was hydrolysed according to Mesbah *et al.* (1989). The resulting deoxyribonucleosides were analysed by HPLC. Ten microlitres of sample were loaded in an HPLC system with a SelectaPore 90M, C₁₈, 5 µm (250 × 4.6 mm) analytical column and the run was performed at 45 °C, with a 0.3 M (NH₄)H₂PO₄/acetonitrile solvent, 40:1 (v/v), pH 4.4, at 1.3 ml min⁻¹ (adapted from Tamaoka & Komagata, 1984). The calibration was done using non-methylated λ DNA (Sigma; G+C content 49.86 mol%) and the G+C content was calculated according to Mesbah *et al.* (1989).

The 16S rRNA genes were amplified by PCR from genomic DNA, purified and sequenced as described by Götz *et al.* (2002). Platinum *Taq* DNA polymerase high fidelity (Invitrogen) was used to confirm the sequence as two single mismatches were detected in the sequence. A total of 1447 nt were sequenced. Sequence alignment and phylogenetic analyses were done as described previously (Götz *et al.*, 2002) using 1379 homologous nucleotides. Due to using a subset of *Aquificales* sequences and based on sequence alignments and secondary structure comparisons, 1430 nt were used to construct distance matrices by pairwise analysis with the Jukes & Cantor (1969) correction.

The new isolate Az-Fu1^T is a thermophilic chemolithoautotrophic 'Knallgas' bacterium isolated from the Furnas hot springs, São Miguel, Azores. Light brown-white filamentous clumps appeared in the liquid medium after 24 h incubation. Based on initial 16S rRNA gene sequence all the isolates (five cultures) were 100–99 % similar in sequence and the isolate designated strain Az-Fu1^T (previously designated Fc8A70; Reysenbach *et al.*, 2002a) was chosen for further study, although optimal growth conditions were confirmed for all strains. Translucent colonies were obtained from gelrite roll tubes under iron-reducing and H₂-oxidizing conditions. Successful transfer of the strains required a 5–10 % mid-exponential-growth-phase inoculum.

The isolate is phylogenetically most closely related to the uncultivated *Aquificales* environmental 16S rDNA sequence SRI-40 (Fig. 4) obtained from Icelandic hot springs (Skirnisdottir *et al.*, 2000; 0.2 % phylogenetic distance), although its closest relative in culture is *Sulfurihydrogenibium subterraneum* (Takai *et al.*, 2003; 2.0 % distance). Furthermore, the Az-Fu1^T 16S rDNA sequence is 3.1 % distant from its Yellowstone relative, strain YNP-SS1 (Reysenbach *et al.*, 2002b) and only about 18 % distant from *Aquifex pyrophilus*. Az-Fu1^T is also 7.7 and 6.8 %

Table 2. Comparison of physiological characteristics of strain Az-Fu1^T with closely related genera and species of chemolithoautotrophic members of the *Aquificales*

Data taken from Takai *et al.* (2002, 2003) for *Sulfurihydrogenibium subterraneum*, Götz *et al.* (2002) for *Persiphonella*, Stöhr *et al.* (2001) for *Hydrogenothermus*, and Huber *et al.* (1992) and Deckert *et al.* (1998) for *Aquifex*.

Strain/species	Marine/terrestrial	Location	Growth temp. (opt.) [°C]	pH (opt.)	Max. O ₂ [% v/v]	NaCl (opt.) [% w/v]	Electron donor	Electron acceptor	Motility	Internal structures	Genome G+C (mol%)
Az-Fu1 ^T	Terrestrial thermal spring	São Miguel, Azores	50–73 (68)	5.5–7.0 (6.0)	9.0* (1.8)	0.0–0.25 (0.1)	H ₂ , S ²⁻ , S ₂ O ₃ ²⁻ , AsO ₄ ³⁻ , Fe ³⁺ , Fe ²⁺ , S ⁰ , Fe ³⁺ , O ₂ , SO ₄ ²⁻	AsO ₄ ³⁻ , SeO ₄ ²⁻	Motile (flagella)	Stacked membranes	33.6†
<i>Sulfurihydrogenibium subterraneum</i>	Subsurface gold mine	Hishikari, Japan	40–70 (65)	6.4–8.8 (7.5)	ND* (ND)	0.0–4.8 (0.5)	H ₂ , S ²⁻ , S ₂ O ₃ ²⁻	Fe ³⁺ , O ₂ , NO ₃ ⁻ , HAsO ₄ ²⁻ , SeO ₄ ²⁻ , SeO ₃ ²⁻	Motile (polar flagella)	No internal structures reported	31.3†
<i>Persiphonella</i>	Deep-sea vents	EPRs, CIRs, MARs, Guaymas Basin	55–80 (70–73)	4.7–7.5 (6.0)	9.0* (2.0–3.0)	1.0–4.5 (2.5)	H ₂ , S ²⁻ , S ₂ O ₃ ²⁻	NO ₃ ⁻ , S ⁰ , O ₂	Motile	Stacked membranes	37.4–38.5‡
<i>Hydrogenothermus</i>	Shallow marine vent	Vulcano, Italy	45–80 (65)	5.0–7.0 (6.8)	8.0 (1.0–2.0)	0.5–6.0 (2.0–3.0)	H ₂	O ₂	Motile (flagella)	No internal structures reported	43†
<i>Aquifex</i>	Shallow marine vent (106 m deep)	Kolbeinsyde Ridge, Iceland; Italy	67–95 (85)	5.4–7.5 (6.8)	6.0* (0.5)	1.0–5.0 (3.0)	H ₂ , S ²⁻ , S ₂ O ₃ ²⁻	O ₂ , NO ₃ ⁻	Motile (flagella)	No internal structures reported	40‡

