Lampropedia cohaerens sp. nov., a biofilm-forming bacterium isolated from microbial mats of a hot water spring, and emended description of the genus Lampropedia

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A biofilm-forming, Gram-stain-negative, aerobic, catalase-positive but oxidase-negative strain, designated CT6T, was isolated from the microbial mats (~45 °C) of a hot water spring, located within the Himalayan ranges at Manikaran, Himachal Pradesh, India. Strain CT6T formed white, smooth colonies with irregular margins. Transmission electron microscopy revealed coccoid, non-flagellated cells with wavy boundaries. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain CT6T belongs to the genus Lampropedia with a sequence similarity value of 95.4% to the sole member of this genus, Lampropedia hyalina ATCC 11041T. Strain CT6T was found to have phosphatidylethanolamine and phosphatidylglycerol as the major polar lipids. The major cellular fatty acids were C16 : 0, summed feature 8 (C18 : 1ω7c and/or C18 : 1ω6c), C14 : 0, C19 : 0 and summed feature 3 (C16 : 1ω7c and/or C18 : 1ω6c). The major respiratory quinone was ubiquinone-8. The major polyamines were putrescine, spermidine and the betaproteobacterial-specific 2-hydroxyputrescine. The DNA G+C content was 63.5 mol%. Based on the genotypic, phenotypic, physiological and biochemical data, strain CT6T is considered to represent a novel species of the genus Lampropedia, for which the name Lampropedia cohaerens sp. nov. is proposed (=DSM 100029T=KCTC 42939T=MCC 2711T).

Square, tablet-forming, coccoid, heterotrophic bacterial cells of the genus Lampropedia (class Betaproteobacteria, family Comamonadaceae) were first described by Schroeter (1886) from polluted pond water. They were later isolated from liquid manure of a dairy farm yard and taxonomically designated Lampropedia hyalina by Pringsheim (1966). Since then, L. hyalina strains have also been reported from the rumen of a fistulated heifer (Hungate, 1966), and from activated sludge (Stante et al., 1997). An emended description of L. hyalina was given by Lee et al. (2004). The genus is currently represented by four strains belonging to a single species, i.e. L. hyalina strains ATCC 11041T, ATCC 43383, ATCC 13691 and ATCC 13871. The genus Lampropedia belongs to the family Comamonadaceae (class Betaproteobacteria), the members of which are characterized by the presence of ubiquinone-8 as the major respiratory quinone, putrescine and 2-hydroxyputrescine as the major polyamines, and phosphatidylethanolamine, phosphatidylglycerol and diphasathidylglycerol as the major polar lipids.

We have been exploring the microbial diversity at one of the hottest water springs of India, located within the Himalayan ranges at Manikaran, India (31° 20’ 25” to 32° 25’ 0” N 76° 56’ 30” to 77° 52’ 20” E), with water temperatures reaching up to 96 °C. We have previously isolated Thermus sp. RL (Dwivedi et al., 2012), Deinococcus sp. RL (Mahato et al., 2014) and Cellulosimicrobium sp. MM (Sharma et al., 2012) from hot spring water (~96 °C), sediments (45 °C) and microbial mats (45 °C), respectively, using culture-dependent approaches, and analysed the culture-independent microbial diversity at the arsenic-rich microbial mat samples from Manikaran (Sangwan et al., 2015).

Abbreviation: FAME, fatty acid methyl ester.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CT6T is KP265299.

Two supplementary figures are available with the online Supplementary Material.
In a continuation of our efforts, we isolated another bacterial strain, CT6<sup>T</sup>, from the hot water spring and classify it here as representing a novel species of the genus Lampropedia. For this, we collected the arsenic-rich (140 p.p.b.) microbial mat samples which covered the surface of stones surrounding the hot water spring (temperature ~45 °C), with surface water temperature reaching up to 57 °C (Sangwan et al., 2015). Mat samples (2 g) were suspended in saline and serially diluted. Dilutions were plated on Luria–Bertani (LB) medium with agar (1.5 %, w/v) and incubated at 45 °C. Dilutions were followed by isolation of several single colonies on LB agar, from which a white colony was selected after inoculation for 48 h and subcultured. The pure isolate was maintained at ~80 °C for long-term storage in 20 % (v/v) glycerol.

