Arenibacter palladensis sp. nov., a novel marine bacterium isolated from the green alga Ulva fenestrata, and emended description of the genus Arenibacter

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The taxonomic position of three novel, marine, heterotrophic, aerobic, pigmented, gliding bacteria, isolated from the green alga Ulva fenestrata in the Sea of Japan, was determined. 16S rRNA gene sequence analysis revealed that the strains belong to the genus Arenibacter. The results of DNA–DNA hybridization experiments supported by phenotypic and chemotaxonomic data showed that the isolates represent a novel species of the genus Arenibacter, for which the name Arenibacter palladensis sp. nov. is proposed. The type strain is KMM 3961T (=LMG 21972T =CIP 108849T).

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of Arenibacter palladensis KMM 3961T is AJ575643.

The genus Arenibacter belongs to the family Flavobacteriaceae (Bernardet et al., 2002) and currently comprises three species: Arenibacter latericius, Arenibacter troitsensis and Arenibacter certesii (Ivanova et al., 2001; Nedashkovskaya et al., 2003a, 2004). Members of the genus are Gram-negative, aerobic, heterotrophic and dark-orange-pigmented marine bacteria. These organisms were isolated from various marine environments, including bottom-sediment samples, the brown alga Chorda filum, the green alga Ulva fenestrata and the edible holothurian Apostichopus japonicus. The genera Muricauda (Bruns et al., 2001) and Zobellia (Barbeyron et al., 2001) are the closest phylogenetic relatives of the Arenibacter species. Novel phenotypic findings and improved determination of some previously described phenotypic properties justify emended descriptions of the genus Arenibacter and A. latericius.

During June 2000 we isolated three novel strains, KMM 3961T, KMM 3979 and KMM 3980, from the green alga Ulva fenestrata, which was collected in Pallada Bay, Gulf of Peter the Great, Sea of Japan. A polyphasic taxonomic study of the algal isolates, cultured on marine agar 2216 (Difco), indicated that they represent a novel species of the genus Arenibacter.

The phylogenetic position of strain KMM 3961T was determined by analysis of the complete 16S rRNA gene sequence. Genomic DNA was prepared according to the protocol of Niemann et al. (1997). 16S rRNA gene amplification, purification and sequencing were performed as described by Vancanneyt et al. (2004) but with the following modifications: PCR-amplified 16S rRNA genes...
were purified by using a NucleoFast 96 PCR Clean-up kit (Macherey-Nagel). Sequencing reactions were performed by using a BigDye terminator cycle sequencing kit (Applied Biosystems) and purified using a Montage SEQ96 Sequencing Reaction Clean-up kit (Millipore). Electrophoresis of sequence reaction products was performed by using an ABI Prism 3100 genetic analyser (Applied Biosystems). Sequence assembly was performed using the program AutoAssembler (Applied Biosystems). The 16S rRNA gene sequence (continuous stretch of 1476 bp) and sequences of strains retrieved from EMBL were aligned and a phylogenetic tree was constructed by the neighbour-joining method, using the BIONUMERICS software package, version 3.50 (Applied Maths). Unknown bases were excluded from the analyses. Bootstrapping analysis was undertaken to test the statistical reliability of the topology of the neighbour-joining tree: 500 bootstrap resamplings of the data were performed (Fig. 1). A comparative analysis revealed that strain KMM 3961T is affiliated to the genus Arenibacter, a member of the family Flavobacteriaceae (Fig. 1). The levels of 16S rRNA gene sequence similarity between strains KMM 3961T and *A. certesii* KMM 3941T, *A. latericius* KMM 426T and *A. troitsensis* KMM 3674T were 94-8, 95-1 and 99-7%, respectively.

