**Cellulomonas carbonis** sp. nov., isolated from coal mine soil

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A Gram-positive, aerobic, motile, rod-shaped bacterium, designated strain T26\(^T\), was isolated from subsurface soil of Tianjin coal mine, China. Colonies were yellow–white, convex, circular, smooth and non-transparent on R2A agar. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain T26\(^T\) was closely related to members of the genus *Cellulomonas* and a member of the genus *Actinobacillus* with 96.8–94.7 % and 96.7 % gene sequence similarities, respectively. The peptidoglycan type of strain T26\(^T\) was A4\(\beta\), containing L-ornithine–D-glutamic acid as the interpeptide bridge. The cell-wall sugars were rhamnose, galactose, xylose and inositol. The major fatty acids (>10 %) were anteiso-C\(_{15:0}\) (33.6 %), anteiso-C\(_{15:1}\) A (22.1 %), C\(_{16:0}\) (14.4 %) and C\(_{14:0}\) (12.1 %). The predominant respiratory quinone was MK-9(H4) and the genomic DNA G+C content was 74.4 mol%. The major polar lipids were diphosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidic acid (D-Asp) (for *C. flavigena*), PG (for *C. bogoriensis* and *C. phragmiteti*). The diagnostic diamino acid in position 3 of the peptidoglycan is ornithine (Orn) with the interpeptide bridge containing either D-aspartic acid (D-Asp) (for *C. flavigena*, *C. persica*, *C. iranensis* and *C. phragmiteti*) or D-glutamic acid (D-Glu) (for all the other 13 species) (Stackebrandt et al., 2006).

The polar lipids have been reported for six species of the genus *Cellulomonas* and included diphosphatidylglycerol (DPG) and phosphatidyglycerol (PG) (for *C. aerilata* and *C. citrullina*), PG (for *C. bogoriensis*), DPG, phosphatidylinositol (PI) and phosphatidylethanolamine (PE) (for *C. composti*), DPG and PI (for *C. flavigena*) and DPG, PI, PE (for *C. terrae*). In recent years, a strain previously identified as *Cellulomonas fermentans* (Bagnara et al., 1985) (Funke et al., 1995), a decayed elm tree (Rivas et al., 2004), sediment (Jones et al., 2005), soil (Lee et al., 2008) and reed periphyton (Rusznyák et al., 2011), respectively. The typical characteristics of members of the genus *Cellulomonas* include rhamnose (Rha) as the major cell-wall sugar in most of the strains, except for *C. gelida*, *C. uda*, *C. composti* (Kang et al., 2007) and *C. aerilata* (Lee et al., 2008). Other diagnostic characteristics for the genus *Cellulomonas* include rhamnose and sedoheptulose (Rha–Sed) as the major cell-wall sugars in most of the strains, except for *C. gelida*, *C. uda*, *C. composti* (Kang et al., 2007) and *C. aerilata* (Lee et al., 2008). The diagnostic diamino acid in position 3 of the peptidoglycan is ornithine (Orn) with the interpeptide bridge containing either D-aspartic acid (D-Asp) (for *C. flavigena*, *C. persica*, *C. bogoriensis*, *C. iranensis* and *C. phragmiteti*) or D-glutamic acid (D-Glu) (for all the other 13 species) (Stackebrandt et al., 2006). The polar lipids have been reported for six species of the genus *Cellulomonas* and included diphosphatidylglycerol (DPG) and phosphatidyglycerol (PG) (for *C. aerilata* and *C. citrullina*), PG (for *C. bogoriensis*), DPG, phosphatidylinositol (PI) and phosphatidylethanolamine (PE) (for *C. composti*), DPG and PI (for *C. flavigena*) and DPG, PI, PE (for *C. terrae*). In recent years, a strain previously identified as *Cellulomonas fermentans* (Bagnara et al., 1985)
Strain T26T was isolated from subsurface soil collected from Tianjin coal mine (39°01′ 49.77″ N 117°11′ 20.20″ E) in Tianjin city, China. The soil texture was of a sandy type with a pH of 7.5. The total soil C, N, P, S and NO3 concentrations were 20.68, 47.44, 2.21, 0.41, 1.61 and 37.83 g kg\(^{-1}\), respectively. Bacteria were isolated using chemically defined (CDM) medium (1 L\(^{-1}\): MgSO4\(\cdot\)7H\(_2\)O, 2.0 g; NH\(_4\)Cl, 1.0 g; Na\(_2\)SO\(_4\), 1.0 g; K\(_2\)HPO\(_4\), 0.013 g; CaCl\(_2\), 2H\(_2\)O, 0.067 g; Na\(_2\)HPO\(_4\), 5.0 g; FeSO\(_4\)\(\cdot\)7H\(_2\)O, 0.033 g; NaHCO\(_3\), 0.798 g and 15.0 g agar, pH 7.2, Weeger et al. (1999) and about 10\(^5\) c.f.u. g\(^{-1}\) soil were obtained. A total of 11 different bacterial strains were isolated. Based on partial 16S rRNA gene (about 1300 bp) sequences, they were pre-identified as *Rhodococcus* sp. T1 (GenBank accession no. HQ727997, 99.8%), *Bacillus* sp. T8 (HQ735298, 100%), *Pseudomonas* sp. T10 (HQ735299, 99.9%), *Pseudomonas* sp. T11 (HQ735300, 99.4%), *Streptomyces* sp. T13 (HQ735301, 100%), *Pseudomonas* sp. T16 (HQ735302, 99.9%), *Hydrogenophaga* sp. T19 (HQ735303, 99.3%), *Pseudomonas* sp. T22 (HQ735304, 99.1%), *Cellulomonas* sp. T26\(^T\) (HQ702749, 96.8%), *Bacillus* sp. T31 (HQ735305, 100%) and *Enisfer* sp. T32 (HQ735306, 100%). Strain T26\(^T\) was chosen for further study due to its potential novelty.

