Pelagibacterium halotolerans gen. nov., sp. nov. and Pelagibacterium luteolum sp. nov., novel members of the family Hyphomicrobiaceae

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Two Gram-negative, motile, aerobic bacterial strains, designated B2T and 1_C16_27T, were respectively isolated from a seawater sample collected from the East China Sea and a semi-coke sample from north-eastern Estonia. Their genetic, phenotypic and chemotaxonomic properties were studied. The isolates were short rods with polar flagella and were positive for catalase and oxidase activities. Q-10 was the predominant respiratory ubiquinone. The major polar lipids were phosphatidylglycerol, diphosphatidylglycerol and two unidentified glycolipids. The major fatty acids were nonadecanoic (C19 : 0cyclo), octadecanoic (C18 : 0and C18 : 03-OH), octadecenoic (C18 : 1) and hexadecanoic (C16 : 0) acids. The G+C content of the genomic DNA was 58.1–59.3 mol%. 16S rRNA gene sequence analysis revealed that the two isolates represent a distinct lineage within the family Hyphomicrobiaceae. The phylogenetically closest relatives were Cucumibacter (92.7–93.7 % 16S rRNA gene sequence similarity), Devosia (92.9–94.4 %) and Zhangella (91.7–92.1 %). Differential phenotypic properties, together with phylogenetic and genetic distinctiveness, revealed that strains B2T and 1_C16_27T could be differentiated from each other and from members of the genera Cucumibacter, Devosia and Zhangella. Therefore, it is proposed that strains B2T and 1_C16_27T represent two novel species in a new genus, for which the names Pelagibacterium halotolerans gen. nov., sp. nov. (the type species; type strain B2T =CGMCC 1.7692T =JCM 15775T) and Pelagibacterium luteolum sp. nov. (type strain 1_C16_27T =CGMCC 1.10267T =JCM 16552T =CELMS EEUT 1C1627T) are proposed.

The family Hyphomicrobiaceae, class Alphaproteobacteria, comprises a morphologically and metabolically heterogeneous group of micro-organisms (Garrity et al., 2005). The establishment of the family Hyphomicrobiaceae was based mainly on phylogenetic relationships of 16S rRNA gene sequences (Garrity et al., 2005; Lee et al., 2005). At the time of writing, the family encompassed 18 genera: Ancalomicrobium, Angulamicrobium, Aquabacter, Blastochloris, Cucumibacter, Devosia, Dichotomicrobium, Filomicrobium, Gemmiger, Hyphomicrobium, Maritalea, Methylorhabdus, Pedomicrobium, Prosthecomicrobium, Rhodomicrobium, Rhodoplanes, Seliberia and Zhangella (Euzéby, 1997).

Most species within the family Hyphomicrobiaceae have been isolated from various non-marine habitats (freshwater, soil, plant roots, sewage, swamps, activated sludge, chicken, saline pond and lake sediment, etc.). Only a few have been isolated from offshore seawater: Cucumibacter marinus, Filomicrobium fusiforme, Hyphomicrobium aestuarii and

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains B2T and 1_C16_27T are EU709017 and EF540455, respectively.

Four supplementary figures and a supplementary table are available with the online version of this paper.

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_Zhangella mobilis_ (Gliesche _et al._, 2005; Schlesner, 2005; Hwang & Cho, 2008; Xu _et al._, 2009). In this paper, we present a polyphasic study describing two novel chemo-
heterotrophic bacteria, isolated from a seawater sample off the
Chinese coast and a semi-coke sample from Estonia, which
belong to this family.