The DNA G+C contents of strains KMM 3961T, *A. certesii* KMM 3941T, *A. latericius* KMM 426T and *A. troitsensis* KMM 3674T were determined. Strains were cultivated on marine agar for 24 h at 37°C. DNA was extracted from 0.75–1.25 g cells (wet weight), using the DNA-extraction protocol of Wilson (1987), as modified by Cleenwerck *et al.* (2002). Cells were lysed in a Tris/EDTA buffer (10 mM Tris/HCl with up to 200 mM EDTA, pH 8.0) containing RNase A (Sigma), SDS (Serva) and protease K (Merck) to final concentrations of 400 μg mL−1, 2% (w/v) and 200 μg mL−1, respectively. NaCl (5 M stock solution) and CTAB/NaCl solution (10% w/v CTAB in 0.7 M NaCl) were added to final concentrations of 1 M and 13.3%, v/v, respectively. For determination of the DNA G+C content, DNA was enzymically degraded into nucleosides as described by Mesbah *et al.* (1989). The nucleoside mixture obtained was then separated by HPLC using a Waters Symmetry Shield C8 column maintained at a temperature of 37°C. The solvent was 0-02 M NH4H2PO4 (pH 4-0) with 1.5% acetonitrile. Non-methylated phage λ DNA (Sigma) was used as the calibration reference.

The DNA G+C contents for all strains tested were in the range 37–39 mol%. Slightly higher values (39–40 mol%) were obtained when the DNAs of strains KMM 3961T, KMM 3979 and KMM 3980 were isolated using the method of Marmur (1961) and when the DNA G+C contents were determined by the thermal denaturation method (Marmur & Doty, 1962).

DNA–DNA hybridizations between strains KMM 3961T, *A. certesii* KMM 3941T, *A. latericius* KMM 426T and *A. troitsensis* KMM 3674T were performed; the DNA was

![Fig. 1. Neighbour-joining evolutionary distance phylogenetic tree based on the 16S rRNA gene sequences of KMM 3961T and representative members of related genera of the family Flavobacteriaceae. The topology of the tree was not changed in the least-squares or maximum-likelihood trees. Numbers at nodes indicate bootstrap values (%). Bar, 0.1 substitutions per nucleotide position.](image-url)
prepared as described above. The microplate method was used as described by Ezaki et al. (1989) and Goris et al. (1998), using an HTS7000 BioAssay Reader (Perkin Elmer) for the fluorescence measurements. Biotinylated DNA was hybridized with single-stranded unlabelled DNA non-covalently bound to microplate wells. Hybridizations were performed at 35 °C in a hybridization mixture [2 x SSC, 5 x Denhardt’s solution, 2-5 % dextran sulfate, 50 % formamide, denatured low-molecular-mass salmon sperm DNA (100 μg ml⁻¹) and biotinylated probe DNA (1250 ng ml⁻¹)]. Each hybridization experiment was performed in triplicate. A binding level of 62 % was found between strains KMM 3961T and A. troitsensis KMM 3674T, indicating that KMM 3961T represents a separate species. The latter two strains had low values for binding (6–20 %) with A. certesii KMM 3941T and A. latericius KMM 426T. To determine the levels of DNA relatedness between strains KMM 3961T, KMM 3979 and KMM 3980, DNA was isolated by the method of Marmur (1961) and DNA–DNA hybridizations were performed spectrophotometrically using the initial renaturation rate method described by De Ley et al. (1970). The levels of DNA–DNA binding between strains KMM 3961T, KMM 3979 and KMM 3980 were found to be 96–99 %. The results of the DNA–DNA hybridization experiments indicate that the strains under study represent a separate and novel Arenibacter species (Wayne et al., 1987).

