Marinibactrum halimedae gen. nov., sp. nov., a gammaproteobacterium isolated from a marine macroalga

Miyuki Nishijima,1,2 Kyoko Adachi,1† Hiroshi Sano1§ and Kazuhide Yamasato1¶

1Marine Biotechnology Institute, Heita, Kamaishi 026-0001, Japan (closed June 2008)
2TechnoSuruga Laboratory Co., Ltd, 330, Nagasaki, Shimizu-ku, Shizuoka 424-0065, Japan

Correspondence
Miyuki Nishijima
mnishiji@tecsrg.co.jp

Phylogenetic and taxonomic characterization was performed for a bacterium, designated strain Q-192T, isolated from the surface of the green macroalga Halimeda sp., collected from the subtropical Ishigaki Island, Japan. The isolate was a polysaccharide-producing, Gram-stain-negative, aerobic, rod-shaped, motile bacterium with a polar flagellum. The isolate was slightly halophilic, required Na\(^{+}\), Mg\(^{2+}\) and Ca\(^{2+}\) ions for growth, but did not require growth factors. The only isoprenoid quinone was ubiquinone-8. The major cellular fatty acids were C\(_{18}:1\) \(\Delta7\)c, C\(_{16}:0\) and C\(_{14}:0\). The main hydroxy fatty acid was C\(_{10}:0\) 3-OH. The DNA G + C content was 45.9 mol%.

Phylogenetic analysis of 16S rRNA gene sequences placed the isolate in the class Gammaproteobacteria. The phylogenetically closest relatives with validly published names were Pseudomaricurvus alkylphenolicus KU41GT, Teredinibacter turnerae T7902T, Pseudoteredinibacter isoporae SW-11T and Simiduia agarivorans SA1T with sequence similarities of 94.5, 94.1, 93.7 and 93.6 %, respectively. The isolate was distinguished from members of these genera by a combination of DNA G + C content, chemotaxonomic characteristics (respiratory quinone system, fatty acid profile and polar lipid composition) and other phenotypic features. Based on phylogenetic, genotypic, chemotaxonomic and phenotypic characteristics, strain Q-192T is considered to represent a novel species of a new genus, for which the name Marinibactrum halimedae gen. nov., sp. nov. is proposed. The type strain of Marinibactrum halimedae is Q-192T (=NBRC 110095T=NCIMB 14932T).

Marine environments are rich in animals, plants and algae that harbour diverse kinds of bacteria. Among them are biochemically active bacteria that have the potential for biotechnological use. In a series of screening studies for marine epiphytic bacteria that produce novel bioactive substances, we have formerly isolated Pseudoalteromonas sp. strain F-420, which produces antibacterial korormicin, from green macroalga (Yoshikawa et al., 1997) and two species of the genus Microbulbifer, Microbulbifer variabilis, which produces anticancer pelagioicins from marine macroalgae and macroalgae, and Microbulbifer epialgicus, which produces UV-absorbing substances, from a green macroalga (Imamura et al., 1997; Nishijima et al., 2009). In the present paper, we describe the phylogenetic position and taxonomic characteristics of a polysaccharide-producing, Gram-stain-negative bacterium which was isolated from the surface of a green macroalga, Halimeda sp., collected from a subtropical area of Japan.

Marine macroalgae were collected from the coastal region of Ishigaki Island in Okinawa Prefecture, a subtropical area of Japan, in 1996 to isolate bacteria. The isolation procedure was conducted immediately after collecting the algal samples at the sampling sites. The method used for bacterial isolation was conducted immediately after collecting the algal samples at the sampling sites. The method used for bacterial isolation was according to that of Nishijima et al. (2009). Briefly, the surface of an alga was rubbed with a small piece of sterile gauze, which was then soaked in sterilized seawater and shaken vigorously. Aliquots (100 μl) of undiluted and 10-fold diluted samples were spread onto agar plates of isolation medium. The isolation medium used was 1/10 marine broth (MB; BD) agar supplemented with a hot-water extract.
from 10 g of a brown alga per litre of medium. The 1/10 agar medium was composed of (per litre) 3.74 g MB powder, 28.8 g Marine Art SF (Tomita Pharmaceuticals) powder [100 % concentration of artificial seawater (denoted as ASW)] is prepared by dissolving 38.4 g powder in 1000 ml distilled water] and 15 g agar, pH 7.6.

