Defluviimonas alba sp. nov., isolated from an oilfield

Xin-Chi Pan,† Shuang Geng,† Xiang-Lin Lv,† Ran Mei,† Jing-Hong Jiangyang,† Ya-Nan Wang,‡ Lian Xu,‡ Xue-Ying Liu,† Yue-Qin Tang,† Ge-Jiao Wang§ and Xiao-Lei Wu†,‡

1College of Engineering, Peking University, Beijing 100871, PR China
2Institute of Biology, Henan Academy of Sciences, Zhengzhou 450008, PR China
3Institute of Engineering (Baotou), College of Engineering, Peking University, Baotou 014030, PR China
4State Key Laboratory of Agricultural Microbiology, College of Life Science and Technology, Huazhong Agricultural University, Wuhan, Hubei 430070, PR China.

Two Gram-stain-negative, rod-shaped bacterial strains, cai42T and b45, were isolated from oil-production water taken from Xinjiang Oilfield, China. Optimum growth was observed at 30 °C, at pH 8 and with 1–3 % (w/v) NaCl. According to phylogenetic analyses, the two strains were members of the genus Defluviimonas, with 16S rRNA gene sequence similarities of 95.5–96.3 % with the type strains of species of the genus. The major cellular fatty acids of strains cai42T and b45 were C10 : 03-OH, C16 : 0 and summed feature 8 (C18 : 1ω7c/C18 : 1ω6c), and the predominant ubiquinone was Q-10, all of these data being typical for the genus Defluviimonas. The polar lipids were phosphatidylethanolamine, phosphatidylglycerol, glycolipid, phosphatidylcholine, two unidentified aminolipids, an unidentified phospholipid and two unidentified lipids. The mean genomic DNA G+C contents of strains cai42T and b45 were 60.8 ± 1.1 and 60.4 ± 1.0 mol%, respectively. On the basis of phylogenetic, physiological and chemotaxonomic analyses, strains cai42T and b45 represent a novel species of the genus Defluviimonas, for which the name Defluviimonas alba sp. nov. is proposed. The type strain is cai42T (≡CGMCC 1.12518T ≡LMG 27406T).

The genus Defluviimonas, belonging to the family Rhodobacteraceae, was first described by Foesel et al. (2011) and, at the time of writing, comprises four recognized species, Defluviimonas denitrificans (Foesel et al., 2011) isolated from the biofilter of a marine aquaculture system, Defluviimonas aestuarii (Math et al., 2013) isolated from a tidal flat of the South Sea in Korea, Defluviimonas indica (Jiang et al., 2014) isolated from a deep-sea hydrothermal vent chimney collected from the South-west Indian Ridge and Defluviimonas aquamixtae (Jung et al., 2014) isolated from the junction between a freshwater spring and the ocean. Typically, cells of members of this genus are Gram-negative, moderately halophilic, catalase- and oxidase-positive rods, with the major fatty acids being summed feature 8 (C18 : 1ω7c/C18 : 1ω6c) and the respiratory quinone being Q-10. During study of the bacterial community in an oilfield in Xinjiang Province, China (Sun et al., 2014), two novel strains, cai42T and b45, were isolated and herein are shown to represent a novel species of the genus Defluviimonas.

Strains cai42T and b45 were isolated by the standard dilution plating method from oil-production water recovered from Xinjiang Oilfield. The isolation medium was Columbia agar base (per litre: special peptone, 23 g; starch, 1 g; NaCl, 5 g; agar, 10 g; pH 7.3 ± 0.2). The morphological, chemical and molecular analyses of the two strains were conducted after the cells were grown on Luria–Bertani agar (LB; per litre: peptone, 10 g; yeast extract, 5 g; NaCl, 10 g; agar, 15 g) for 24 h at 30 °C, pH 8, except where otherwise indicated. D. denitrificans DSM 18921T, D. aestuarii JCM 18630T and Rhodobacter veldkampii CGMCC 15006T, used as reference strains, were obtained from Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Japan Collection of Microorganisms and China General Microbiological Culture Collection Center, respectively. Reference strains Haematobacter massiliensis CCUG 47968T and Haematobacter missouriensis CCUG 52307T were kindly provided by Gejiao Wang, State

†These authors contributed equally to this work.
‡Present address: College of Architecture and Environment, Sichuan University, Chengdu, 610065, PR China.
§These authors contributed equally to this work.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains cai42T and b45 are KC222646 and KC222647, respectively.