Phylogenetic analysis based on the 16S rRNA gene sequence was performed to identify the position of isolate CT6<sup>T</sup>. The 16S rRNA gene was amplified using standard eubacterial primers 8f and 1542r (Lane, 1991). Sanger sequencing of the 16S rRNA gene was carried out using an ABI 3700/3730 X1 sequencer (Applied Biosystems) at the Department of Plant and Molecular Biology, University of Delhi, South Campus, New Delhi, India. Universal sequencing primers 8f, 341f: CTACGGAGGCAGCAGTGGG 786f: GATATTACCCCTGGTAG and 1542r were used for sequencing. The sequences were manually assembled using Sequencing Analysis version 5.1.1 (Applied Biosystems) and a continuous nucleotide sequence of about 1425 nt was obtained. Sequences were manually checked for sequence quality. Searches via the BLAST program (ncbi.nlm.nih.gov/Blast.cgi; Altschul et al., 1990) on NCBI and the EzTaxon-e server (www.ezbiocloud.net/eztaxon; Kim et al., 2012) were used to retrieve the nearest neighbours of strain CT6<sup>T</sup>. Sequence alignment was done using CLUSTAL X (Thompson et al., 1997). Phylogenetic analyses were performed using the software package MEGA version 6 (Tamura et al., 2013). Phylogenetic trees were reconstructed using the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1993) algorithms. The method of Jukes & Cantor (1969) was used to calculate evolutionary distances. Statistical evaluation of the tree topology using 1000 resamplings was done by bootstrap analysis (Felsenstein, 1985).

Analysis of 16S rRNA gene sequences showed that strain CT6<sup>T</sup> was related most closely to members of the family Comamonadaceae of the class Betaproteobacteria. In the phylogenetic tree reconstructed with the maximum-likelihood algorithm, strain CT6<sup>T</sup> clustered with L. hyalina ATCC 11041<sup>T</sup> (Fig. 1) with a bootstrap value of 95 %. The phylogenetic position of this strain was further confirmed by the neighbour-joining method. Strain CT6<sup>T</sup> exhibited 16S rRNA gene sequence similarity of 95.4 % to L. hyalina ATCC 11041<sup>T</sup>. This was below the 97 % threshold recommended for the discrimination of separate bacterial species (Stackebrandt & Goebel, 1994). Physiological and biochemical tests were performed with L. hyalina ATCC 11041<sup>T</sup> to further confirm that strain CT6<sup>T</sup> represents a novel species.

Cell shape and size were examined by transmission electron microscopy (TEM 269D; Morgagni, Fei) at All India Institute of Medical Sciences (AIIMS), New Delhi, India. Images obtained revealed cocoid, non-flagellated cells with wavy margins (Fig. S1, available in the online Supplementary Material). Gliding motility was tested by the hanging drop method using motility agar (Farmer, 1999) and strain CT6<sup>T</sup> was found to be non-motile. Growth was checked on LB agar, polypeptide yeast extract agar, brain heart infusion agar, green top agar and tryptone soy agar at 37 °C. All the above media supported the growth of this strain. Strain CT6<sup>T</sup> formed white, smooth colonies with irregular margins on LB agar. Biofilm formation was seen when strain CT6<sup>T</sup> was inoculated in LB broth as the cells aggregated to form clusters and stuck to the sides of glass tubes. A Gram-stain test was performed with a Gram staining kit (HiMedia) according to the manufacturer’s instructions and strain CT6<sup>T</sup> was found to be Gram-stain-negative. Temperature tolerance was checked at 10, 20, 30, 40, 50, 55 and 60 °C by inoculating a pure culture of strain CT6<sup>T</sup> in LB broth and growth was monitored for 7 days. Salinity tolerance tests were performed in LB medium prepared by adding all components separately and using NaCl concentrations from 0 to 11 % (w/v) (at increments of 1 %). pH tolerance tests were performed in LB medium with pH gradients maintained from 4 to 12 (at increments of 1 pH unit). The following buffered media were used to stop the post-autoclaving variation, particularly for maintaining higher pH: K<sub>2</sub>HPO<sub>4</sub>–KH<sub>2</sub>PO<sub>4</sub> (for pH 4–8); NaHCO<sub>3</sub>–NaOH (for pH 9–11); NaCO<sub>3</sub>–NaOH (for pH 12). The pH of the media was confirmed after autoclaving. The final pH in the media after growth was also recorded. Salinity and pH tolerance tests were performed at 37 °C according to Arden Jones et al. (1979). In all the above tests, growth was measured at OD<sub>600</sub>. Tolerance tests showed that strain CT6<sup>T</sup> was able to grow over the temperature range 20–55 °C (optimum 37 °C); salinity tolerance was 1–3 % (w/v) NaCl (optimum 1 %); and pH was tolerated in the range 6–9 (optimum pH 8–9). Final pH in the growth media was recorded as 8.2–8.4.