To determine their whole-cell fatty acid profiles, strain KMM 3961T, A. certesii strain KMM 3941T, A. latericius strains KMM 426T, KMM 3522, KMM 3523, KMM 3528 and KMM 3557 and A. troitsensis strain KMM 3674T were grown at 25 °C for 48 h on marine agar. Analysis of the fatty acid methyl esters was carried out according to the standard protocol of the Microbial Identification System (Microbial ID). The predominant cellular fatty acids of KMM 3961T were of the straight-chain unsaturated, branched-chain unsaturated and saturated types: iso-C₁₅:₀ (8-7 %), iso-C₁₅:₁ (12-7 %), C₁₅:₀ (15-0 %), iso-C₁₇:₀ 3-OH (17-4 %) and summed feature 3 (11-1 %); comprising iso-C₁₅:₀ 2-OH and/or C₁₆:₀(107) (Table 1). The presence of a significant amount of iso-C₁₇:₀ 3-OH (6-9–21-9 %) in all strains tested should be emphasized as it is one of the characteristic fatty acids of members of the family Flavobacteriaceae. Previously, Ivanova et al. (2001) had reported the absence of hydroxy fatty acids in Arenibacter strains.

Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Akagawa-Matsushita et al. (1992). Menaquinones were detected by using monitoring at 270 nm and were identified by comparison with known quinones from the reference strain Salegentibacter salegens DSM 5424T. The main isoprenoid quinone was MK-6.

### Table 1. Cellular fatty acid compositions (percentage content) of Arenibacter species

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
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<th>4</th>
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<tbody>
<tr>
<td>iso-C₁₅:₀</td>
<td>8-7</td>
<td>7-7</td>
<td>6-9–15-8</td>
<td>8-1</td>
</tr>
<tr>
<td>anteiso-C₁₅:₀</td>
<td>3-3</td>
<td>6-3</td>
<td>4-8–13-5</td>
<td>9-3</td>
</tr>
<tr>
<td>iso-C₁₅:₁</td>
<td>12-7</td>
<td>7-2</td>
<td>4-9–14-0</td>
<td>14-0</td>
</tr>
<tr>
<td>anteiso-C₁₅:₁</td>
<td>0-5</td>
<td>0-8</td>
<td>0-6–2-9</td>
<td>2-9</td>
</tr>
<tr>
<td>C₁₅:₀</td>
<td>15-0</td>
<td>11-5</td>
<td>4-2–16-0</td>
<td>14-2</td>
</tr>
<tr>
<td>iso-C₁₇:₀ (106c)</td>
<td>2-6</td>
<td>1-9</td>
<td>1-0–2-3</td>
<td>2-3</td>
</tr>
<tr>
<td>iso-C₁₆:₀</td>
<td>0-2</td>
<td>1-7</td>
<td>0-5–1-3</td>
<td>0-5</td>
</tr>
<tr>
<td>C₁₆:₀</td>
<td>0-6</td>
<td>1-0</td>
<td>1-0–2-7</td>
<td>1-9</td>
</tr>
<tr>
<td>iso-C₁₇:₀ (109c)</td>
<td>4-0</td>
<td>4-7</td>
<td>2-2–4-6</td>
<td>2-9</td>
</tr>
<tr>
<td>C₁₇:₀ (108c)</td>
<td>0-5</td>
<td>2-4</td>
<td>0-5–2-0</td>
<td>1-3</td>
</tr>
<tr>
<td>C₁₇:₀ (106c)</td>
<td>1-4</td>
<td>3-0</td>
<td>0-7–2-9</td>
<td>2-4</td>
</tr>
<tr>
<td>C₁₅:₀ 2-OH</td>
<td>0-4</td>
<td>0-6</td>
<td>0-7–1-0</td>
<td>0-6</td>
</tr>
<tr>
<td>iso-C₁₅:₀ 3-OH</td>
<td>5-3</td>
<td>3-5</td>
<td>4-6–5-7</td>
<td>5-6</td>
</tr>
<tr>
<td>C₁₅:₀ 3-OH</td>
<td>2-2</td>
<td>0-6</td>
<td>0-0–1-4</td>
<td>0-4</td>
</tr>
<tr>
<td>iso-C₁₆:₀ 3-OH</td>
<td>1-6</td>
<td>7-2</td>
<td>2-1–5-7</td>
<td>2-1</td>
</tr>
<tr>
<td>C₁₆:₀ 3-OH</td>
<td>2-0</td>
<td>0-8</td>
<td>0-6–1-3</td>
<td>1-3</td>
</tr>
<tr>
<td>iso-C₁₇:₀ 3-OH</td>
<td>17-4</td>
<td>13-3</td>
<td>6-9–14-4</td>
<td>6-9</td>
</tr>
<tr>
<td>C₁₇:₀ 2-OH</td>
<td>1-0</td>
<td>3-8</td>
<td>2-1–5-1</td>
<td>2-1</td>
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<tr>
<td>Summed feature 3</td>
<td>11-1</td>
<td>13-5</td>
<td>9-8–11-9</td>
<td>9-8</td>
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</tbody>
</table>