Three supplementary figures are available with the online Supplementary Material.
Key Laboratory of Agricultural Microbiology, Huazhong Agricultural University, China. D. denitrificans DSM 18921T, D. aestuarii JCM 18630T and R. veldkampii CGMCC 15006T were cultured in marine broth 2216 (MB; per litre: peptone, 5 mg; ferric phosphate, 0.1 mg; yeast extract, 1 mg; NaCl, 19.45 mg; MgCl₂, 5.98 mg; Na₂SO₄, 3.42 mg; CaCl₂, 1.8 mg; KCl, 0.55 mg; Na₂CO₃, 0.16 mg; KBr, 0.08 mg; Cl₂Sr, 0.0034 mg; boric acid, 0.022 mg; sodium silicate, 0.004 mg; NaF, 0.0024 mg; NaNO₃, 0.0016 mg; Na₂HPO₄, 0.008 mg; pH 7.0) at 30 °C (Math et al., 2013); H. massiliensis CCUG 47968T and H. missouriensis CCUG 52307T were grown under clinical culture conditions in brain heart infusion (BHI) medium (Helsel et al., 2007) at 35 °C.

The morphology of the cells was observed under a transmission electron microscope (JEM-1230; JEOL). The temperature and pH range for growth were determined using LB medium at 4, 15, 20, 25, 30, 37, 40, 45, 50 and 55 °C, and at pH values from 4 to 10 (at 1 pH unit intervals), respectively (Takai et al., 2002). Salt tolerance was tested in LB medium (pH 8) ranging from 0 to 9% (w/v) NaCl (at 1% intervals).

Enzyme activities were tested using an API ZYM kit (bioMérieux) according the method described by Cai et al. (2011). Oxidase activity was examined using oxidase reagent (bioMérieux). Catalase activity and hydrolysis of Tween 80 and starch were analysed according to Dong & et al. (2012). Oxidase activity was examined using oxidase reagent (bioMérieux) after incubation at 30 °C for 24 h. Antibiotic susceptibility tests were carried out with disc diffusion method (Fraser & Jorgensen, 1997; Andrews et al., 2008), and the compounds included amikacin (30 μg), ceftazidime (30 μg), neomycin (30 μg), cefotaxime (30 μg), kanamycin (30 μg), vancomycin (30 μg), chloramphenicol (30 μg), tetracycline (30 μg), ciprofloxacin (5 μg), ofloxacin (5 μg), gentamicin (10 μg), penicillin (10 μg), amoxicillin (10 μg), rifampicin (5 μg), erythromycin (15 μg), clindamycin (2 μg), novobiocin (5 μg) and midazdacyn (15 μg). After cells of strains cai42T and b45 were cultured in 50 ml LB liquid medium at 30 °C in the dark for 24 h, pigments were sprayed with 1-naphthol for detection of sugars, nirhydin for aminolipids, molybdenum blue for phospholipids, D reagent (3.5 ml bismuthyl nitrate solution (1.7%, w/v, dissolved in 20% acetic acid), 5 ml potassium iodide (40%, w/v), 20 ml acetic acid, 50 ml double distilled water) for phosphatidylycholine, phosphatidylethanolamine and phosphatidimethylmethylethanolamine components, and molybdotrophosphoric acid for total lipids.

The genomic DNA of strains cai42T and b45 was extracted according to Marmur (1961) from cells grown in LB medium for 24 h at pH 8 and 30 °C. The 16S rRNA gene was PCR-amplified using the universal bacterial primer set 8 F and 1492 R (Embley, 1991). After sequencing, the 16S rRNA gene sequences were compared with sequences obtained from the EzTaxon-e database (Kim et al., 2012). Phylogenetic trees were reconstructed and evaluated using MEGA software (Tamura et al., 2011) with the neighbour-joining (Saitou & Nei, 1987), minimum-evolution (Rzhetsky & Nei, 1993) and maximum-likelihood (Felsenstein, 1981) algorithms, and the bootstrap analysis was based on 1000 resamplings.