For analyses of morphological, physiological and biochemical characteristics, strain T26\(^T\) and four reference strains, *C. cellasea* DSM 20118\(^T\), *C. bogoriensis* DSM 16987\(^T\), *C. flavigena* DSM 20109\(^T\) and *A. fermentans* DSM 3133\(^T\), were cultivated on R2A agar or broth and incubated at 28 °C for 3 days unless otherwise stated. Cell morphology was observed using a scanning electron microscope and a transmission electron microscope (H-7650; Hitachi). Gram staining was determined using the method described by Dussault (1955). Growth at different temperatures (4, 15, 20, 28, 37, 42, 45 and 50 °C), various pH values (4.0–11.0) and NaCl (1–10 %, w/v) ranges were assessed after incubation for 7 days with shaking at 150 r.p.m. Aerobic growth was investigated on R2A agar, nutrient agar, MacConkey agar, full-strength trypticase soy agar (TSA) and Luria–Bertani (LB) agar (all from Difco). Anaerobic growth was determined by incubation in an anaerobic chamber (Mitsubishi Gas Chemical Co, Inc.) at 28 °C for 15 days on R2A agar.

Tests to determine hydrolysis of casein, gelatin, starch, Tween 80, DNA, tyrosine, urea and carboxymethyl cellulose were performed as described by Cowan & Steel (1965). Nitrile reduction was tested according to the method described by Lányi (1987). Methyl red and Voges–Proskauer tests and tests for the production of H\(_2\)S and indole were performed as recommended by Smibert & Krieg (1994). Catalase activity was determined by assessing bubble production in 3 % (v/v) H\(_2\)O\(_2\), and oxidase activity was determined using 1 % (w/v) tetramethyl-\(\beta\)-phenylenediamine (Cappuccino & Sherman, 2002). Acid production from carbohydrates was assessed using phenol red broth (Rhoades et al., 1989) and determined as described by Hinz et al. (1998). Antibiotic-susceptibility tests were performed by spreading bacterial suspensions on culture plates and applying filter-paper discs containing different antibiotics (Hangzhou Microbial Reagent Co., Ltd). Susceptibility to the antibiotic was confirmed when the inhibition zone diameter was >10 mm. Enzyme activities, other biochemical characteristics and utilization of carbohydrates were determined using API ZYM, API 20 NE and API ID 32 GN kits, respectively, according to the manufacturer’s instructions (bioMérieux). The API ZYM test strips were read after incubation at 28 °C for 5 h, the API 20 NE and API ID 32 GN tests were examined after incubation at 28 °C for 48 h and 72 h.