Inoculated isolation plates were incubated at 25°C for 7 days. The strain isolated from a green macroalga, Halimeda sp., was subjected to phylogenetic and taxonomic characterization. Cells of the isolate were grown on 1/10 MB agar at 25°C for 2 days, suspended in sterilized seawater supplemented with 20 % (v/v) glycerol and stored at 80°C.

Cultivation of the isolated bacterium was conducted at 25°C using 1/10 MB agar and R2A-ASW agar, which was composed of (per litre ASW) 3.2 g R2A broth (Nihon Pharmaceutical) powder and 15 g agar, pH 7.2. Anaerobic cultivation was conducted by absorbing oxygen using an Anaero Pack gas system (Anaero Pack disposable; Mitsubishi Gas Chemical). Methods for observation of cell morphology, characterization of conventional phenotypic features, determination of growth range as well as optimal pH, temperature and salinity were as described previously (Nishijima et al., 2009). Additionally, examination of requirements for inorganic ions and growth factors and examination of utilization of ammonical nitrogen and carbon compounds were also performed as described previously (Nishijima et al., 2009). API 20 NE, API 20 E and API ZYM kits (bio-Mérieux) were used for assessing biochemical features and enzyme activity according to the manufacturer’s instructions, except that the cells for inoculation were suspended in 75 % (v/v) ASW composed of 28.8 g Marine Art SF powder and 1000 ml distilled water to incubate under an optimal range of NaCl concentration for growth. The incubation time in the API ZYM tests was extended to 24 h, as the scores of most tests for the isolates and the reference strains (Teredinibacter turnerae ATCC 39867T and Pseudoteredinibacter isopora DSM 22368T) were negative at a shorter incubation time (4–4.5 h in the manufacturer’s instructions) but were positive when incubated for 24 h. The API 50CH kit (bio-Mérieux) was also used for tests of acid production from carbohydrates under aerobic conditions according to the manufacturer’s manual except that the cells for inoculation were suspended in 75 % ASW instead of suspension media provided by the manufacturer. Acid production was checked using phenol red as a pH indicator. To determine flagella arrangement, cells were grown at 25°C for 48 h on 1/5 marine agar (MA), which was composed of (per litre 75 % ASW) 7.48 g MB powder and 1.5 g agar, pH 7.6, and were observed by electron microscopy (JEM-2000FX; JEOL) using the negative staining method with uranyl acetate.

The isolate was Gram-stain-negative, catalase- and oxidase-positive and non-endospore-forming. Cells were straight to slightly curved rods with a polar flagellum (Fig. S1, available in the online Supplementary Material). The isolate possessed a respiratory-type metabolism, growing aerobically and incapable of growing under anaerobic conditions. The number of colonies that developed in an agar medium by pour-plating of a cell suspension was >10 times that which developed on the surface of agar plates by spread-plating. In the cell propagation initiation process, strain Q-192T was sensitive to the atmospheric oxygen concentration and a slightly reduced concentration was preferable for its growth.

Colonies grown on 1/10 MB agar were transparent and white to pale yellow. They did not produce water-soluble pigments, whereas colonies grown on MB agar were pale yellow, becoming brown when old, and water-soluble brown pigments were produced on/in MB and R2A-ASW agar/broth media. The isolate produced a large amount of polysaccharide in R2A-ASW broth medium. The isolate required divalent cations, Mg2+ and Ca2+, as well as Na+ ions for growth. It was capable of using ammonical nitrogen and required no growth factors, growing in a medium composed of 1 % glucose, 0.078 % (NH4)2SO4, 0.1 % NaNO3 and 75 % ASW. Growth was not improved by the addition of algal extract to the growth medium even though the isolate was originally isolated on an algal-extract-containing medium. The isolate grew in the presence of 1.0–5.0 % (w/v) NaCl with an optimum of 3.5 %, at pH 6.5–9.0 with an optimum of pH 8.0 and at 10–37°C with an optimum of 25–30°C. Other phenotypic features of the isolate are given in Table 1 and in the genus and species descriptions.