The genomic DNA G+C contents of strains cai42T and b45 were determined from the midpoint value (Tm) of the thermal denaturation profile (Mandell et al., 1970) with Escherichia coli K-12 as reference. DNA–DNA hybridization between strains cai42T and b45 was performed in triplicate according to the methods of De Ley et al. (1970) and Huss et al. (1983).

Strains cai42T and b45 shared a similarity of 99.9% in the nearly complete 16S rRNA gene sequence (1428 nt), and the mean (±SD) level of DNA–DNA relatedness between the two strains was 73.9±8.2%. The results showed that they were different strains belonging to the same species. The two strains shared 96.3–96.4% 16S rRNA gene sequence similarity with R. veldkampii CGMCC 15006T, 96.0–96.2% with strains in the genus Haematobacter and 95.5–96.3% with strains in the genus Defluviimonas. However, in the phylogenetic trees reconstructed using the neighbour-joining (Fig. 1), minimum-evolution (Fig. S1, available in the online Supplementary Material) and
maximum-likelihood algorithms (Fig. S2), strains cai42T and b45 formed a stable and distinct clade with species of the genus *Defluviimonas* and separated from other genera.

For better confirmation of the taxonomic position of the two new isolates, the closest related type strains in the genera *Defluviimonas*, *Haematobacter* and *Rhodobacter* were used as reference strains, namely *D. denitrificans* DSM 18921T (95.5–95.6 % 16S rRNA gene sequence similarity), *D. aestuarii* JCM 18630T (96.2–96.3 %), *H. missouriensis* CCUG 52307T (96.0–96.1 %), *H. massiliensis* CCUG 47968T (95.8–95.9 %) and *R. veldkampii* CGMCC 15006T. The mean genomic DNA G+C contents of strains cai42T and b45 were 60.8 ± 1.1 and 60.4 ± 1.0 mol %, respectively, values similar to that of *D. aestuarii* JCM 18630T (61.6 mol%), but significantly lower than the four other reference strains.

After growth on LB agar (pH 8) for 48 h, colonies of strains cai42T and b45 were creamy, circular and with a diameter of 0.5–1.0 mm. Cells of the two strains were Gram-stain-negative, rod-shaped, 1.0–1.5 μm in length and 0.5–0.7 μm in width (Fig. 2). Cells of strain cai42T had a cluster of one polar pili, which was different from *D. denitrificans* DSM 18921T and *D. aestuarii* JCM 18630T.

Growth was observed at 20–37 °C, at pH 7–9 and with 0–5 % (w/v) NaCl. Optimum growth occurred at 30 °C, at

---

**Fig. 1.** Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strains cai42T and b45 within the genus *Defluviimonas* and closely related members in the family *Rhodobacteraceae*. Bootstrap values (based on 1000 replications) greater than 50 % are shown at branch points. Bar, 0.02 nt substitutions per nucleotide position. Filled circles indicate branches also found in the minimum-evolution and maximum-likelihood phylogenetic trees.
pH 8 and with 1–3 % (w/v) NaCl. Strains cai42T and b45 were positive for oxidase and catalase activities, and weakly positive for starch hydrolysis. The results of API ZYM and API 20NE tests are listed in Table 1. Generally, the biochemical characteristics of strains cai42T and b45 better matched those of *D. denitrificans* DSM 18921T and *D. aestuarii* JCM 18630T than *H. massiliensis* CCUG 47968T, *H. missouriensis* CCUG 52307T and *R. veldkampii* CGMCC 15006T. However, strains cai42T and b45 were negative for activities of alkaline phosphatase and naphthol-AS-Bl-phosphoamidase, and positive for utilization of gluconate and malic acid as sole carbon sources, which were notably opposite to those for both *D. denitrificans* DSM 18921T and *D. aestuarii* JCM 18630T. The results of antibiotic tests showed that strains cai42T and b45 were sensitive to clindamycin and midecamycin. Neither photosynthetic pigments nor the photosynthetic reaction centre gene *pufM* was detected in the two isolates, results that were consistent with the genera *Defluviimonas* and *Haematobacter*, but different from *R. veldkampii* CGMCC 15006T. Anaerobic growth of the two isolates was not detected while *D. denitrificans* DSM 18921T showed facultatively anaerobic growth by using NaNO3 and NaNO2 as electron acceptors. Differential characteristics between strains cai42T and b45 and the reference strains are listed in Table 1.

