Description of *Naumannella cuiyingiana* sp. nov., isolated from a ca. 1500-year-old mural painting, and emended description of the genus *Naumannella*

Tian Tian,¹ Fasi Wu,² Yantian Ma,³ Ting Xiang,¹ Wenxia Ma,¹ Weigang Hu,¹ Guangwen Wu,⁴ Lizhe An,¹ Wanfu Wang²,* and Huyuan Feng¹,*

**Abstract**

Strain AFT² was isolated from a mural painting sample from a ca. 1500-year-old tomb located in Shanxi Province, China. The isolate was a Gram-stain-positive, non-motile, non-spore-forming, aerobic and oval to short-rod-shaped bacterium that formed white-pigmented colonies. Phylogenetic analyses based on 16S rRNA gene sequence revealed that strain AFT² was most closely (97.01%) correlated and formed a monophyletic clade with *Naumannella halotolerans* WS4616 (=DSM 24323). The G+C content of the genomic DNA was 71.97 mol%, and the strain showed 37.27% DNA-DNA relatedness to *N. halotolerans* DSM 24323. The major cellular fatty acid was anteiso-C₁₅:₀ (55.32%), and MK-9(H₂) was the only respiratory quinone. The polar lipids comprised phosphatidylglycerol, diphosphatidylglycerol, two unknown phospholipids and five unknown glycolipids. L-L-Diaminopimelic acid was detected in the cell wall peptidoglycan (type A3γ), and the whole-cell sugars consisted of ribose, mannose, arabinose and galactose. On the basis of its phenotypic and phylogenetic characteristics, it is proposed that strain AFT² should be classified as a representative of a novel species of the genus *Naumannella*, for which the name *Naumannella cuiyingiana* sp. nov. is proposed. The type strain is AFT² (=CCTCC AB 2015428=DSM 103164).

It is well known that ancient mural paintings preserved in cultural heritage sites may be easily colonized and deteriorated by micro-organisms [1–3]. Culture-dependent and -independent studies have clearly suggested that bacterial communities inhabiting these works of art are dominated by members of the phyla *Actinobacteria* and *Proteobacteria*, among which several novel species have been described [4–6]. During the course of classification of heterotrophic bacteria isolated from mural paintings in a ca. 1500-year-old tomb (tomb of Xuxianxiu) of the Northern Qi Dynasty in Shanxi Province, China, we isolated a bacterium, designated AFT², belonging to the genus *Naumannella* of the family *Propionibacteriaceae*.

The genus *Naumannella* was first proposed by Rieser et al. [7] based on phenotypic and genetic differences between the bacterium and closely related members of the genera *Propionicicella*, *Propionicimonas*, *Micropolium* and *Microlu- natus*. At the time of writing, there is only a single recognized species (*Naumannella halotolerans*) affiliated with the genus *Naumannella* (www.bacterio.net/naumannella.html). Members of the genus *Naumannella* are Gram-stain-positive, aerobic, non-spore-forming and non-motile bacteria. The cell wall peptidoglycan is of the A3γ type, containing L-L-diaminopimelic acid (DAP), alanine, glycine and glutamic acid. The major polar lipids are diphosphatidylglycerol and phosphatidylglycerol, and anteiso-C₁₅:₀ is the dominant cellular fatty acid. Based on the differences in results obtained from phenotypic characterization including chemotaxonomy and phylogenetic properties of strain AFT² and *N. halotolerans* DSM 24323, in current study we propose that strain AFT² should be placed in the genus *Naumannella* as the type strain of a novel species.

Strain AFT² was isolated from a mural painting sample collected from a ca. 1500-year-old tomb in China. The mural sample was taken by scraping off the paint layer with a sterile scalpel [8] and incubated in PYGV liquid medium.

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**Keywords:** new actinobacterium; *Naumannella*; mural painting; China.

**Abbreviations:** DAP, diaminopimelic acid; CCTCC, China Center for Type Culture Collection; GDDCM, Guangdong Detection Center of Microbiology.

The GenBank/EMBL/DDJB accession number for the 16S rRNA gene sequence of strain AFT² is KF041479.