The 16S rRNA gene sequence (1451 bp) of strain Q-192T was determined as described previously (Nishijima et al., 2009) with minor modifications. Briefly, the near full-length 16S rRNA gene was amplified by PCR using a pair of universal primers, 9F (5’-GAGTTGTGATCCCTGCGG-TCAG-3’) (Nakagawa et al., 2002) and 1510R (5’-GGCTATTCCCTGTTACGA-3’) (Uchino et al., 1997), and the PCR product was sequencing by using an ABI BigDye v3.1 cycle sequencing kit and ABI 3130 xl DNA sequencer (Applied Biosystems). Phylogenetic trees were reconstructed using the software MEGA version 6.0 (Tamura et al., 2013) and two tree-making algorithms, neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981; Nei & Kumar, 2000; Tamura et al., 2013). The reliability of cluster formation was assessed by a bootstrap analysis (Felsenstein, 1985). Both algorithms gave similar tree topologies and similar bootstrap values of robustness (Fig. 1). Comparison against the 16S rRNA gene sequences in DDBJ (http://www.ddbj.nig.ac.jp/) indicated that the isolate belonged to the class Gammaproteobacteria. Among its members with validly published names, those sharing the highest level of 16S rRNA gene sequence similarity with the new isolate were Pseudomaricurvu alkylenophenolicus KU41G T (Iwaki et al., 2014), Teredinibacter turnerae T7902 T (Distel et al., 2002), Pseudoteredinibacter isopora SW-11 T (Chen et al., 2011) and Simiduia agavivorans SA1 T (Shieh et al., 2008), with values of 94.5, 94.1, 93.7 and 93.6 %, respectively. The taxa sharing the next highest 16S rRNA gene sequence similarity were Maricurvu nonylphenolicus KU41E T (Iwaki et al., 2012),
Table 1. Differential characteristics between strain Q-192T and members of related genera

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Motility/single polar flagellum</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−*</td>
</tr>
<tr>
<td>Growth on marine agar</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>NaCl range for growth (% w/v)</td>
<td>1–5</td>
<td>2–3</td>
<td>0.6–3.5</td>
<td>2–4</td>
<td>0.5–7</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>6.5–9</td>
<td>7–10</td>
<td>6–10.5</td>
<td>7–8</td>
<td>7–10</td>
</tr>
<tr>
<td>Temperature range for growth (°C)</td>
<td>10–37</td>
<td>15–30</td>
<td>20–35</td>
<td>10–45</td>
<td>15–40</td>
</tr>
<tr>
<td>Reduction of nitrate to nitrite</td>
<td>−</td>
<td>−</td>
<td>−†</td>
<td>−†</td>
<td>−+</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gelatin</td>
<td>+</td>
<td>−</td>
<td>−‡</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Tween 80</td>
<td>+</td>
<td>+</td>
<td>+‡</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Agar</td>
<td>−</td>
<td>ND</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Cellulose</td>
<td>−</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Enzyme activities (API ZYM tests)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Trypsin</td>
<td>−</td>
<td>−</td>
<td>−†</td>
<td>−†</td>
<td>+</td>
</tr>
<tr>
<td>Lipase (C14)</td>
<td>+</td>
<td>+</td>
<td>−‡</td>
<td>+†</td>
<td>−§</td>
</tr>
<tr>
<td>Cystine arylamidase</td>
<td>+</td>
<td>−</td>
<td>−†</td>
<td>+†</td>
<td>−</td>
</tr>
<tr>
<td>N-Acetyl-β-glucosaminidase</td>
<td>−</td>
<td>−</td>
<td>+†</td>
<td>−†</td>
<td>+</td>
</tr>
<tr>
<td>Carbon utilization of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cellobiose</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Fructose</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Mannose</td>
<td>+</td>
<td>+</td>
<td>−‡</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Sucrose</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Pyruvate</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+§</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>45.9</td>
<td>53.3</td>
<td>49.0</td>
<td>51.6</td>
<td>55.6</td>
</tr>
<tr>
<td>Isoprenoid quinone(s)</td>
<td>Q-8 (100 %)</td>
<td>Q-8 (98.5 %), Q-7 (1.5 %)</td>
<td>Q-8 (77.7 %), Q-9 (4.4 %), Q-7 (1.4 %), MK-8 (16.5 %)</td>
<td>Q-8 (96.5 %), Q-7 (2.9 %), Q-9 (0.5 %)</td>
<td>Q-8§</td>
</tr>
<tr>
<td>Polar lipids</td>
<td>PE, PG, lysoPE, DPG, UPL</td>
<td>ND</td>
<td>PE, PG, GL, 2 AL†</td>
<td>PE, PG, lysoPE, DPG†</td>
<td>PE, PG, AL, 3 GL, 2 L§</td>
</tr>
<tr>
<td>Isolation source</td>
<td>Macroalga</td>
<td>Seawater</td>
<td>Bivalve</td>
<td>Coral</td>
<td>Seawater</td>
</tr>
</tbody>
</table>