Microplate system according to the manufacturers’ instructions.

The physiological, morphological and biochemical characteristics of the strains studied are listed in the species description and in Table 2. Similarities in the phenotypic characteristics support the inclusion of strains KMM 3961T, KMM 3979 and KMM 3980 in the genus Arenibacter. However, the three strains differ clearly from currently described Arenibacter species by their ability to move on substrate surfaces by means of gliding and to grow in media containing no sea water or Na⁺ ions. Also, the novel isolates cannot reduce nitrites to nitrates or form acid from D-lactose or L-raffinose, in contrast to the other Arenibacter strains tested in this study. Moreover, only strains KMM 3961T, KMM 3979 and KMM 3980 produced acid from D-lxylene and were resistant to oleanomycin. The novel bacteria can be further differentiated from A. latericius and A. certesii by the absence of urea hydrolysis, by the lack of susceptibility to ampicillin and by the higher G+C content of the DNA (Table 2). Other phenotypic characteristics, such as growth at 8 % NaCl, the maximum growth temperature (38 °C), oxidation of D-galactose, D-glucose, D-melibiose and N-acetylglucosamine, resistance to tetracycline and the absence of Tween 40 hydrolysis and H₂S

Microbial Identification System: iso-C₁₅:₀ 2-OH, C₁₆:₀(107)c and C₁₆:₀(107)c.
production also distinguish the novel isolates from the closest relative, *A. troitsensis* (Table 2).

The above-mentioned phenotypic features (Table 1), in association with molecular divergence, support strongly the differentiation of the strains studied from the *Arenibacter* species with validly published names.

Originally, the genus *Arenibacter* was described as consisting of non-gliding bacteria requiring Na\(^+\) ions for growth and unable to decompose gelatin (Ivanova et al., 2001). In the course of our study of these novel algal isolates and *A. troitsensis* KMM 3674\(^T\), several phenotypic traits were found to be helpful for the differentiation of *Arenibacter* species.

### Table 2. Phenotypic characteristics of *A. palladensis* sp. nov. and other *Arenibacter* species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>3</th>
<th>4</th>
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</thead>
<tbody>
<tr>
<td>Gliding motility</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Na(^+) requirement for growth</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>H(_2)S production</td>
<td>-</td>
<td>-</td>
<td></td>
<td>+</td>
</tr>
<tr>
<td>Degradation of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gelatin</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>DNA</td>
<td>-</td>
<td>V(^-) (-)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Urea</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Tween 20</td>
<td>-</td>
<td>V(^+) (-)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Tween 40</td>
<td>V</td>
<td>V(^-) (-)</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Growth with:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8% NaCl</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>10% NaCl</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Growth at 42(^\circ) C</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Galactose, D-glucose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>D-Lactose, L-raffinose</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Melibiose</td>
<td>+</td>
<td>V(^+) (+)</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>L-Fucose</td>
<td>+</td>
<td>V(^+) (-)</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>L-Rhamnose</td>
<td>+</td>
<td>V(^-) (+)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>DL-Xylose</td>
<td>+</td>
<td>-</td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>Glycerol</td>
<td>-</td>
<td>+</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N-Acetylglucosamine</td>
<td>+</td>
<td>V(^-) (+)</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Production of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Esterase (C4), lipase (C14)</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>(\beta)-Glucuronidase</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Susceptibility to:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ampicillin</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Carbenicillin</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Oleandomycin</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>-</td>
<td>-</td>
<td></td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>40</td>
<td>37–38</td>
<td>38</td>
<td>40</td>
</tr>
</tbody>
</table>
Thus, we propose the placement of strains KMM 3961\textsuperscript{T}, KMM 3979 and KMM 3980 in the genus Arenibacter, as *Arenibacter palladensis* sp. nov., and the emendation of the description of the genus Arenibacter.