Catalase activity was tested by observing if bubbles are produced after adding 3 % (v/v) hydrogen peroxide solution (McCarthy & Cross, 1984) to fresh colonies grown on LB agar. Oxidase activity was tested using oxidase reagent (N,N,N’,N’-tetramethyl-1,4-phenylenediamine; bioMérieux). Citrate utilization was tested using Simmons citrate agar (HiMedia). Biochemical tests were performed according to the manufacturer’s instructions using the API 20NE kit (bioMérieux). Hydrolysis of Tween 20 and 80 was checked according to Arden Jones et al. (1979). Degradation of xanthine and hypoxanthine was determined as described by Gordon et al. (1974). Arsenic tolerance was determined by checking growth on LB medium supplemented with 80 p.p.b. working concentration of arsenic trioxide. Arsenic trioxide stock solution (1000 p.p.m.) was prepared in low pH water. Strain CT6<sup>T</sup> was positive for...
catalase but negative for oxidase. It was able to hydrolyse Tweens 20 and 80, but it could not hydrolyse gelatin or aesculin. Strain CT6 raised tolerance to arsenic trioxide up to 80 p.p.b. Strain CT6 tested negative for nitrate reduction, indole production, urease, arginine dihydrolase and β-galactosidase but positive for the assimilation of malic acid, capric acid and citric acid and fermentation of glucose (Table 1). Simultaneously, all the above tests were also performed for L. hyalina. Antibiotic sensitivity tests were performed on Muller Hinton agar plates using ready-made antibiotic discs (HiMedia) with varying amounts of antibiotics. Antibiotics tested were as follows (μg per disc in parentheses): vancomycin (30), nalidixic acid (30), penicillin-G (10), ampicillin (10), rifampicin (5), polymyxin-B (300), kanamycin (30), amikacin (30), gentamicin (10) and tetracycline (30). Antibiotic tests were carried out by plating the cultures uniformly onto agar plates and impregnating antibiotic discs into them. Antibiotic sensitivity was scored based on observing a visible zone of clearance near the antibiotic discs for up
to 7 days. Strain CT6\textsuperscript{T} along with \textit{L. hyalina} showed similar antibiotic resistance profiles. Both were resistant to vancomycin, penicillin-G, ampicillin and rifampicin but sensitive to the other antibiotics tested.

For fatty acid methyl ester (FAME) analysis, biomass was harvested at the late exponential phase from strain CT6\textsuperscript{T} and \textit{L. hyalina}, both grown in LB medium at 28\textdegree{C}. The physiological age of cultures was standardized according to the protocol of the Sherlock Microbial Identification System (MIDI) (Sasser, 1990). FAME analysis was performed at Royal Life Sciences, Secunderabad, India, by subjecting the cells to saponification, methylation and extraction as described by Miller (1982) and Kuykendall et al. (1988). The mixture of FAMEs was separated using a GC device (Agilent 6890) equipped with flame-ionization detector. Identification of FAMEs was done using the Aerobe TSBA, 60 version 6.0 B database (MIDI). The predominant fatty acids detected were C\textsubscript{16}:0 (34.5\%), summed feature 8 (C\textsubscript{18:1}\textsubscript{v7c} and/or C\textsubscript{18:1}\textsubscript{w6c}, 12.6\%), C\textsubscript{14:0} (10.3\%), C\textsubscript{19:0} cyclo (9.8\%) and summed feature 3 (C\textsubscript{16:1}\textsubscript{w7c} and/or C\textsubscript{16:1}\textsubscript{w6c}, 7.5\%) (Table 2).