*Less than 1 % of cells showed motility with monotrichous flagella (Shieh et al., 2008).
†Data obtained in this study.
‡Data from Chen et al. (2011).
§Data from Park et al. (2014).

Saccharophagus degradans 2-40T (González & Weiner, 2000; Ekborg et al., 2005) and Eionea nigra 17X/A02/237T (Urios et al., 2011) with values of 92.7, 92.6 and 92.5 %, respectively. Levels of similarity to other described genera were <92.5 %. Levels of divergence in the 16S rRNA gene sequences between the new isolate and the aforementioned seven genera were 5.5–7.5 %. The isolate did not form a cluster with any of them. In terms of phylogenetic distance, the isolate is suggested to constitute an independent taxon at the genus level (Yarza et al., 2008; Tindall et al., 2010). The neighbour-joining tree was reconstructed for uncharacterized bacterial isolates and uncultured bacterial clones.
sharing ≥94 % sequence similarity with strain Q-192T, which is shown in Fig. S2. Strain Q-192T also formed an independent lineage in the tree: the closest neighbour was unclassified bacterial clone FII-OX039 (accession no. JQ579688), obtained from marine sediments, sharing 95.5 % similarity and the next closest neighbours were an unclassified bacterium ('Pseudomonas' group; accession no. AF102866), isolated from a marine wood-boring shipworm, and an uncultured bacterial clone (accession no. FJ203036), detected from a diseased coral, both sharing 94.8 % similarity with strain Q-192T.

The isoprenoid quinone system was determined from cells grown in R2A-ASW broth at 30°C for 48 h aerobically with shaking. Methods for extraction and measurement of quinones were as described by Nishijima et al. (1997, 2009) using HPLC (Waters HPLC system 600 series). The isolate possessed only ubiquinone-8 (Q-8); no other ubiquinones or menaquinones were detected.

For determination of the cellular fatty acid composition, cells were grown on R2A-ASW agar plates at 30°C for 3 days. Fatty acid methyl esters were prepared and analysed according to the instructions given for the Microbial Identification System version 6.0 and identified using the TSBA40 database (MIDI). The majority of fatty acids of the new isolate were saturated and mono-unsaturated straight chains with even numbers of carbons. The fatty acid profile was as follows: C14:0 (15.1 %), C15:0 (2.4 %), C16:0 (15.9 %), C18:1ω7c (24.8 %), anteiso-C17:0 (2.0 %), C11:0 2-OH (1.9 %), C10:0 3-OH (7.3 %), unknown 11.799 (13.1 %) and summed feature 3 (10.2 %).