A sample was collected from the East China Sea (30° 58′
16° N 125° 59′ 24″ E) from a depth of 70 m (temperature
16.7 °C; salinity 33.95 %). Approximately 100 μl seawater
was plated on marine agar 2216 (MA). After 3 days of
aerobic incubation at 30 °C, one light-yellowish colony,
designated 
1_C16_27T, was picked. Strain 1_C16_27T was isolated
from a sample collected from an oil shale chemical industry
solid waste (semi-coke) depository area in north-eastern
Estonia (59° 23′ 44″ N 27° 13′ 05″ E) in October 2003. Ten
subsamples of semi-coke from a depth of 5–15 cm were
taken with a soil corer and then mixed to form a composite
sample. Microbial cells were suspended from the soil
sample into sterile 0.9 % NaCl solution by vortexing. After
setting of the soil particles, 100 μl of the clear supernatant
was plated onto minimal medium agar plates (M9 salts
supplemented with trace elements) with hexadecane as the
sole carbon and energy source (a piece of filter paper,
soaked with hexadecane, was placed inside the cover lid of
the agar plate) (Truu _et al._, 2003). After a week of aerobic
incubation at 22 °C, one yellowish colony, designated
1_C16_27T, was picked. The two strains were purified by
repeated restreaking; purity was confirmed by the unifor-
mity of cell morphology. Unless otherwise stated, strains
B2T and 1_C16_27T were maintained in yeast extract broth
(YEB; basal medium supplemented with 5 g yeast extract
and 8.3 g NaCl 1−1) (Mikhailov _et al._, 2006). The basal
medium (BM) contained (per l distilled water) 1.0 g
NH4Cl, 0.044 g K2HPO4, 0.028 g FeSO4 .7 H2O, 500 ml
artificial seawater and 50 ml Tris/HCl (1 M, pH 7.5). The
artificial seawater contained (per l distilled water) 23.4 g
artificial seawater and 50 ml Tris/HCl (1 M, pH 7.5). The
corresponding filter-sterilized sugar
(1.5 % (w/v) NaCl. The corresponding filter-sterilized sugar
(0.2 %), alcohol (0.2 %), organic acid (0.1 %) or amino acid
(0.1 %) was added to liquid medium. Acid production was
tested by using modified MOF medium supplemented with
1 % sugars or alcohols (Leifson, 1963; Xu _et al._, 2008).

Nitrate reduction, gluconate oxidation, lecithinase and
urease activities and the ability to hydrolyse aesculin, casein,
DNA, gelatin and Tweens 40, 60 and 80 were determined
according to Dong & Cai (2001). Susceptibility to antibiotics
was detected on marine 2216 agar (MA; BD) or PYM agar
plates using antibiotic discs containing the following
amounts (μg unless otherwise stated): amoxicillin (10),
ampicillin (10), bacitracin (0.04 IU), cefoxime (30),
cefotaxin (30), chloramphenicol (30), erythromycin (15),
kanamycin (30), neomycin (30), nitrofurantoin (300),
novobiocin (30), nystatin (100), penicillin (10), polymyxin
(300 IU), rifampicin (5), streptomycin (10), tetracycline
(30) and tobramycin (10). Additional enzyme activities
and biochemical characteristics were determined by using API 20
NE and API ZYM kits at 30 °C as recommended by the
manufacturer (bioMérieux).

Isoprenoid quinones were analysed as described previously
(Komagata & Suzuki, 1987) by reversed-phase HPLC. Fatty
acid methyl esters obtained from cells grown on MA at
30 °C were analysed according to the instructions of the
Microbial Identification System (MIDI; Microbial ID).

Polar lipids were extracted using a chloroform/methanol
system and separated by two-dimensional TLC using silica
gel 60 F254 aluminium-backed thin-layer plates (Merck)
(Kates, 1986). The solvent systems chloroform/methanol/ water
(65:24:4, by vol.) and chloroform/glacial acetic acid/methanol/water
(80:12:13:4, by vol.) were used in
the first and second dimensions. Separated components
were visualized by treating the plates with 10 % (w/v)
molybdoadiphosphoric acid followed by heating at 150 °C
for 5 min. Genomic DNA was obtained using the method
described by Marmur (1961). The purified DNA was
hydrolysed with P1 nuclease and the nucleotides were
dephosphorylated with calf intestine alkaline phosphatase
(Mesbah & Whitman, 1989). The G+C content of the result-
ing deoxyribonucleosides was determined by
reversed-phase HPLC and calculated from the ratio of
deoxyguanosine (dG) and thymidine (dT) (Mesbah &
Whitman, 1989).

The 16S rRNA gene was amplified and analysed as described
previously (Xu _et al._, 2007). Sequence data were aligned with
CLUSTAL W 1.8 (Thompson _et al._, 1994). The sequence was
compared with closely related sequences of reference
organisms from the EzTaxon service (Chun _et al._, 2007).
Phylogenetic trees were constructed by the neighbour-
joining (Saitou & Nei, 1987) and maximum-parsimony
(Fitch, 1971) methods with the MEGA 4 program package
(Tamura _et al._, 2007) and the maximum-likelihood method
(Felsenstein, 1981) with the TreePuzzle 5.2 program.