Four supplementary figures and one supplementary table are available with the online Supplementary Material.
for 15 days at 20 °C for microbial enrichment. PYGV liquid medium contained peptone (0.025 %, w/v), yeast extract (0.025 %, w/v), glucose (0.025 %, w/v), 20 ml per litre of mineral salt solution (l⁻¹: 10 g nitritrolactic acid, 29.7 g MgSO₄·7H₂O, 3.34 g CaCl₂·2H₂O, 12.67 mg Na₂MoO₄·2H₂O, 99 mg FeSO₄·7H₂O and 50 ml metal salt solution (l⁻¹: 250 mg sodium EDTA, 1095 mg ZnSO₄·7H₂O, 500 mg FeSO₄·7H₂O, 154 mg MnSO₄·H₂O, 39.2 mg CuSO₄·5H₂O, 24.8 mg Co(NO₃)₃·6H₂O and 17.7 mg Na₂B₄O₇·10H₂O), pH 7.2) and 5 ml per litre of vitamin solution (l⁻¹: 4 mg biotin, 4 mg folic acid, 20 mg pyridoxine hydrochloride, 10 mg riboflavin, 10 mg thiamine hydrochloride dihydrate, 10 mg nicotinamide, 10 mg calcium pantothenate, 0.2 mg vitamin B₁₂ and 10 mg p-aminobenzoic acid [9]. Strain AFT₂ᵀ was subsequently isolated on tryptic soy agar (TSA; Solarbio) after 3 days of incubation at 37 °C. Briefly, the enriched cultures were serially diluted with autoclaved NaCl solution (0.85 %, w/v) after microbial enrichment. A 0.1 ml aliquot of each dilution was then plated on TSA to isolate strain AFT₂ᵀ.

For morphological, physiological and biochemical analyses, the novel strain was studied together with the type strain of the type species of the genus *Naumannella* (*N. halotolerans* DSM 24323ᵀ) under the same experimental conditions. Strain AFT₂ᵀ and the reference strain were maintained as glycerol suspensions (15 %, w/v) at −80 °C.

Morphological characteristics were observed after cultivation for 3 days on TSA at 37 °C. Cell morphology, dimensions, motility and endospore formation were observed by using a biological microscope (BX43, Olympus), transmission electron microscope (H-8000, Hitachi) and scanning electron microscope (S-3400N, Hitachi). The Gram reaction was determined by the KOH-lysis method [10] and a staining-based method [11]. Growth under anaerobic conditions was examined in an anaerobic chamber by the Guangdong Detection Centre of Microbiology (GDDCM; Guangzhou, China) by incubating the strains on TSA and substituting the upper air layer with nitrogen gas. Catalase activity was assessed, based on bubble production from a 3 % (v/v) hydrogen peroxide solution. Oxidase activity was determined using *N*,*N*,*N*,*N*'-tetramethyl-p-phenylenediamine reagent [12]. The hydrolysis of starch and casein was tested as described by Smibert and Krieg [11]. Biochemical tests, including acid production from carbohydrates, enzyme activities and assimilation of single carbon sources for growth were carried out using commercially available systems (API 50 CH, API ZYM and API 20 NE) according to the manufacturer’s instructions (bioMérieux). In addition, oxidation of carbon sources was assayed with Biolog GP2 MicroPlates. Tolerance to NaCl was determined in tryptone soy broth (TSB; l⁻¹: 17 g tryptone, 3 g soya peptone, 2.5 g K₂HPO₄, 2.5 g glucose and 5 g NaCl, pH 7.2) supplemented with 0, 1, 3, 5, 7, 8, 9, 10, 12, 14 % (w/v) NaCl, respectively. Temperature range for growth was tested at 4, 10, 15, 20, 25, 30, 37, 40 and 45 °C. Growth at different pH values (pH 4.0–14.0 at intervals of 1.0 pH unit) was investigated with TSB as the basal medium following the protocols of Zhu *et al.* [13] and Zhao *et al.* [14]. Characteristics of strain AFT₂ᵀ are given in the species description, while differences between the novel strain and *N. halotolerans* DSM 24323ᵀ are shown in Table 1.