*Can grow anaerobically with an alternative electron acceptor.

†Value obtained by HPLC.

‡Mean value from melting point and HPLC.

§EPR, East Pacific Rise; CIR, Central Indian Ridge; MAR, Mid Atlantic Ridge.

distant from the recently described lineages *Persephonella marina* and *Hydrogenothermus marinus*, respectively, and differs significantly from these lineages in their physiological growth requirements (Table 2). The G + C content of the DNA of strain Az-Fu1^T is 33.6 mol%. Two mismatches were detected in the 16S rRNA gene sequence which were confirmed to be real by RT-PCR and by cloning. These are located at *Escherichia coli* 16S rRNA positions 818 and 888. Furthermore, two 16S rRNA genes were detected in the *Sulfurihydrogenibium* strain Az-Fu1^T genome sequence (A.-L. Reysenbach & J. F. Heidelberg, unpublished data).

The cells of Az-Fu1^T strain are motile Gram-negative rods, varying from 0.9 to 2.0 µm in length and from 0.4 to 0.5 µm in width. Transmission electron microscopy of

Fig. 1. Transmission electron micrograph of negatively stained Az-Fu1^T cells revealing flagella extending from the cell surface. Some flagella have been deformed during the process of staining so that their helicity has been lost. The longer cell is dividing and shows that cell division is by the typical Gram-negative constrictive process (arrow). Bar, 0.5 µm.

negatively stained bacteria revealed flagella extending from the cell surface of many of the cells and constrictive division sites typical of actively growing cultures of Gram-negative rods (Fig. 1). The flagella were unsheathed and had a diameter of ~15 nm, which is typical for many bacteria (Wilson & Beveridge, 1993). Endospores were not observed. Thin sections showed a typical Gram-negative cell envelope complete with outer and plasma membranes (Fig. 2) although, like *Persephonella marina* (Götz *et al.*, 2002), it was difficult to differentiate the peptidoglycan layer as a distinct entity. When grown with H₂ the cells tended to cluster, forming macrofilaments (clumps of filaments), even while agitated. Under iron-oxidizing and iron-reducing conditions, Az-Fu1^T cells were often found attached to minerals. Thin sections of samples grown under H₂-oxidizing conditions, in the presence of S⁰, revealed unidentified structures that resembled internal stacked membranes with a particle periodicity on them (Fig. 3). Similar, but smaller membranous structures, have previously been reported for another member of the *Aquificales*, i.e. *Persephonella* (Götz *et al.*, 2002). Such structures

Fig. 2. Detail of the typical Gram-negative envelope of Az-Fu1^T shown in thin section. OM, outer membrane; PM, plasma membrane; PS, periplasmic space. Bar, 100 nm.

Fig. 3. Thin section of Az-Fu1^T revealing the typical Gram-negative envelope (large arrow) as well as cytoplasmic structures that resemble stacked membranes (small arrow). Bar, 0.5 µm.

were not reported for *Sulfurihydrogenibium subterraneum* (Takai *et al.*, 2002, 2003). Although internal membranes are often used to align enzymes for complex metabolic reactions, the function of these membranous structures is not yet known. Alternatively, these structures may resemble cytoplasmic axial filaments as have been reported for *Escherichia coli* (Okada *et al.*, 1994); however, this is speculative without purification and extensive characterization of these structures.