Evolutionary distances were calculated according to the
algorithm of Kimura’s two-parameter model (Kimura,
1980) for the neighbour-joining method.
The two isolates were Gram-negative, rod-shaped, motile, oxidase-positive and possessed Q-10 as the predominant quinone. Cell division occurred by binary fission. Electron micrographs of negative stained cells did not reveal prosthetae (Supplementary Fig. S1, available in IJSEM Online). Other physiological and chemotaxonomic characteristics of strains B2T and 1_C16_27T are summarized in the species descriptions. Phenotypic characteristics that serve to differentiate the two strains from their closest phylogenetic relatives are listed in Table 1.

16S rRNA gene sequence comparisons to representative bacteria with validly published names indicated that strains B2T and 1_C16_27T were affiliated with the family *Hyphomicrobiaceae*. Based on analysis by the EzTaxon service, the two strains were related most closely to type strains of the genera *Devosia* (92.9–94.4 % similarity), *Zhangella* (91.7–92.1 %) as well as *Prosthecococcus pneumoniae* (93.1–93.2 %), and they showed <90 % sequence similarity to other described species of the *Hyphomicrobiaceae*. Phylogenetic trees constructed with all three treeing methods indicated that the two strains clustered with the genera *Cucumibacter* and *Zhangella* (Fig. 1 and Supplementary Figs S2 and S3). Within this cluster, strain B2T was found to be closely related to strain 1_C16_27T, as supported by a high bootstrap resampling value (99 % by the neighbor-joining method) (Fig. 1). Therefore, the relatively low sequence similarities between strains B2T and 1_C16_27T and their phylogenetic neighbours indicate strongly that these two strains are members of a new genus in the family *Hyphomicrobiaceae*.

The dominant fatty acid for strains B2T and 1_C16_27T was C18:1ω7c, characteristic of the vast majority of species within the *Alphaproteobacteria*. The relative amounts of C19:0 cyclo ω8c, 11-methyl C18:1ω7c and C18:1ω10c varied according to the age of the culture (Supplementary Table S1). The respective contents of C18:1ω7c of strains B2T and 1_C16_27T decreased from 61.3 and 75.3 % after 1 day to 58.0 and 74.6 % after 2 days and 12.1 and 59.0 % after 3 days. The proportions of C19:0 cyclo ω8c and 11-methyl C18:1ω10c increased accordingly. Together, C19:0 cyclo ω8c, 11-methyl C18:1ω7c and C18:1ω10c made up 67–83 % of the total fatty acids of strains B2T and 1_C16_27T. In general, the percentages of unsaturated fatty acids of strains B2T (68.2–75.3 %) and 1_C16_27T (68.2–80.4 %) were close to that of *Zhangella mobilis* CGMCC 1.7002T (71.8–83.5 %) and were greater than those of *Cucumibacter marinus* DSM 18995T, *Devosia riboflava* DSM 7230T and *Devosia geojensis* DSM 19414T (42.0–62.5 %). 10-Methyl C19:0 was detected in extracts of strains B2T and 1_C16_27T but not in the four reference strains; iso-C19:0 was detected extracts from 2- and 3-day cultures of *C. marinus* DSM 18995T and *Z. mobilis* CGMCC 1.7002T but was absent in strains B2T and 1_C16_27T.

The results of two-dimensional TLC analysis of polar lipids extracted from strains B2T and 1_C16_27T as well as three

### Table 1. Taxonomic characteristics that differentiate strains B2T and 1_C16_27T from related members of the family *Hyphomicrobiaceae*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<td>Colony colour</td>
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<td>Y</td>
<td>C</td>
<td>PY</td>
<td>C</td>
<td>WH</td>
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<tr>
<td>Growth at 10 % NaCl (w/v)</td>
<td>++</td>
<td>+</td>
<td>++</td>
<td>–</td>
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<td>–</td>
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<tr>
<td>Nitrate reduction</td>
<td>–</td>
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<td>++</td>
<td>–</td>
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<tr>
<td>Urease</td>
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<tr>
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<tr>
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<td>Rhamnose</td>
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<td>–</td>
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<td>Sensitivity to:</td>
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<td>Neomycin (30 μg)</td>
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<tr>
<td>Novobiocin (30 μg)</td>
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<td>+</td>
<td>+</td>
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<td>API ZYM results</td>
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<td>Alkaline phosphatase</td>
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<td>z-Chymotrypsin</td>
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<td>W</td>
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<td>Cystine arylamidase</td>
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<td>+</td>
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<td>β-Galactosidase</td>
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<td>z-Glucoamidase</td>
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<td>Tryptophase</td>
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<td>DNA G+C content (mol%)</td>
<td>59.3</td>
<td>58.1</td>
<td>62.9a</td>
<td>53.1b</td>
<td>61.4e</td>
<td>60.8d</td>
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</table>