For phylogenetic analysis, genomic DNA was extracted from purified isolates by the boiling lysis method [15] and the 16S rRNA genes were amplified using the universal primer pair 27F (5’-AGGTTTGTATCCGTGCTCAG-3’) and 1492R (5’-TACGTTATCCTGTAGACATT-3’) [16]. Amplification reactions were performed in a total volume of 25 µl containing 1 U Taq polymerase (New England Biolabs), 1× Taq buffer, 2 mM MgCl₂, 0.2 mM each deoxynucleoside triphosphate (dNTP), 0.5 µM each primer and 2.5 µl (approx. 10 ng) of template DNA. The thermal conditions consisted of an initial denaturation of 3 min at 94 °C, followed by 30 cycles at 94 °C for 1 min, 58 °C for 1 min and 72 °C for 1.5 min; with a final extension at 72 °C for 10 min. The PCR product was validated on 1.5 % (w/v) agarose gel with ethidium bromide staining and sequenced by Major Biotech (Shanghai, China). An almost-complete 16S rRNA gene sequence (1484 bp) of strain AFT₂ᵀ was submitted to the online database of the EzTaxon-e server [17] to determine the closest phylogenetic relatives. All DNA sequences were then multiply aligned using the CLUSTAL W program [18]. Phylogenetic trees were reconstructed using the MEGA 5.0 [19] program based on the General Time Reversible model with invariable sites and gamma site rate variation (GTR+I+G) using the maximum-likelihood, neighbour-joining and maximum-parsimony methods. The reliability of the tree branch points was assessed by bootstrap analysis of 1000 replicates. The 16S rRNA gene sequence of strain AFT₂ᵀ was most closely related to that of *N. halotolerans* DSM 24323ᵀ (97.01 %) followed by *Microlunatus panaciteraen* Gsoil 954ᵀ (94.91 %) and *Microlunatus parietis* 12-Be 011ᵀ (94.73 %). Evaluation of the tree topology revealed that strain AFT₂ᵀ formed a monophyletic clade with *N. halotolerans* DSM 24323ᵀ with a high level of bootstrap support (99 %; Fig. 1). Phylogenetic trees reconstructed using different treeing algorithms showed the same type of clustering and tree topology (Figs S1 and S2, available in the online Supplementary Material).

The DNA G+C content and DNA–DNA hybridization experiments were performed by the GDDCM. For the measurement of the DNA G+C content, nucleosides were separated by HPLC (model 1200, Agilent) using a XDB-C18 column (5 µm, 4.6×250 mm; ZORBAX Eclipse, Agilent) as described by Mesbah *et al.* [20]. The DNA G+C content of strain AFT₂ᵀ was 71.97 mol%, which is close to that of *N. halotolerans* DSM 24323ᵀ (67.7 mol%). DNA–DNA hybridization was carried out according to the fluorometric method of Ezaki *et al.* [21] in triplicate. The mean of tripli- cate determinations of DNA–DNA relatedness between strain AFT₂ᵀ and *N. halotolerans* DSM 24323ᵀ was only 37.27 %, considerably lower than the recommended threshold for species delineation [22], supporting that strain
Table 1. Differential features between strain AFT2<sup>T</sup> and *N. halotolerans* DSM 24323<sup>T</sup>

Data for both strains were obtained during this study under the same experimental conditions, unless indicated otherwise. +, Positive; −, negative; w, weakly positive. DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PL, unknown phospholipid(s); GL, unknown glycolipid(s).