Strain Az-Fu1^T grew from 50 to 73 °C with optimal growth at 68 °C (doubling time about 2.5 h with no agitation). Growth occurred between pH 5.5 and 7.0 and was optimal at pH 6. Strain Az-Fu1^T grew at salt concentrations from 0 to 0.25 % (w/v) NaCl, although growth rate was low at 0.25 % NaCl. This physiological trait confirms that Az-Fu1^T is the first freshwater isolate to be characterized

within this phylogenetic lineage. Strain Az-Fu1^T is a strict chemolithoautotroph and uses CO₂ as sole carbon source. Furthermore, strain Az-Fu1^T does not use NO₃⁻ as electron acceptor. Strain Az-Fu1^T grew with up to 9.0 % oxygen, with optimal growth between 1.8 and 2.0 % (v/v). There was no growth in the presence of 12.0 % (v/v) oxygen. Growth under hydrogen-oxidizing conditions was enhanced by the presence of sulfur compounds (S⁰, S₂O₃²⁻ or SO₃²⁻) as reported for *Hydrogenobacter* (Bonjour & Aragno, 1986). Az-Fu1^T is able to use ferrous iron (Fe²⁺) as electron donor in the presence of O₂ or S⁰, and like *Sulfurihydrogenibium subterraneum* (Takai *et al.*, 2002, 2003) ferric iron (Fe³⁺) can be used as electron acceptor in the presence of H₂ and S⁰. *Sulfurihydrogenibium subterraneum* was also tested for iron oxidation and, like Az-Fu1^T, it is capable of using ferrous iron (Fe²⁺) as electron donor in the presence of O₂.

Comparison with related genera and species

Together with *Sulfurihydrogenibium subterraneum*, Az-Fu1^T forms a distinct bacterial lineage within the *Aquificales* (Fig. 4), with a similar low G + C content. Both strains share many characteristics with the rest of the *Aquificales*, such as microaerophilic growth. However, their distinct ability to use heavy metals and iron compounds as electron donors or acceptors (Tables 1 and 2) distinguish them from other members of the *Aquificales*.

There are several distinguishing features that set Az-Fu1^T apart from *Sulfurihydrogenibium subterraneum*, such as salt tolerance and pH growth optima (Table 2). These differences may reflect their different habitats; Az-Fu1^T has been obtained from terrestrial hot springs whereas *Sulfurihydrogenibium subterraneum* was obtained from a warm subterranean gold mine. Furthermore, unlike *Sulfurihydrogenibium subterraneum*, Az-Fu1^T cannot grow aerobically, nor can it use nitrate as an electron acceptor. With the exception of *Hydrogenothermus marinus* and 'Aqulfex aeolicus' (Table 2), all marine *Aquificales* isolates described to date are able to grow with O₂ and NO₃⁻ as electron acceptors and H₂ as an electron donor, suggesting that perhaps *Sulfurihydrogenibium subterraneum* is more marine in origin. Furthermore, based on a conservative estimate and comparing only homologous nucleotides, Az-Fu1^T is 2 % different from *Sulfurihydrogenibium subterraneum* in the 16S rRNA sequence. Based on the phylogenetic position and distinct physiological characteristics of Az-Fu1^T, we propose that this isolate be named *Sulfurihydrogenibium azorense*.

Description of *Sulfurihydrogenibium azorense* sp. nov.

Sulfurihydrogenibium azorense (a.zo.ren'se. N. L. neut. adj. *azorense* from the Azores, the place of isolation).

Motile rods, 0.4–0.5 × 0.9–2.0 µm. Cells can occur singly, in pairs or in filamentous clumps. Colonies are translucent. Grows best in the presence of sulfur compounds.

Fig. 4. Maximum-likelihood phylogenetic tree showing the position of strain Az-Fu1^T. The scale bar represents the number of fixed mutations per nucleotide position. The numbers at the branch nodes are bootstrap values based on 100 bootstrap resamplings. The additional sequences used to generate the tree were *Thermotoga maritima* MSB-8^T (M21774), *Thermosiphon melanesiensis* BI429^T (Z70248), *Thermus thermophilus* HB8^T (X07998), *Heliobacterium chlorum* DSM 3682^T (M11212), *Bacillus subtilis* W168 (K00637), *Escherichia coli* (J01695) and *Flexibacter flexilis* DSM 6793^T (M62794). '*Methanocaldococcus jannaschii*' JAL-1^T (M59126) was used as the outgroup.

Optimal growth occurs at 68 °C and growth occurs from 55 to 73 °C. The optimal pH for growth is 6.0, with a range from 5.5 to 7.0. Grows fastest with 0.1 % (w/v) NaCl; growth is inhibited with NaCl concentrations above 0.25 %. Not capable of growth at 12 % (v/v) O₂ final concentration. Doubling time of 2.5 h with O₂ as electron acceptor and H₂ as electron donor. Cells utilize H₂, thiosulfate, S⁰ or Fe²⁺ as electron donors and O₂, S⁰ and Fe³⁺ as electron acceptors, but cannot use nitrate as electron acceptor. The G+C content is 33.6 mol%. Isolated from a terrestrial hot spring (68.4 °C, pH 5.9) in the Água do Caldeirão area, Furnas, on São Miguel Island, Azores. The type strain is Az-Fu1^T (=DSM 15241^T=OCM 825^T). The GenBank accession number for the 16S rRNA sequence of Az-Fu1^T is AF528192.

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