In accordance with the genera *Haematobacter*, *Rhodobacter* and *Defluviimonas*, the major quinone in strains cai42T and b45 was Q-10. The major fatty acids (>5 % of the total) of strains cai42T and b45 were C10:0 3-OH (8.0–8.6 %), C16:0 (5.6–7.0 %) and summed feature 8 (C18:1ω7c/C18:1ω6c, 73.6–74.8 %), all of which were found in *D. aestuarii* JCM 18630T and *D. denitrificans* DSM 18921T (Table 2). However, strains cai42T and b45 lacked C18:0 3-OH and C19:0 cyclo ω8c (trace amount), components that were found in *D. aestuarii* JCM 18630T and *D. denitrificans* DSM 18921T; furthermore, the two new isolates contained specific components present in trace amounts, namely summed feature 5 (C18:2ω6, 9c/anteiso-C18:0; 0.8 %), which also differed from *D. aestuarii* JCM 18630T and *D. denitrificans* DSM 18921T. *H. massiliensis* CCUG 47968T and *H. missouriensis* CCUG 52307T lacked 11-methyl C18:1ω7c but contained C19:0 cyclo ω8c and summed feature 2 (C14:0 3-OH/iso-C16:1 I; 1.5–1.6 %) compared with strains cai42T and b45. *R. veldkampii* CGMCC 15006T showed clear differences in fatty acid features with the two new isolates. The polar lipids of strains cai42T and b45 were phosphatidylethanolamine (PE), phosphatidylglycerol (PG), glycolipid (GL), phosphatidylcholine (PC), two unidentified aminolipids (AL1 and 2), an unidentified phospholipid (PL2) and two unidentified lipids (L1 and 2) (Figs 3 and S3). Although strains cai42T and b45 shared similar PE, PG, AL2 and PC components with *D. denitrificans* DSM 18921T, *D. aestuarii* JCM 18630T (Math et al., 2013), *H. massiliensis* CCUG 47968T and *H. missouriensis* CCUG 52307T (Wang et al., 2014), they contained unique PL, GL, AL1 and two other unknown lipids.

From the above analysis, strains cai42T and b45 grouped together with the cluster of type strains of the genus *Defluviimonas* and shared 95.5–96.3 % 16S rRNA gene sequence similarity with them. Strains cai42T and b45 did not have photosynthetic pigments or the *pufM* gene, in contrast to the genus *Rhodobacter*. The DNA G+C contents of the two isolates were approximately 60.4–60.8 mol%, values much lower than for *Haematobacter* (65.0–65.5 mol%). Regarding fatty acids, strains cai42T and b45 lacked C18:0 3-OH and C19:0 cyclo ω8c components but contained trace amounts of C18:2ω6, 9c/anteiso-C18:0 compared with *D. aestuarii* JCM 18630T and *D. denitrificans* DSM 18921T. The two new isolates contained particular polar lipid components, PL, GL, AL1 and two other unknown lipids, which were not found in *D. aestuarii* JCM 18630T or *D. denitrificans* DSM 18921T. Furthermore, strains cai42T and b45 were negative for activity of alkaline phosphatase and naphthol-AS-Bl-phosphoamidase and positive for utilization of gluconate and malic acid, which also differed from the two *Defluviimonas* strains. The phylogenetic, physiological and chemotaxonomic analyses showed that strains cai42T and b45 represented a species of the genus *Defluviimonas* that was clearly distinct from existing species. Therefore, strains cai42T and b45 are considered to represent a novel species of the genus *Defluviimonas*, for which the name *Defluviimonas alba* sp. nov. is proposed.
**Table 1.** Differential characteristics between strains cai42<sup>T</sup> and b45 and the five reference type strains