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>AFT2&lt;sup&gt;T&lt;/sup&gt;</th>
<th><em>N. halotolerans</em> DSM 24323&lt;sup&gt;T&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Morphology</td>
<td>Oval to short rods</td>
<td>Cocci</td>
</tr>
<tr>
<td>Pigmentation (on TSA)</td>
<td>White</td>
<td>Pale yellow</td>
</tr>
<tr>
<td>NaCl tolerance (% w/v)</td>
<td>0–12</td>
<td>0–10</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>6–10</td>
<td>6–8</td>
</tr>
<tr>
<td>Temperature range for growth (°C)</td>
<td>20–37</td>
<td>15–37</td>
</tr>
<tr>
<td>Respiratory quinones</td>
<td>MK-9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>MK-8(H&lt;sub&gt;4&lt;/sub&gt;) (27%), MK-9(H&lt;sub&gt;4&lt;/sub&gt;) (73%)</td>
</tr>
<tr>
<td>Polar lipids</td>
<td>DPG, PG, PL1, PL2, GL1, GL2, GL3, GL4, GL5</td>
<td>DPG, PG, PL, GL1, GL2, GL3</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gelatin</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Production of oxidase</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Assimilation of:</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>N</em>-Acetylglucosamine</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Malate</td>
<td>+</td>
<td>−</td>
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<tr>
<td>Gluconate</td>
<td>W</td>
<td>+</td>
</tr>
<tr>
<td>Adipate</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>71.97</td>
<td>67.7&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Isolation</td>
<td><em>ca.</em> 1500-year-old mural painting</td>
<td>Pharmaceutical clean room and food</td>
</tr>
</tbody>
</table>

<sup>a</sup>Data from Rieser et al. [7].

AFT2<sup>T</sup> should be classified as a representative of a novel species of the genus *Naumanniella*.

Fatty acid analyses were carried out by the China Centre for Type Culture Collection (CCTCC; Wuhan, China) according to the instructions of the Microbial Identification System (MIDI) as described by Sasser [23]. The fatty acid methyl esters of strain AFT2<sup>T</sup> and of *N. halotolerans* DSM 24323<sup>T</sup> were obtained from cells grown on TSA plates for 24 h at 28 °C by saponification, methylation and extraction, and then analysed with a Hewlett Packard 6890 N gas chromatograph. The identities and percentages of fatty acids were determined by Sherlock MIS software (MIDI) based on the TSBA6 database. The predominant cellular fatty acid of AFT2<sup>T</sup> was anteiso-C<sub>15:0</sub> (55.32 %). A comparison of complete fatty acid profiles between strain AFT2<sup>T</sup> and *N. halotolerans* DSM 24323<sup>T</sup> is given in Table S1.

Cell-wall peptidoglycan and whole-cell sugars were analysed by the Identification Service of the CCTCC according to the methods of Schleifer and Kandler [24] and Staneck and Roberts [25]. Cell walls were hydrolysed with hot trichloroacetic acid (10 %) and trypsin. The hydrolysate was placed into a small ampoule with 0.2 ml of 6 M hydrochloric acid. The sealed ampoule was kept at 105 °C for 24 h, and dried at 65 °C. This residue was dissolved in 0.05 ml distilled water and centrifuged at 12 000 r.p.m. (~13 400 × g) for 5 min. The composition of peptidoglycan was then identified by TLC on silica gel plates. The cell-wall peptidoglycan of strain AFT2<sup>T</sup> was of the type A<sub>3</sub>y (LL-DAP–Gly), containing LL-DAP, alanine, glycine and glutamic acid. Whole-cell sugars were determined from 25 mg (dry weight) of lyophilized cells. Cells were hydrolysed with 1.5 ml 0.5 M H<sub>2</sub>SO<sub>4</sub> and heated for 2 h in a boiling water bath. The hydrolysate was applied to the base line of the TLC sheet along with two standard solutions, and the sugars were then analysed by TLC. The whole-cell sugars contained ribose, mannose, arabinose and galactose.

Polar lipid analysis was performed by the Identification Service of the CCTCC. Lipids were separated by two-dimensional TLC on silica gel plates (layer thickness 0.2 mm; Merck) according to the protocols of Tindall [26]. The polar lipid pattern included diphosphatidylglycerol and phosphatidylglycerol as the major components and two unknown phospholipids and five unknown glycolipids (Fig. S3). Respiratory quinones were determined by the Identification Service of the CCTCC according to the method of Yokota [27]. Quinones were extracted with chloroform/methanol (2:1, v/v) and separated by TLC. The components of the quinone were then tested by HPLC (UltiMate 3000, Dionex). MK-9(H<sub>4</sub>) was the only respiratory quinone detected, which was different from *N. halotolerans* DSM 24323<sup>T</sup> (Table 1).