Polar lipids were analysed from cells grown in R2A-ASW broth at 30°C for 48 h aerobically with shaking. Methods for extraction and measurement of polar lipids using two-dimensional TLC were as described by Nishijima et al. (2009) except that the total lipid components were detected by 10 % (w/v) molybdatophosphoric acid. Lysophosphatidylethanolamine (lysoPE) was identified by comparing with a standard phospholipid preparation (Phospholipid kit; Doosan SRL) via TLC. The major phospholipids of strain Q-192T were phosphatidylethanolamine (PE) and phosphatidylglycerol (PG). LysoPE, diphasphatidylglycerol (DPG) and one unidentified phospholipid were detected as minor components (Fig. S3).

Genomic DNA was extracted and purified according to the combined methods of Marmur (1961) and Saito & Miura.
Pseudomaricurvus alkylphenolicus (Iwaki et al., 2011) and 55.6 mol% for was reported to possess Q-8 (Kim (2.9 %) (Iwaki 2002), 51.6 mol% for (data from this study) and (this study) possessed Q-8 (98.5 % of the total) isoporae + Q-7 (1.5 %), Q-8 (77.7 %) + Q-9 (4.4 %) + Q-7 (1.4 %) + MK-8 (16.5 %), and Q-8 (96.5 %) + Q-7 (2.9 %) + Q-9 (0.5 %), respectively. Simiduia agarivorans was reported to possess Q-10 as a major qui- none in the original paper (Shieh et al., 2008). With respect to chemotaxonomic fea-
tures, the isolate possessed only Q-8, whereas Pseudomari-
curvus alkylphenolicus (Iwaki et al., 2014), Teredinibacter turnerae (data from this study) and Pseudoteredinibacter isoporae (this study) possessed Q-8 (98.5 % of the total) + Q-7 (1.5 %), Q-8 (77.7 %) + Q-9 (4.4 %) + Q-7 (1.4 %) + MK-8 (16.5 %), and Q-8 (96.5 %) + Q-7 (2.9 %) + Q-9 (0.5 %), respectively. Simiduia agarivorans

The major polar lipids of strain Q-192T were phosphatidy-
lethanolamine and phosphatidylglycerol, which were also observed for Teredinibacter turnerae (this study), Pseudo-

The new isolate and related bacteria were all found in marine environments (Table 1). The new isolate seems to be a free-living bacterium dwelling on the surface of macroalga and differs ecologically and biochemically from Teredinibacter, which is a specific symbiont associated with wood-boring shipworms and fixes atmospheric nitrogen (Distel et al., 2002), and from Pseudoteredinibacter, a coral-associated bacterium (Chen et al., 2011).

Based on a combination of phylogenetic divergence, geno-
typic differences, chemotaxonomic characteristics and eco-
logical features, the isolate should be regarded as a member of a new genus distinct from the phylogenetically related genera Pseudomaricurvus, Teredinibacter, Pseudoteredi-
nibacter and Simiduia. The isolate is further distinguished from these most closely related genera by morphological, physiological and biochemical features as listed in Table 1. Based on the data described above, strain Q-192T should be classified as representing a novel species of a new genus, for which the name Marinibactrum halimedae gen. nov., sp. nov. is proposed.

Marinibactrum gen. nov. Marinibactrum [Ma.ri.ni.bac’trum. L. adj. marinus of the sea; Gr. neut. n. baktron a staff or stick; N.L. neut. n. Marinibactrum rod of (inhabiting) the sea].

Cells are Gram-stain-negative, motile with a polar flagel-

um and non-endospore-forming rods. Possesses a respira-

tory-type metabolism. Catalase- and oxidase-positive. Requi-

The type species is Marinibactrum halimedae.

**Description of Marinibactrum halimedae sp. nov.**

Marinibactrum halimedae (ha.li.me’dae. N.L. gen. n. hal-

M. Nishijima and others

(1963). The G+C content of the DNA was determined by HPLC with a Develosil ODS-HG-5 column (4.6 × 250 mm; Nomura Chemical) and a UV 8010 detector (Shimadzu) at 270 nm. The DNA G+C content of strain Q-192T was 45.9 mol%.