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2&lt;sup&gt;a&lt;/sup&gt;</th>
<th>3&lt;sup&gt;b&lt;/sup&gt;</th>
<th>4&lt;sup&gt;c&lt;/sup&gt;</th>
<th>5&lt;sup&gt;d&lt;/sup&gt;</th>
<th>6&lt;sup&gt;e&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolation source</td>
<td>Water</td>
<td>Aquaculture</td>
<td>Tidal flat</td>
<td>Clinical specimens</td>
<td>Clinical specimens</td>
<td>Freshwater</td>
</tr>
<tr>
<td>Colour of colonies</td>
<td>Creamy</td>
<td>Yellow</td>
<td>White</td>
<td>White</td>
<td>Yellow</td>
<td>Yellow brown</td>
</tr>
<tr>
<td>Pili</td>
<td>+</td>
<td>+&lt;sup&gt;a&lt;/sup&gt;</td>
<td>-&lt;sup&gt;b&lt;/sup&gt;</td>
<td>-&lt;sup&gt;c&lt;/sup&gt;</td>
<td>-&lt;sup&gt;c&lt;/sup&gt;</td>
<td>-&lt;sup&gt;e&lt;/sup&gt;</td>
</tr>
<tr>
<td>Optimum temperature (°C)</td>
<td>30</td>
<td>30–40&lt;sup&gt;a&lt;/sup&gt;</td>
<td>30&lt;sup&gt;b&lt;/sup&gt;</td>
<td>35&lt;sup&gt;d&lt;/sup&gt;</td>
<td>35&lt;sup&gt;d&lt;/sup&gt;</td>
<td>30–35&lt;sup&gt;e&lt;/sup&gt;</td>
</tr>
<tr>
<td>Optimum pH</td>
<td>8</td>
<td>6.5–7&lt;sup&gt;a&lt;/sup&gt;</td>
<td>7–7.5&lt;sup&gt;b&lt;/sup&gt;</td>
<td>7&lt;sup&gt;d&lt;/sup&gt;</td>
<td>7&lt;sup&gt;d&lt;/sup&gt;</td>
<td>7.5&lt;sup&gt;e&lt;/sup&gt;</td>
</tr>
<tr>
<td>Optimum NaCl (%)</td>
<td>1–3</td>
<td>0.5–2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1–1.5&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1–2</td>
<td>1–2</td>
<td>Not required&lt;sup&gt;f&lt;/sup&gt;</td>
</tr>
<tr>
<td>Anaerobic growth</td>
<td>–</td>
<td>FA&lt;sup&gt;a&lt;/sup&gt;</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Pigment</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**API ZYM results:**
- Alkaline phosphatase: –<sup>a</sup> +<sup>b</sup> +<sup>c</sup> +<sup>d</sup> +<sup>e</sup> +
- Esterase lipase (C-8): –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> +<sup>d</sup> –<sup>e</sup> +
- Leucine aminopeptidase: +<sup>a</sup> +<sup>b</sup> +<sup>c</sup> +<sup>d</sup> +<sup>e</sup> –
- Valine aminopeptidase: –<sup>a</sup> w<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- Acid phosphatase: –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> +
- Naphthal-AS-BI-phosphoamidase: –<sup>a</sup> +<sup>b</sup> +<sup>c</sup> w<sup>d</sup> +<sup>e</sup> –
- β-Galactosidase: –<sup>a</sup> –<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> +
- α-Glucosidase: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –

**API 20NE results:**
- Nitrate reduction: –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- Urease: –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> w<sup>d</sup> w<sup>e</sup> –
- Gelatinase: –<sup>a</sup> –<sup>b</sup> +<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- Glucose: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> w<sup>d</sup> w<sup>e</sup> +
- Arabinose: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- Mannose: –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- Mannon: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> –
- N-Acetylg glucosamine: –<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> +
- Maltose: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> +
- Gluconate: +<sup>a</sup> +<sup>b</sup> –<sup>c</sup> –<sup>d</sup> –<sup>e</sup> +
- Adipic acid: –<sup>a</sup> –<sup>b</sup> –<sup>c</sup> –<sup>d</sup> +<sup>e</sup> +
- Malic acid: +<sup>a</sup> –<sup>b</sup> –<sup>c</sup> +<sup>d</sup> +<sup>e</sup> +
- Sodium citrate: –<sup>a</sup> –<sup>b</sup> –<sup>c</sup> –<sup>d</sup> +<sup>e</sup> +
- Phenylacetic acid: –<sup>a</sup> –<sup>b</sup> –<sup>c</sup> –<sup>d</sup> +<sup>e</sup> +