*N. halotolerans* DSM 24323<sup>T</sup> and strain AFT2<sup>T</sup> shared similar characteristics such as the presence of ribose, mannose, arabinose and galactose as the dominant cell-wall sugars, type A<sub>3</sub>y of peptidoglycan with LL-DAP, anteiso-C<sub>15:0</sub> as the predominant cellular fatty acid, and...
Propionibacterium thoenii NCFB 568\textsuperscript{T} (AJ704572)
Propionibacterium jensenii DSM 20535\textsuperscript{T} (AJ704571)
Propionibacterium microaerophilum M5\textsuperscript{T} (AF234623)
Propionibacterium acidopropionici NCFB 570\textsuperscript{T} (AJ704570)
Propionibacterium granulosum DSM 20700\textsuperscript{T} (AJ003057)
Propionibacterium propionicus DSM 43307\textsuperscript{T} (AJ704570)
Propionibacterium avidum DSM 4901\textsuperscript{T} (AJ003055)
Propionibacterium cyclohexanicum TA-12\textsuperscript{T} (D82046)
Propionibacterium acidifaciens C3M_31\textsuperscript{T} (EU979537)
Luteococcus sediminum XH208\textsuperscript{T} (KC986353)
Luteococcus peritonei CCUG 38120\textsuperscript{T} (AJ132334)
Luteococcus sanguinis CCUG 33897\textsuperscript{T} (AJ416758)
Luteococcus japonicus DSM 10546\textsuperscript{T} (Z78208)
Tessaracoccus oleaigri SL014B-20A1\textsuperscript{T} (GU111566)
Tessaracoccus flavescentes SST-39\textsuperscript{T} (AM393882)
Tessaracoccus bendigoensis ACM 5119\textsuperscript{T} (AF038504)
Tessaracoccus lubricatus KSS-17Se\textsuperscript{T} (FM178840)
Tessaracoccus lapidicaptus IPBSL-7\textsuperscript{T} (KF668596)
Aestuariimicrobium kwangyangense DSM 21549\textsuperscript{T} (ATXE0100005)
Naumannella cuiyingiana AFT2\textsuperscript{T} (KF041479)
Naumannella halotolerans WS4616\textsuperscript{T} (FR832425)
Propionicillium innocua ATCC 49929\textsuperscript{T} (AF227165)
Mariniluteococcus flavus YIM M13146\textsuperscript{T} (KF564278)
Granulicoccus phenolivorans DSM 17626\textsuperscript{T} (AUHH01000073)
Propionicimonas paludicola DSM 15597\textsuperscript{T} (FR733712)
Micropruina glycogenica Lg2\textsuperscript{T} (AB012607)
Friedmanniella lucida FA2\textsuperscript{T} (AB445454)
Friedmanniella lacustris EL-17a\textsuperscript{T} (AJ132943)
Friedmanniella capsulata Ben 108\textsuperscript{T} (AF084529)
Friedmanniella luteola FA1\textsuperscript{T} (AB445453)
Friedmanniella okinawensis FB1\textsuperscript{T} (AB445455)
Friedmanniella flava W6\textsuperscript{T} (HQ839787)
Friedmanniella sagamiharensis FB2\textsuperscript{T} (AB445456)
Friedmanniella spumicola ACM 5121\textsuperscript{T} (AF062535)
Friedmanniella antarctica DSM 11053\textsuperscript{T} (Z78206)
Microlunatus ginsengisoli Gsoil 633\textsuperscript{T} (AB245389)
Microlunatus phosphovorus NM-1\textsuperscript{T} (AP012204)
Microlunatus aurantiacus YIM 45721\textsuperscript{T} (EF601828)
Microlunatus parietis 12-Be-011\textsuperscript{T} (FN566016)
Microlunatus soli CC-12602\textsuperscript{T} (FJ807672)
Kribbella flavida KACC 20248\textsuperscript{T} (AY253863)

**Fig. 1.** Phylogenetic tree derived from 16S rRNA gene sequences of strain AFT2\textsuperscript{T}, *N*. halotolerans DSM 24323\textsuperscript{T} and other closely related members of the family *Propionibacteriaceae*. The tree was reconstructed using the maximum-likelihood method with the GTR+I+G model, and rooted to the outgroup *Kribbella flavida* KACC 20248\textsuperscript{T} (AY253863). Bootstrap values above 50\% are shown as a percentages of 1000 replicates. Bar, 0.02 expected changes per nucleotide position.
The description of the genus *Naumannella* is as given by Rieser et al. [7], except for the following features from this study. Cells are cocci to short rods. Minor polar lipids are unknown phospholipids and unknown glycolipids. The major respiratory quinones are MK-9(H4) and/or MK-8 (H4).