The fatty acid profile of strain CT6\textsuperscript{T} revealed qualitative and quantitative differences as compared with \textit{L. hyalina} ATCC 11041\textsuperscript{T}, suggesting that strain CT6\textsuperscript{T} may represent a novel species.

Polar lipids were extracted from 100 mg of lyophilized cell culture and analysed with the help of two-dimensional TLC using 9 x 9 cm silica-gel F\textsubscript{254} plates (Merck) (Bligh & Dyer, 1959). Total polar lipids were detected by spraying with 10% phosphomolybdic acid. Additionally, 1% aqueous primulin dissolved in acetone was used as another spraying agent for total polar lipids, followed by visualization under UV light. For detection of amino lipids, 0.3% ethanolic ninhydrin was sprayed and the TLC plate was kept at 110\textdegree{C} for 15 min. Pink spots on the plate indicated amino lipids, including phosphatidylethanolamine and phosphatidylserine. Major polar lipids detected in strain CT6\textsuperscript{T} were phosphatidylethanolamine, phosphatidylglycerol and an unknown glycolipid. Additionally, diphosphatidylglycerol, phosphatidylserine, two phospholipids and a glycolipid were detected in minor amounts. \textit{L. hyalina}

### Table 1. Differential morphological and physiological characteristics between CT6\textsuperscript{T} and \textit{L. hyalina} ATCC 11041\textsuperscript{T}

All data are from this study. Both strains give negative reactions for the following: Gram staining, oxidase, nitrate reduction, indole production, arginine dihydrolase, \textit{fi}-galactosidase, aesculin hydrolysis, utilization of phenyl acetic acid, N-acetylg glucosamine, L-arabinose, D-mannose, D-mannitol, maltose, potassium gluconate and adipic acid. Both strains show positive reactions for catalase and starch hydrolysis. +, Positive; −, negative.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>CT6\textsuperscript{T}</th>
<th>\textit{L. hyalina} ATCC 11041\textsuperscript{T}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolation source</td>
<td>Microbial mat</td>
<td>Polluted aquatic sample</td>
</tr>
<tr>
<td>Growth conditions</td>
<td>NaCl concentration (%)</td>
<td>1–3</td>
</tr>
<tr>
<td>Temperature (\textdegree{C})</td>
<td>20–55</td>
<td>10–40</td>
</tr>
<tr>
<td>pH tolerance</td>
<td>6–9</td>
<td>6–9</td>
</tr>
<tr>
<td>Final pH in growth media</td>
<td>8.2–8.4</td>
<td>8.4–8.6</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td>Tween 20</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>Tween 80</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>Gelatin</td>
<td>−</td>
</tr>
<tr>
<td></td>
<td>Urea</td>
<td>−</td>
</tr>
<tr>
<td>Fermentation of glucose</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Assimilation of:</td>
<td>Capric acid</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>Malic acid</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>Citric acid</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>63.5</td>
<td>63.2</td>
</tr>
</tbody>
</table>

### Table 2. Cellular fatty acid profiles (%) of CT6\textsuperscript{T} and \textit{L. hyalina} ATCC 11041\textsuperscript{T}

All data are from this study. ND, Not detected.