**Emended description of the genus Arenibacter Ivanova et al. 2001**

This description is based on that of Ivanova et al. (2001). Some species may display gliding motility and grow without sea water or Na\textsuperscript{+} ions. Aerobic. Produce non-diffusible carotenoid pigments. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. The major respiratory quinone is MK-6. The predominant cellular fatty acids are straight-chain saturated and unsaturated and branched-chain unsaturated fatty acids C\textsubscript{15:0}, iso-C\textsubscript{15:0}, iso-C\textsubscript{15:1}, iso-C\textsubscript{17} 3-OH and summed feature 3 (comprising iso-C\textsubscript{15:0} 2-OH and/or C\textsubscript{16:1}ω7). The main polar lipid is phosphatidylethanolamine. The type species is *Arenibacter laticius*.

**Description of Arenibacter palladensis sp. nov.**

*Arenibacter palladensis* (pal.la.den’sis. N.L. masc. adj. *palladensis* pertaining to Pallada Bay, where the first strains were isolated).

The main characteristics are the same as those given for the genus. In addition, cells range from 0.4 to 0.5 mm in width and from 1.6 to 2.3 mm in length, and move by means of gliding. On marine agar, colonies are 2–4 mm in diameter, circular with entire edges and dark orange in colour. Growth is detected at 10–42 °C. The optimal temperature for growth is 23–25 °C. Growth occurs at 0–10% NaCl. Does not hydrolyse agar, casein, gelatin, alginate, starch, Tween 20, DNA, urea, cellulose (CM-cellulose and filter paper) or chitin. Forms acid from D-glucose, D-lactose, D-maltose and D-sucrose, but not from L-arabinose, D-galactose, D-sorbitose, N-acetylglucosamine, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Utilizes L-arabinose and D-mannose, but not mannitol, inositol, sorbitol, malonate or citrate. Nitrate is not reduced. Indole, H\textsubscript{2}S and acetoin (Voges–Proskauer reaction), arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are not produced. According to the results of testing with the Biolog GN2 Microplate system, the type strain utilizes dextrin, cellobiose, D-fructose, L-fucose, D-galactose, gentiobiose, α-D-glucose, α-Lactose, α-D-lactose, lactulose, maltose, D-mannose, D-melibiose, methyl β-D-glucoside, D-rhamnose, sucrose, D-trehalose, turanose, methylpyruvate, α-ketobutyric acid, DL-lactic acid, N-acetyl-D-glucosamine, L-glutamic acid, L-threonine and glucose 1-phosphate. Does not utilize α-cyclodextrin, Tween 40 or 80, adonitol, L-arabinose, D-arabitol, i-erythritol, *myo*-inositol, D-mannitol, psicose, L-rhamnose, xylitol, monomethyl succinate, acetic acid, citric acid, formic acid, D-galactonic acid lactone, D-glucic acid, D-glucosaminic acid, D-glucuronic acid, α- and β-hydroxybutyric acids, p-hydroxyphenylacetic acid, itaconic acid, α-ketogluartic acid, α-ketovaleric acid, malonic acid, propionic acid, quinic acid, D-saccharic acid, sebamic acid, succinic acid, bromosuccinic acid, succinic acid, glucuronamide, alaninamide, D-alanine, L-alanyl glycine, L-asparagine, glycy1 L-glutamic acid, L-histidine, hydroxy-L-proline, L-leucine, L-ornithine, L-phenylalanine, L-pyroglutamic acid, D- and L-serine, DL-carnitine, γ-amino butyric acid, uronic acid, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol or glucose 6-phosphate. The predominant fatty acids in the type strain are straight-chain saturated and unsaturated and branched-chain unsaturated fatty acids C\textsubscript{15:0} (15.0%), iso-C\textsubscript{15:0} (8.7%), iso-C\textsubscript{15:1} (12.7%), iso-C\textsubscript{17} 3-OH (17.4%) and summed feature 3 (11.1%); comprising iso-C\textsubscript{15:0} 2-OH and/or C\textsubscript{16:1}ω7. The G+C content of the DNA is 39–40 mol%. The type strain is KMM 3961\textsuperscript{T} (=LMG 21972\textsuperscript{T} = CIP 108849\textsuperscript{T}), isolated from the green alga *U. fenestrata*, collected in Pallada Bay, Sea of Japan.