**DESCRIPTION OF NAUMANNELLA CUIYINGIANA SP. NOV.**

*Naumannella cuiyingiana* (cui.ying.i’a’na. N.L. fem. adj. cuiyingiana pertaining to the Cuiying Arch, the original location of Lanzhou University in which the type strain was identified).

Cells are Gram-stain-positive, aerobic, non-spore-forming, non-motile and oval to short-rod-shaped (0.3–0.7×0.6–1.0 μm; Fig. S4). Colonies on TSA are white, low-convex, smooth and up to 2 mm in diameter after 3 days of incubation at 37°C. The NaCl, pH and temperature ranges for growth are 0–12% (w/v) NaCl, pH 6–10 and 20–37°C, respectively. Positive results are observed for hydrolysis of starch, gelatin and aesculin and production of 3 days of incubation at 37°C. The NaCl, pH and temperature ranges for growth are 0–12% (w/v) NaCl, pH 6-10 and 20–37°C, respectively. Positive results are observed for hydrolysis of starch, gelatin and aesculin and production of 2-ketogluconate or 5-ketogluconate. With the API 20NE test, positive for assimilation of glucose, gluconate (weakly), mannose, man- nitol, N-acetylgalactosamine, maltose and malate; negative for assimilation of arabinose, caprate, adipate, citrate and phe- nylacetate. With GP2 MicroPlates, the following carbon sources can be oxidized: β-cyclodextrin, inulin, Tween 40, Tween 80, N-acetylgalactosamine, L-arabinose, D-arabinose, arbutin, D-fructose, trehalose, D-galactose, D-galacturonic acid, gentiobiose, D-glucuronate, D-glucose, lactose, lactulose, maltose, malottriose, D-mannitol, D-mannose, melibiose, methyl α-D-galactoside, methyl β-D-galactoside, 3-methylglucose, methyl α-D-glucopyranoside, methyl α-D-mannopyranoside, 6-O-D-galactose, D-psicose, raffi- nose, L-rhamnose, D-ribose, salicin, D-sorbitol, stachyose, D- alanine, L-aspartic acid, L-glutamic acid, glycy1-L-glutamic acid, L-serine, butanediamine, 2-deoxyadenosine, 5′-uridine monophosphate, D-fructose 6-dihydrogenphosphate and D-gluc- 6-phosphate; it does not oxidize α-cyclodextrin, dextrin, glyco- gen, mannann, amygdalin, inositol, β-D-glucopyranose, sucrone, α-ketoglu- taric acid, α-oxopentanoic acid, lactamide, pyruvate, acetyl glutamic acid, L-alanine, L-alanine, L-alanyl glycine, L- pyroglutamic acid, 2,3-butanediol, glycerol, adenosine, inosine, thymidine, uridine, 5′-adenosine monophosphate, 5′-thymidine monophosphate, α-D-glucose 1-phosphate or Dl-α-glycerophosphoric acid. The major cellular fatty acid is anteiso-C₁₅:0. The cell-wall peptidoglycan is of the type A3γ (LL-DAP-Gly), containing LL-DAP, alanine, glycine and glutamic acid. The whole-cell sugar pattern includes ribose, mannose, arabinose and galactose. The major polar lipids are diphosphatidylglycerol and phosphatidylglycerol. Minor polar lipids are two unknown phospholipids and five unknown glycolipids. The sole respiratory quinone is MK-9(H₄).

The type strain, AFT2=DSM 24323=DSM 103164, was isolated from a mural painting sample from a ca. 1500-year-old tomb in China. The genomic DNA G+C content of the type strain is 71.97 mol%.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.
References

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