An almost complete 16S rRNA gene sequence was amplified as described by Fan et al. (2008) and compared with the sequences available in NCBI GenBank using BLASTN search. Multiple alignments were performed with the CLUSTAL_X program (Thompson et al., 1997). Phylogenetic analysis was performed using MEGA 4.0 (Tamura et al., 2007) and the PHYLML online web server (Guindon et al., 2005). Distances and clustering were determined using the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods with bootstrap analyses based on 1000 replications.

For cellular fatty acid analysis, strains T26\(^T\), *C. cellasea* DSM 20118\(^T\), *C. bogoriensis* DSM 16987\(^T\), *C. flavigena* DSM 20109\(^T\) and *A. fermentans* DSM 3133\(^T\) were grown on R2A broth at 28 °C. Biomass was collected in the late exponential phase and analysed by GC (6890; Hewlett Packard) according to the standard protocol of the Sherlock Microbial Identification System (MIDI Sherlock version 4.5, MIDI database TSBA40 4.10) (Kroppenstedt, 1985; Sasser, 1990). Polar lipid analysis was determined under the same experimental conditions by two dimensional TLC as described by Tindall (1990). Cell-wall peptidoglycan was analysed according to the method of Schleifer & Kandler (1972). Sugar analysis of whole cells was carried out as described by Staneck & Roberts (1974). The DNA G+C content was determined by HPLC following the method of Mesbah et al. (1989). Respiratory quinone analysis was conducted by HPLC as described by Minnikin et al. (1984).

Cells of strain T26\(^T\) were Gram-staining-positive, aerobic, motile and rod-shaped. Colonies were yellow–white, convex, circular, smooth and non-transparent after 3 days incubation on R2A agar at 28 °C. The strain grew on R2A agar, nutrient agar, full-strength TSA and LB agar, but did not...
**Table 1.** Differential phenotypic characteristics of strain T26\(^T\) and type strains of members of the genera *Cellulomonas* and *Actinotalea*

| Characteristic | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 |
| Motility      | + | + | + | + | + | + | + | + | + | + | + | - | - | - | - | + | + | + | + | + |
| Morphology    | R | P | R | R | R | R | R | R | R | R | R | R | R | R | R | R | R | CR | R | R |
| Mycelium      | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Colony colour |YW|WH|Y|Y|Y|YW|YW|YW|YW|YW|YW|YW|Y|LO|Y|PY|–|–|–|–|–|
| Nitrate reduction | ++ | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Urease        | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – |
| Aesculin      | + | + | + | + | + | + | + | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND |
| Catalase      | + | + | + | + | + | + | + | ND | ND | ND | ND | + | + | + | + | + | + | + | + | + |
| DNase         | – | – | – | – | – | – | – | – | ND | ND | ND | ND | – | – | ND | ND | ND | ND | ND | ND |
| Gelatin       | + | + | + | + | + | ND | W | W | W | W | W | W | + | + | + | + | + | + | + | + |
| Cellulolytic activity | + | + | + | + | + | ND | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Hydrolase     | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – |
| Utilization of: | | | | | | | | | | | | | | | | | | | | | |
| D-Ribose      | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – |
| L-Rhamnose    | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – | – |
| Gluconate     | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Raffinose     | W | + | + | + | + | + | + | ND | ND | ND | ND | – | – | – | – | – | – | – | – | – |
| Lactose       | + | + | + | + | + | + | + | ND | ND | ND | ND | – | – | – | – | – | – | – | – | – |
| Mannitol      | – | – | – | – | – | – | – | – | ND | ND | ND | ND | – | – | – | – | – | – | – | – |
| Acetate       | – | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Lactate       | – | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Cell-wall sugars* | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, | Rha, Rha, |
| DNA G+C content (mol%) | 74.4 | 75.8 | 75 | 71.5 | 73.8 | 73.9 | 73 | 73 | 73 | 73 | 73 | 73 | 73 | 73 | 73 | 73 | 74 | 74 | 74 | 76 | 68.5 |

*6dTal, 6-Deoxytalose; Rha, rhamnose; Gal, galactose; Xyl, xylose; Ino, inositol; Glc, glucose; Rib, ribose; Man, mannose; GlcN, glucosamine; Fuc, fucose.