**Emended description of Arenibacter latericius Ivanova et al. 2001**

The description is as for the genus and is based on that of Ivanova et al. (2001). In addition, cells range from 0.4 to 0.6 mm in width and from 2.1 to 5.0 mm in length. Gliding motility not observed. Growth is detected at 10–42 °C and in 1–8% NaCl. Decomposes urea. Some strains may hydrolyse DNA and Tweens 20 and 40. Does not hydrolyse agar, casein, gelatin, starch, alginic acids, Tween 80, cellulose (CM-cellulose and filter paper) or chitin. Forms acid from D-cellobiose, D-galactose, D-glucose, D-lactose, D-maltose, L-raffinose, D-sucrose and glycerol. Can oxidize D-melibiose, L-fucose, L-rhamnose and N-acetylgulcosammine. Does not produce acid from L-arabinose, L-sorbose, DL-xyllose, adonitol, inositol, dulcitol, mannitol, malate, fumarate or citrate. According to the Biolog system, α-D-glucose, L-glutamic acid, L-ornithine, uridine, glycerol, DL-α-glycerol phosphate, glucose 1-phosphate, glucose 6-phosphate are utilized. Dextrin, N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, cellobiose, D-fructose, α-D-lactose, α-D-lactose, lactulose, glycerogen, maltose, D-mannitol, D-mannose, D-melibiose, methyl β-D-glucoside, D-raffinose, sucrose, D-trehalose, DL-lactic acid, turanose, succinic acid, glucuronamide, alaninamide, L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, glycol L-aspartic acid, glycol L-glutamic acid, L-proline, D- and L-serine and L-threonine are weakly utilized. Susceptible to erythromycin, ampicillin, carbenicillin, oleandomycin, cephaloridin and lyncomycin. Not susceptible to kanamycin, benzylpenicillin, oxacillin, neomycin, streptomycin, gentamicin, polymyxin B or tetracycline. Hydrogen sulfide, indole and acetoin are not produced. Nitrates are reduced to nitrites. The cellular fatty acids are predominantly odd-numbered and iso-branched (about 70%): C\textsubscript{15:0} (4.2–16.0%), iso-C\textsubscript{15:0} (6.9–15.8%), anteiso-C\textsubscript{15:0} (4.8–13.5%), iso-C\textsubscript{15:1} (4.9–14.0%), iso-C\textsubscript{15:0} 3-OH (4.6–5.7%), iso-C\textsubscript{17:0} 3-OH (6.9–14.4%) and summed feature 3 (9.8–11.9%); comprising C\textsubscript{16:1}ω7 and/or iso-C\textsubscript{15:0} 2-OH.)
The type strain is KMM 426T (= VKM B-2137D T = LMG 19693 T = CIP 106861 T).

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