* a, Cream; LY, light yellow; PY, pale yellow; WH, white; Y, yellow.
† Data from: a, Hwang & Cho (2008); b, Xu et al. (2009); c, Nakagawa et al. (1996); d, Ryu et al. (2008).
reference strains, *C. marinus* DSM 18995^T^, *D. geojensis* DSM 19414^T^ and *Z. mobilis* CGMCC 1.7002^T^, are shown in Supplementary Fig. S4. The polar lipid profiles of all five strains were dominated by phosphatidylglycerol, diphosphatidylglycerol and two unidentified glycolipids (GL1 and GL3). Strains B2^T^ and 1_C16_27^T^ did not contain relatively large amounts of unknown lipid L16, in marked contrast to the phylogenetically related genera *Cucumibacter* and *Zhangella*. Seven polar lipids (L1, L2, L3, L5, L6, L8 and L11) were detected in both strains B2^T^ and 1_C16_27^T^ in minor amounts. Four of them (L2, L3, L6 and L8) were also found in the three reference strains, but L5 and L11 are characteristic lipids of strains B2^T^ and 1_C16_27^T^.

In addition, L15, found in the three reference strains, was not detected in strains B2^T^ and 1_C16_27^T^, and 10-Methyl C19:0 was found in both strains B2^T^ (0.6–0.9 %) and 1_C16_27^T^ (0.3–0.4 %), but not in related organisms (Supplementary Table S1). In addition to these differences, some phenotypic characteristics of strain B2^T^ and 1_C16_27^T^, e.g., β-galactosidase, hydrolysis of casein and utilization of gluconate, distinguish the two novel isolates from the previously described species *C. marinus*, *Z. mobilis*, *D. riboflavina* and *D. geojensis* (Table 1). Therefore, chemotaxonomic and physiological features suggest that strains B2^T^ and 1_C16_27^T^ represent a novel genus of the family *Hyphomicrobiaceae*. The main respiratory quinone of strains B2^T^ and 1_C16_27^T^ was Q-10 (94.2 and 96.2 %, respectively), while Q-9 was a minor component (5.8 and 3.8 %, respectively).

Strains B2^T^ and 1_C16_27^T^ could be differentiated from each other by their fatty acid compositions and a number of phenotypic characteristics (Table 1) and on the basis of their 16S rRNA gene sequences. The total content of C19:0 cyclo ω8c, 11-methyl C18:1ω7c and C18:1ω9c of strain B2^T^ (66.8–73.3 %) was lower than that of strain 1_C16_27^T^ (78.1–79.0 %) grown under the same conditions. The two strains could also be distinguished by their different abilities to produce acid from rhamnose, their NaCl range for growth, utilization of lactose, susceptibility to kanamycin and enzyme activities such as alkaline phosphatase, α-glucosidase and trypsin (Table 1). The 16S rRNA gene sequence divergence between strain B2^T^ and 1_C16_27^T^ was 3.4 %, which exceeded the commonly accepted threshold of 3 % for the distinction of different genomic species (Stackebrandt & Goebel, 1994). On the basis of the physiological and chemotaxonomic characteristics presented and 16S rRNA gene sequence comparisons, it is proposed that strains B2^T^ and 1_C16_27^T^ represent two novel species in a new genus, for which the names *Pelagibacterium halotolerans* gen. nov., sp. nov. and *Pelagibacterium luteolum* sp. nov. are proposed.

**Description of *Pelagibacterium* gen. nov.**

*Pelagibacterium* (Pe.la.gi bac.te.ri.um. L. n. pelagus the sea; N.L. n. bacterium from Gr. n. bakterion a small rod; N.L. neut. n. Pelagibacterium a rod isolated from the sea).