†Data that were different to those found in previous studies.
grow on MacConkey agar. Detailed results of the morpho-
logical, physiological and biochemical characteristics are given
in the species description. A scanning electron and transmis-
sion electron micrographs showing the general morphology of
cells of strain T26T are available as Fig. S1a and b, respectively.
The main phenotypic differences between strain T26T and
closely related type strains are shown in Table 1.

The 1442 bp 16S rRNA gene sequence of strain T26T was
analysed to determine the phylogenetic position of the
novel strain. Strain T26T shared gene sequence similarities
of 96.8–94.7% with other species of the genus Cellu-
lononas and a member of the genus Actinotalea. Strain
T26T showed the highest 16S rRNA gene sequence simi-
larities with C. cellasea DSM 20118T (96.8 %), A. fermentans
DSM 3133T (96.7 %), C. hominis DMMZ CE40T (96.6 %), C.
denverensis W6929T (96.5 %) and C. bogoriensis 69B4T
(96.4 %). A phylogenetic tree constructed using the
neighbour-joining algorithm showed that strain T26T was
always very closely associated with C. bogoriensis 69B4T;
other species of the genus Cellulomonas fell into other nearby
clusters, but all in a large cluster (Fig. 1). This cluster also
included four strains of the genus Oerskovia and
Paraerskovia marina CTT-37T; however, strain T26T was
distinct from members of the genus Oerskovia based on the
peptidoglycan structure (see below). In addition, P. marina
CTT-37T could be distinguished from strain T26T on the
basis of the cellular fatty acid content and peptidoglycan
structure (Khan et al., 2009). The maximum-parsimony
and the maximum-likelihood trees (Fig. S2a, b) also supported
the phylogenetic position obtained with the neighbour-
joining algorithm.

Fig. 1. A neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain T26T.
Bootstrap values (>70%) based on 1000 replications are shown at branch nodes. Bar, 10 substitutions per 1000 nt.
Strain T26<sup>T</sup> gave a negative result in tests for urease activity but a positive result for the hydrolysis of carboxymethyl cellulose and aesculin. The major cellular fatty acids (>10%) were anteiso-C<sub>15:0</sub> (33.6%), anteiso-C<sub>15:1</sub> A (22.1%), C<sub>16:0</sub> (14.4%) and C<sub>14:0</sub> (12.1%) on R2A medium (details are shown in Table 2). The fatty acid profile of the novel strain was very similar to that of the type species of the genus *Cellulomonas*, *C. flavigena* DSM 20109<sup>T</sup>. The major respiratory quinone was MK-9(H<sub>4</sub>) (Fig. S3), which was the same as that of members of the genus *Cellulomonas* and was different from *A. fermentans* which contained MK-10(H<sub>4</sub>) as the major respiratory quinone (Yi et al., 2007). Strain T26<sup>T</sup> exhibited similar major polar lipids, DPG and PG, when compared with other type strains of the genus *Cellulomonas*. In addition, strain T26<sup>T</sup> also contained phosphatidylinositol mannosides (PIM), phosphatidylinositol (PI), an unknown phospholipid (PL) and an unknown phosphoglycolipid (PGL) (Fig. S4). *C. cellasea* DSM 20118<sup>T</sup> and *C. bolgiensis* DSM 16987<sup>T</sup> and *A. fermentans* DSM 3133<sup>T</sup> were analysed in this study and showed very similar polar lipids to strain T26<sup>T</sup> (Fig. S4). The polar lipid data and 16S rRNA gene sequence phylogenies of both strain T26<sup>T</sup> and *C. bolgiensis* DSM 16987<sup>T</sup> were consistent with their assignment to the genus *Cellulomonas*. The DNA G+C content of strain T26<sup>T</sup> was 74.4 mol%. The cell-wall peptidoglycan type was A4<sub>4β</sub>, containing L-Orn–D-Glu. The cell-wall sugars were rhamnose (80.9%), galactose (3.3%), xylose (5.3%) and inositol (6.3%). All of these results for strain T26<sup>T</sup> were very similar to those of the type species of the genus *Cellulomonas*, *C. flavigena* DSM 20109<sup>T</sup>, and to other species of the genus. Strain T26<sup>T</sup> could be differentiated from members of the genera *Actinotalea* and *Oerskovia* on the basis of differences in the respiratory quinone [MK-9(H<sub>4</sub>) vs MK-10(H<sub>4</sub>)] and peptidoglycan type (L-Orn–D-Glu vs L-Lys–L-Thr←D-Asp or L-Lys–L-Thr←D-Glu), respectively.