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>CT6\textsuperscript{T}</th>
<th>\textit{L. hyalina} ATCC 11041\textsuperscript{T}</th>
</tr>
</thead>
<tbody>
<tr>
<td>C\textsubscript{16:0}</td>
<td>34.53</td>
<td>19.25</td>
</tr>
<tr>
<td>C\textsubscript{14:0}</td>
<td>10.29</td>
<td>5.87</td>
</tr>
<tr>
<td>C\textsubscript{18:0}</td>
<td>4.68</td>
<td>ND</td>
</tr>
<tr>
<td>C\textsubscript{20:0} cyclo</td>
<td>9.75</td>
<td>ND</td>
</tr>
<tr>
<td>C\textsubscript{16:1}\textsubscript{w7c}</td>
<td>1.42</td>
<td>ND</td>
</tr>
<tr>
<td>11-methyl C\textsubscript{18:1}\textsubscript{w7c}</td>
<td>1.23</td>
<td>ND</td>
</tr>
<tr>
<td>C\textsubscript{10:0} 3-OH</td>
<td>3.09</td>
<td>4.35</td>
</tr>
<tr>
<td>C\textsubscript{12:0} 3-OH</td>
<td>3.41</td>
<td>1.70</td>
</tr>
<tr>
<td>Summed features</td>
<td>7.49</td>
<td>27.45</td>
</tr>
<tr>
<td>3 (C\textsubscript{16:1} w7c/C\textsubscript{16:1} w6c)</td>
<td>1.25</td>
<td>ND</td>
</tr>
<tr>
<td>8 (C\textsubscript{18:1} w7c/C\textsubscript{18:1} w6c)</td>
<td>12.56</td>
<td>39.28</td>
</tr>
</tbody>
</table>
ATCC 11041^T exhibited the presence of phosphatidylethanolamine, phosphatidylmonomethylethanolamine and phosphatidylglycerol as major polar lipids (Fig. S2).

Quinones were extracted from 200 mg of dry cell mass using 10% aqueous solution of 0.3% (w/v) NaCl in methanol and petroleum ether (1:1). The upper phase was dried in a rotary evaporator (Rotavapor R-210; Büchi) and the residue was dissolved in 100 μl acetone. The extract was loaded and analysed on a TLC plate (Silica gel 60 F_254; 20 × 20 cm; Merck) using petroleum ether and diethyl ether (85:15, v/v) as solvent. The purified ubiquinone was dissolved in acetone and analysed by reversed-phase TLC according to Collins & Jones (1981). Ubiquinone-8 was detected as the major respiratory quinone in strain CT6^T as well as in its neighbour L. hyalina. The presence of ubiquinone is consistent with reports of Q-8 being the major quinone among Comamonadaceae.

Bacterial polyamines were extracted from 40 mg of dry cell mass of late exponential phase cultures for both strain CT6^T and L. hyalina ATCC 11041^T as described by Busse & Auling (1988). 1,8-Diaminooctane was used as an internal standard. Extracted dansylated polyamines (20 μl) were analysed by HPLC (Agilent Technologies 1220 Infinity LC) using reversed-phase C18 column chromatography and visualized at an excitation wavelength of 365 nm. Commercially prepared standards (Sigma Aldrich) were also prepared and analysed simultaneously and peak identification for the polyamines of strain CT6^T and L. hyalina was made by comparing the elution time of the standards. The major polyamines identified in strain CT6 and L. hyalina ATCC 11041^T were putrescine, spermidine and the diagnostic polyamine 2-hydroxyputrescine. The polyamine pattern was in good agreement with that reported for betaproteobacteria (Hamana et al., 2006). However, there were quantitative differences in the polyamine patterns for the two strains. Putrescine and spermidine were present in higher amounts than 2-hydroxyputrescine in strain CT6^T, whereas 2-hydroxyputrescine was present in a higher amount than putrescine and spermidine in L. hyalina ATCC 11041^T.

The DNA G+C content of strain CT6^T was calculated according to the method described by Gonzalez & Saiz-Jimenez (2002) using an Applied Biosystems 7500 Real-Time PCR machine. Additionally, the G+C content was also calculated from the Illumina sequencing data recently generated for strain CT6^T (R. Lal, unpublished data; accession number NZ_LBNQ00000000.1). The DNA G+C content of strain CT6^T was 63.9 mol% (RT-PCR) and 63.5 mol% (genomic data).