Gram-negative, non-spore-forming bacteria. Divide by binary division. Motile. Catalase- and oxidase-positive. Aerobic chemoheterotrophs. Major polar lipids are phosphatidylglycerol, diphosphatidylglycerol and two unidentified glycolipids. Small amounts of seven unidentified lipids (L1, L2, L3, L5, L6, L8 and L11) are detected. Major fatty acids include nonadecanoic (C19:0 cyclo), octadecanoic (C18:0) and 11-methyl C18:1ω7c and C18:1ω9c of strain B2^T^. The G+C content of the genomic DNA is 58.1–59.3 mol%. Belongs to the class *Alphaproteobacteria*. Analysis of 16S rRNA gene sequences, showing the phylogenetic relationships of the novel isolates and related members of the *Hyphomicrobiaceae*. Bootstrap values are based on 1000 replicates; values >50 % are shown. Filled circles indicate nodes recovered in both maximum-likelihood and maximum-parsimony trees. Bar, 0.02 substitutions per nucleotide position.
sequences showed that Pelagibacterium species are most closely related to the members of the genera Cucumibacter, Devosia and Zhangella. The type species is Pelagibacterium halotolerans.

**Description of Pelagibacterium halotolerans sp. nov.**

Pelagibacterium halotolerans (ha.lo.to’le.rans. Gr. n. hals, halos salt; L. part. adj. tolerans tolerating; N.L. part. adj. halotolerans salt-tolerating, referring to the organism’s ability to tolerate high salt concentrations).

Cells are 0.4–0.6 μm wide and 2–3 μm long. Motile by means of several polar flagella. Young cultures consist of slightly curved rods. Colonies are 1–2 mm in diameter, circular, smooth, elevated, semi-transparent and light yellowish after 3 days at 30 °C. Growth occurs at 0–13.0 % (w/v) NaCl, with optimum growth at 3.0–4.0 % (w/v). Grows at pH 6.0–9.5 and 10–42 °C (optimum growth at pH 7.0 and 30 °C). Nitrate is not reduced. Aesculin and casein are hydrolysed. Gelatin, DNA, starch and Tweens 40, 60 and 80 are not hydrolysed. Glucanase oxidation, glucose fermentation, β-galactosidase and urease activities are positive. Negative for arginine dihydrolase, indole production and lecithinase. The following substrates are utilized for growth: acetate, L-alanine, cellobiose, citrate, ethanol, D-galactose, glucosone, glucose, glycerol, L-glutamine, myo-inositol, lactate, malate, malonic acid, mannitol, D-mannose, L-ornithine, pyruvate, ribose, rhamnose, salinic acid, L-arginine, succinates, sucrose, trehalose and D-xylose. The following compounds are not utilized as sole carbon sources: L-aspartate, L-asparagine, L-arabinose, L-asparagine, L-aspartyte, cellobiose, citrate, ethanol, D-galactose, glucosone, glucose, glycerol, L-glutamine, myo-inositol, lactate, malate, malonic acid, mannitol, D-mannose, L-ornithine, pyruvate, ribose, rhamnose, salinic acid, L-arginine, succinates, sucrose, trehalose and D-xylose. The following compounds are not utilized as sole carbon sources: L-arginine, L-cysteine, glycine, formate, fumarate, L-histidine, isoleucine, lactose, L-lysine, malonic acid, L-methionine, propionate, raffinose, sorbitol and sorbose. Acid is produced from L-arabinose, ethanol, D-galactose, glucose, glycerol, inositol, malose, mannitol, D-mannose, ribose, rhamnose, salinic acid, sucrose, trehalose and D-xylose. Susceptible to (μg per disc unless otherwise stated) amoxicillin (10), ampicillin (10), bacitracin (0.04 IU), cefotaxime (30), cefoxitin (30), chloramphenicol (30), erythromycin (15), neomycin (30), nitrofurantoin (300), polymixin (300 IU), streptomycin (10) or tobramycin (10). In the API ZYM system, acid production, N-acetyl-β-glucosaminidase, esterase (C4), esterase lipase (C8), β-glucosidase, leucine arylamidase (weak reaction) and naphthol-AS-Bl-phosphohydrolase activities are present, whereas alkaline phosphatase, α-chymotrypsin, cystine arylamidase, α-fucosidase, α- and β-galactosidase, α-glucuronidase, lipase (C14), α-mannosidase and valine arylamidase activities are absent. In addition to the major polar lipids described for the genus, contains a third unidentified glycolipid. Trace amounts of nine unidentified lipids are detected. The major fatty acids are C₁₇:₀, C₁₉:₀ cyclo ω₈c, C₂₀:₀ 11-methyl C₁₈:₁ w7c, C₁₈:₀ w7c, C₁₆:₀ and C₁₈:₀. The DNA G+C content of the type strain is 59.3 mol% (HPLC).