On the basis of the close relationship and distinctive phenotypic and phylogenetic differences between strain T26<sup>T</sup> and other closely related species, it is proposed that strain T26<sup>T</sup> represents a novel species of *Cellulomonas*, with the name *Cellulomonas carbonis* sp. nov.

**Description of *Cellulomonas carbonis* sp. nov.**

*Cellulomonas carbonis* (car.bo'nis. L. gen. n. carbonis of coal, of charcoal).

Cells are Gram-positive-staining, aerobic, motile and rod-shaped (0.5–0.8 × 2.0–2.4 µm). Colonies are yellow–white, convex, circular, smooth and non-transparent after incubation on R2A agar at 28 °C for 3 days. Grows on R2A agar, nutrient agar, full-strength TSA and LB agar, but does not grow on MacConkey agar. Temperature range for growth is 4–45 °C, and optimal temperature for growth is 28 °C. Growth occurs with NaCl concentrations in the range 0–7% and with pH 6–10 (optimum, pH 7.0). Catalase-positive and oxidase-negative. Positive in tests for β-galactosidase activity but negative result for arginine dihydrolase and urease. Hydrolyses carboxymethyl cellulose, starch, gelatin, aesculin, but not DNA, casein,

### Table 2. Cellular fatty acid contents (%) of strain T26<sup>T</sup> and some type strains of members of the genera *Cellulomonas* and *Actinotalea*