The morphological, physiological and chemotaxonomic comparisons between strain CT6^T and L. hyalina ATCC 11041^T suggest that strain CT6^T belongs to the genus Lampropedia. 16S rRNA gene sequence similarity with its nearest neighbour was 95.4%, which is well below the threshold limit for delineation of a novel species. The FAME profile of strain CT6^T shows marked differences with that of L. hyalina, but similar profiles are obtained for polar lipids, polyamines and quinones. Both strain CT6^T and L. hyalina have phosphatidylethanolamine and phosphatidylglycerol as major polar lipids. The polyamine pattern revealed the presence of the diagnostic polyamine 2-hydroxyputrescine along with putrescine and spermidine in both strains. Ubiquinone-8 was the major respiratory quinone in both strains. Additionally, both L. hyalina and strain CT6^T show similar pH tolerance, and both show negative reactions for nitrate reduction, β-galactosidase and aesculin hydrolysis and a positive reaction for starch hydrolysis. However, strain CT6^T shows differences with L. hyalina in terms of temperature and NaCl tolerance, hydrolysis of Tween 20, Tween 80, gelatin and urea, fermentation of glucose, and assimilation of capric acid, malic acid and citric acid. Tw eens 20 and 80 are hydrolysed by strain CT6^T, but are not hydrolysed by L. hyalina. Gelatin and urea are not hydrolysed by strain CT6^T whereas they are hydrolysed by L. hyalina. Glucose is fermented and capric acid, malic acid and citric acid are assimilated by CT6^T whereas they are not by L. hyalina. Differences are also seen in the relative amounts of the major polyamines; 2-hydroxyputrescine is present in higher amounts in L. hyalina whereas putrescine and spermidine are predominant in strain CT6^T. This difference may be attributed to the fact that strain CT6^T has been isolated from a slightly thermophilic environment and spermidine is known to be present along with putrescine and 2-hydroxyputrescine in slightly thermophilic betaproteobacteria (Hamana et al., 2006). On the basis of morphological, physiological, genotypic and chemotaxonomic characteristics, strain CT6^T is considered to represent a novel species of the genus Lampropedia, for which the name Lampropedia cohaerens sp. nov. is proposed.

Emended description of the genus Lampropedia

Based on the properties of Lampropedia given by Lee et al. (2004) and properties tested in this study, an emended description of the genus Lampropedia is provided. Gram-stain-negative, coccoid, aerobic, catalase-positive and oxidase-negative. Growth is observed at 10–55 °C, at pH 6–9 and with 1–3% (w/v) NaCl. Phosphatidylethanolamine and phosphatidylglycerol are the major polar lipids. The major polyamines are putrescine, 2-hydroxyputrescine and spermidine. The major quinone is ubiquinone-8. Starch is hydrolysed, but nitrate and aesculin are not. Indole, β-galactosidase and arginine dihydrolase are not produced. Unable to utilize carbohydrates in general but can utilize some organic acids. The DNA G+C content is 60–67 mol%.

Description of Lampropedia cohaerens sp. nov.

Lampropedia cohaerens (co.hae’rens. L. part. adj. cohaerens sticking together).

Cells are Gram-stain-negative, aerobic, coccoid, 0.48–0.62 μm in length and 0.32–0.39 μm in width. Growth
occurs on LB agar, polypeptone yeast extract agar, tryptic soy agar, brain heart infusion agar, green top agar and Simmons citrate agar. Colonies are white, smooth and with irregular margins after 24 h of incubation. Growth occurs at 20–55°C. Growth occurs with 1–3% (w/v) NaCl and at pH 6–9. Catalase-positive but oxidase-negative. Hydrolyses Tweens 20 and 80 but does not hydrolyse gelatine, aesculin, urea or nitrate. Starch is hydrolysed. Arsenic trioxide is tolerated up to 80 p.p.b. β-Galactosidase and arginine dihydrolase are not produced. Indole production is negative. Citrate, xanthine and hypoxanthine are utilized. Can utilize malic acid, trisodium citrate and capric acid but cannot utilize N-acetylgalosamine, potassium gluconate, adipic acid, phenylacetic acid, L-arabinose, D-mannose, D-mannitol or maltose. Forms acid from glucose. Major fatty acids are C16:0, summed feature 8 (C18:1ω7c and/or C18:1ω6c), C14:0, C19:1ω9c cyclo and summed feature 3 (C16:1ω7c and/or C16:1ω6c).

The type strain is CT6T (=DSM 100029T = KCTC 42939T = MCC 2711T), isolated from arsenic-rich microbial mats surrounding a hot water spring located at Manikaran, India. The DNA G+C content of the type strain is 63.5 mol%.

Acknowledgements

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