The type strain, B2ᵀ (=CGMCC 1.7692ᵀ =JCM 15775ᵀ), was isolated from a seawater sample collected from the East China Sea.

**Description of Pelagibacterium luteolum sp. nov.**

Pelagibacterium luteolum (lu.te.o’lum. L. neut. adj. luteolum yellowish).

Cells are 0.5–0.9 μm wide and 1.5–2.5 μm long. Short rod-shaped. Motile by means of a single polar flagellum. Colonies are 1–2 mm in diameter, circular, smooth, elevated, semi-transparent and yellowish after 3 days at 30 °C. Growth occurs at 0–5.0 % (w/v) NaCl, with optimum growth at 0.5 % (w/v). Grows at pH 6.0–9.5 and 4–37 °C (optimum growth at pH 7.5 and 30 °C). Nitrate is not reduced. Aesculin and casein are hydrolysed. Gelatin, DNA, starch and Tweens 40, 60 and 80 are not hydrolysed. Gluconate oxidation, glucose fermentation, β-galactosidase and urease activities are positive. Negative for arginine dihydrolase and indole production. The following substrates are utilized for growth: acetate, L-alanine, cellobiose, citrate, ethanol, D-galactose, glucosone, glucose, glycerol, L-glucose, myo-inositol, lactate, lactose, maltose, mannitol, D-mannose, L-ornithine, pyruvate, ribose, rhamnose, salinic acid, L-arginine, succinate, sucrose, trehalose and D-xylose. The following compounds are not utilized as sole carbon sources: L-aspartate, L-asparagine, L-arabinose, L-asparagine, L-aspartyte, cellobiose, citrate, ethanol, D-galactose, glucosone, glucose, glycerol, L-glutamine, myo-inositol, lactate, malate, malonic acid, mannitol, D-mannose, L-ornithine, pyruvate, ribose, rhamnose, salinic acid, L-arginine, succinate, sucrose, trehalose and D-xylose. The following compounds are not utilized as sole carbon sources: L-arginine, L-cysteine, glycine, formate, L-histidine, isoleucine, lactose, L-lysine, malonic acid, L-methionine, propionate, raffinose, sorbitol and sorbose. Acid is produced from L-arabinose, ethanol, D-galactose, glucose, glycerol, inositol, malose, mannitol, D-mannose, ribose, rhamnose, salinic acid, sucrose, trehalose and D-xylose. Susceptible to (μg per disc unless otherwise stated) amoxicillin (10), ampicillin (10), bacitracin (0.04 IU), cefotaxime (30), cefoxitin (30), chloramphenicol (30), erythromycin (15), kanamycin (30), neomycin (30), nitrofurantoin (300), polymixin (300 IU), streptomycin (10) or tobramycin (10). In the API ZYM system, acid production, N-acetyl-β-glucosaminidase, esterase (C4), esterase lipase (C8), β-glucosidase, leucine arylamidase (weak reaction) and naphthol-AS-Bl-phosphohydrolase activities are present, whereas alkaline phosphatase, α-chymotrypsin, cystine arylamidase, α-fucosidase, α- and β-galactosidase, α-glucuronidase, lipase (C14), α-mannosidase, trypsin and valine arylamidase activities are absent. Trace amounts of ten unidentified lipids are detected. The major fatty acids are C₁₈:₀ 11-methyl C₁₈:₁ w7c, C₁₈:₀ cyclo ω₈c, C₁₇:₀ and C₁₉:₀. The DNA G+C content of the type strain is 58.1 mol% (HPLC).

The type strain, 1C₁₆:₀ 27ᵀ (=CGMCC 1.10267ᵀ =JCM 16552ᵀ =CELMS EUT 1C1627ᵀ), was isolated from a semi-coke sample collected from north-eastern Estonia.
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References