<table>
<thead>
<tr>
<th>Fatty acid</th>
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<th>10</th>
<th>11</th>
<th>12</th>
<th>13</th>
<th>14</th>
<th>15</th>
<th>16</th>
<th>17</th>
</tr>
</thead>
<tbody>
<tr>
<td>C&lt;sub&gt;13:0&lt;/sub&gt;</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>1.8</td>
<td>1.0</td>
<td>2.0</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
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<td>–</td>
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</tr>
<tr>
<td>anteiso-C&lt;sub&gt;13:0&lt;/sub&gt;</td>
<td>1.2</td>
<td>2.5</td>
<td>1.1</td>
<td>1.0</td>
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<td>–</td>
<td>–</td>
<td>–</td>
<td>1.3</td>
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<tr>
<td>C&lt;sub&gt;14:0&lt;/sub&gt;</td>
<td>12.1</td>
<td>20.4</td>
<td>4.1</td>
<td>9.6</td>
<td>12.1</td>
<td>8.0</td>
<td>4.0</td>
<td>4.0</td>
<td>4.0</td>
<td>4.0</td>
<td>7.3</td>
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<td>4.6–4.8</td>
<td>–</td>
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<td>3.9</td>
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<td>7.9</td>
<td>10.8</td>
<td>3.4</td>
<td>1.0</td>
<td>2.0</td>
<td>2.0</td>
<td>8.9</td>
<td>4.6</td>
<td>5.1–5.9</td>
<td>7.8–8.9</td>
<td>7.7–9.6</td>
<td>3.0</td>
<td>–</td>
<td>5.1</td>
<td>1.6</td>
<td>–</td>
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<td>–</td>
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<td>4.1</td>
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<td>–</td>
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<td>2.1</td>
<td>–</td>
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<td>1.9–2.6</td>
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<td>–</td>
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<td>6.8</td>
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<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
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<td>4.0</td>
<td>4.0</td>
<td>7.4</td>
<td>–</td>
<td>15.2–18.5</td>
<td>10.9–12.2</td>
<td>18.6–22.1</td>
<td>3.0</td>
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<td>34</td>
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<td>43.0</td>
<td>43.0</td>
<td>41.2</td>
<td>44.9</td>
<td>44.5–45.6</td>
<td>32.8–44.1</td>
<td>40.1–45.5</td>
<td>61.3</td>
<td>44.0</td>
<td>49.7</td>
<td>37.8</td>
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<td>27.6</td>
<td>5.2</td>
<td>30.5</td>
<td>12.6</td>
<td>16.0</td>
<td>17.0</td>
<td>17.0</td>
<td>9.6</td>
<td>12.7</td>
<td>8.0–9.5</td>
<td>11.2–12.8</td>
<td>9.5–10.6</td>
<td>2.9</td>
<td>14.6</td>
<td>20.0</td>
<td>23.3</td>
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<tr>
<td>iso-C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>6.1</td>
<td>6.2</td>
<td>9.6</td>
<td>2.1</td>
<td>1.5</td>
<td>3.0</td>
<td>3.0</td>
<td>3.0</td>
<td>8.8</td>
<td>7.6</td>
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<td>1.8–2.7</td>
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<td>1.2</td>
<td>–</td>
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<td>0.8–1.6</td>
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<td>3.9</td>
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<td>7.0</td>
<td>7.0</td>
<td>7.0</td>
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<td>–</td>
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<td>3.0</td>
<td>1.0</td>
<td>1.0</td>
<td>1.9</td>
<td>5.4</td>
<td>7.1–8.2</td>
<td>0.8–1.8</td>
<td>10.7–13.0</td>
<td>3</td>
<td>7.9</td>
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tyrosine or Tween 80. Does not produce indole from tryptophan, but H₂S is produced from cysteine and NH₃ is produced from peptone. Positive in tests for nitrate reduction but negative result in methyl-red and Voges–Proskauer tests. Assimilates D-glucose, L-arabinose, mannose, N-acetylglucosamine, maltose, gluconate, sucrose, glycogen, salicin, melibiose, D-sorbitol, xylose, lactose, D-galactose, D-fructose and raffinose. Does not assimilate L-rhamnose, D-ribose, inositol, mannitol, L-fucose, L-serine, L-proline, L-alanine, L-histidine, capric acid, adipic acid, malic acid, citric acid, phenylacetic acid, trisodium citrate, itaconic acid, suberate, sodium malonate, sodium acetate, lactate, propionate, caprate, valerate, potassium 5-ketogluconate, 3-hydroxybenzoate, potassium 2-ketogluconate, 3-hydroxybutyrate or 4-hydroxybenzoate (API 20NE and API ID 32 GN). In API ZYM tests, positive result for esterase (C4), acid phosphatase, ß-galactosidase, ß-glucosidase, naphthol-AS-BI-phosphohydrolase, N-acetyl-ß-glucosaminidase and leucine arylamidase activities, but negative result for alkaline phosphatase, esterase (C4), acid phosphatase, ß-glucosidase, ß-glucuronidase and ß-mannosidase. Acid is produced from D-glucose, cellubiose, D-fructose, D-mannose, D-galactose, maltose, sucrose, D-xylene, trehalose, lactose, raffinose, turanose, L-arabinose, D-sorbitol, melibiose and N-acetylglucosamine, but not from D-mannitol, D-ribose, D-arabinose, inositol, L-sorbose, melezitose, L-rhamnose, ribitol or propylene glycol. Sensitive to polyoxin B (25 µg), novobiocin (5 µg), teicoplanin (30 µg), cefalotin (30 µg), chloramphenicol (30 µg), rifampicin (5 µg), ampicillin (10 µg), carbenicillin (100 µg), lincomycin (2 µg), cephalexin (10 µg), tetracycline (10 µg), amoxicillin (30 µg), ofloxacin (5 µg), norfloxacin (10 µg), erythromycin (15 µg), minocin (30 µg), oxacillin (10 µg), clindamycin (30 µg) and nitrofurantoin (300 µg). The peptidoglycan type is A1α, containing 1-ornithine–d-glutamic acid. Cell-wall sugars are rhamnose, galactose, xylose and inositol. Major fatty acids are anteiso-C₁₅:0, C₁₆:0, C₁₄:0 and anteiso-C₁₅:1 A. The major respiratory quinone is MK-9(H₄). Major polar lipids are DPG, PG, PIM and PI.

The type strain, T26T (=CGMCC 1.10786T=KCTC 19824T =CCTCC AB2010450T), was isolated from coal mine soil from Tianjin, China. The G+C content of the genomic DNA of the type strain is 74.4 mol%.

Acknowledgements

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References