**Polar lipids:**
- PE, PG, GL, PC, AL, PL, L<sup>a</sup> PE, DPG, AL, PL, L<sup>b</sup> PE, DPG, AL, PL, L<sup>b</sup> PG, PE, AL, PL<sup>d</sup> PG, PE, AL, PL<sup>d</sup> NT
- DNA G+C content (mol%): 60.4–60.8 65.1<sup>a</sup> 61.6<sup>b</sup> 65.0<sup>d</sup> 65.5<sup>d</sup> 64.4–67.5<sup>e</sup>

*Data from: a, Foesel et al. (2011); b, Math et al. (2013); c, Helsel et al. (2007); d, Wang et al. (2014); e, Hansen & Imhoff (1985).*

†FA, facultatively aerobic.

‡PE, phosphatidylethanolamine, PG, phosphatidylglycerol, GL, glycolipid, PC, phosphatidylycholine, AL, unidentified aminolipid, PL, unidentified phospholipid, L, unidentified lipid.
Description of Defluvimonas alba sp. nov.

Defluvimonas alba (al’ba. L. fem. adj. alba white, the colour of colonies).

Cells are aerobic, Gram-stain-negative, rod-shaped, 1.0–1.5 μm long and 0.5–0.7 μm wide. After growth on LB agar (pH 8) for 48 h, colonies are creamy and circular (with a diameter of 0.5–1.0 mm). Growth occurs at 20–37 °C, at pH 7–9 and with 0–5 % (w/v) NaCl. Optimum growth occurs at 30 °C, at pH 8 and with 1–3 % (w/v) NaCl. Positive for activities of oxidase, catalase, esterase (C4), leucine aminopeptidase and z-glucosidase, weakly positive for starch hydrolysis, but negative for activities of alkaline phosphatase, esterase lipase (C8), lipase (C14), valine aminopeptidase, cystine aminopeptidase, trypsin, x-chymotrypsin, acid phosphatase, x-galactosidase, naphthol-AS-BI-phosphoamidase, β-galactosidase, N-acetyl-β-glucosaminidase, β-glucuronidase, β-glucosidase, x-mannosidase, β-fucosidase, nitrate reduction, indole reduction, D-glucose fermentation, arginine dihydrolase and urease activities, and hydrolysis of gelatin and aesculin. Utilizes D-glucose, malic acid, but not D-mannose, N-glucosidase, weakly positive for starch hydrolysis, but negative for activities of alkaline phosphatase, esterase lipase (C4), lipase (C14), valine aminopeptidase, cystine aminopeptidase, trypsin, x-chymotrypsin, acid phosphatase, x-galactosidase, naphthol-AS-BI-phosphoamidase, β-galactosidase, N-acetyl-β-glucosaminidase, β-glucuronidase, β-glucosidase, x-mannosidase, β-fucosidase, nitrate reduction, indole reduction, D-glucose fermentation, arginine dihydrolase and urease activities, and hydrolysis of gelatin and aesculin. Utilizes D-glucose, arabinose, mannitol, maltose, potassium gluconate and malic acid, but not D-mannose, N-acetyl-β-glucosamine, capric acid, adipic acid, citrate or phenylacetic acid. Cannot use nitrate or nitrite as electron acceptors. The predominant ubiquinone is Q-10. The major cellular fatty acids are C10:0 3-ОH, C16:0 and summed feature 8. The DNA G+C content is 60.4–60.8 mol%. The polar lipids are phosphatidylethanolamine (PE), phosphatidylglycerol (PG), glycolipid (GL), phosphatidylincholine (PC), two unidentified aminolipids (AL1 and 2), an unidentified phospholipid (PL2) and two unidentified lipids (L2 and 2).

The type strain, caït4T (=CGMCC 1.12518T=LMG 27406T), was isolated from oil-production water of Xinjiang Oilfield, China.

Acknowledgements

We acknowledge the Institute of Microbiology, Chinese Academy of Sciences, for help with transmission electron microscopy. This study was supported by National Natural Science Foundation of China (31225001), and the National High Technology Research and Development Program (863 Project: 2012AA02A703).

References


Defluviimonas alba sp. nov.