The characteristics that differentiate the new isolate from its closest described relatives are shown in Table 1. The new isolate was distinguished by its genomic DNA G+C content, being 45.9 mol% versus 53.3 mol% for Pseudomaricurvus alkylphenolicus (Iwaki et al., 2014), 49–51 mol% for Teredinibacter turnerae (Distel et al., 2002), 51.6 mol% for Pseudoteredinibacter isoporae (Chen et al., 2011) and 55.6 mol% for Simiduia agarivorans (Shieh et al., 2008). With respect to chemotaxonomic fea-
tures, the isolate possessed only Q-8, whereas Pseudomari-
curvus alkylphenolicus (Iwaki et al., 2014), Teredinibacter turnerae (data from this study) and Pseudoteredinibacter isoporae (this study) possessed Q-8 (98.5 % of the total) + Q-7 (1.5 %), Q-8 (77.7 %) + Q-9 (4.4 %) + Q-7 (1.4 %) + MK-8 (16.5 %), and Q-8 (96.5 %) + Q-7 (2.9 %) + Q-9 (0.5 %), respectively. Simiduia agarivorans was reported to possess Q-10 as a major qui- none in the original paper (Shieh et al., 2008).

The major polar lipids of strain Q-192T were phosphatidy-
lethanolamine and phosphatidylglycerol, which were also observed for Teredinibacter turnerae (this study), Pseudo-

can be classified as representing a novel species of a new
genus, for which the name Marinibactrum halimedae gen. nov., sp. nov. is proposed.

Marinibactrum [Ma.ri.ni.bac’trum. L. adj. marinus of the sea; Gr. neut. n. baktron a staff or stick; N.L. neut. n. Marinibactrum rod of (inhabiting) the sea].

Has the following characteristics in addition to those given for the genus. Colonies are convex with thinly spreading,
rhizoid to undulate peripheries, transparent, glistening and white to pale yellow, 1.5–2.0 mm in diameter on 1/10 MB agar plates after 3 days of incubation at 25 °C. An oxygen concentration slightly lower than that of atmos-
pheric oxygen is preferable for growth initiation. Cells are 1.2–4.0 μm long and 0.4–0.6 μm wide on 1/10 MB agar. The range of NaCl concentration for growth is 1.0–5.0 % (w/v) with an optimum of 3.5 % (w/v). Growth occurs at pH 6.5–9.0 with an optimum of pH 8.0 and at 10–37 °C with an optimum of 25–30 °C. Produces a large amount of polysaccharide. Gelatin, casein, Tween 80, starch and aesculin are hydrolysed. Argar, cellulose, carrageenan, alginate, pectin and laminarin are not hydrolysed. Nitrate reduction, ONPG (p-nitrophenyl-β-D-galactopyranoside), ONPG, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase and urease are negative. Production of acetoin (Voges–Pros-
kauer test), H2S and indole, and citrate utilization are nega-
tive. Acid is produced from D-ribose, D-xylene, D-glucose, aesculin, maltose, starch, glycogen and 2-ketogluconate, but not from glycerol, D-arabinose, L-arabinose, L-xylene, D-adonitol, methyl β-D-xylene, D-galactose, L-sorbos

e 25–30 °C. Produces a large amount of polysaccharide. Gelatin, casein, Tween 80, starch and aesculin are hydrolysed. Argar, cellulose, carrageenan, alginate, pectin and laminarin are not hydrolysed. Nitrate reduction, ONPG (p-nitrophenyl-β-D-galactopyranoside), ONPG, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase and urease are negative. Production of acetoin (Voges–Proskauer test), H2S and indole, and citrate utilization are negative. Acid is produced from D-ribose, D-xylene, D-glucose, aesculin, maltose, starch, glycogen and 2-ketogluconate, but not from glycerol, D-arabinose, L-arabinose, L-xylene, D-adonitol, methyl β-D-xylene, D-galactose, L-sorbos
lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase are positive. Esterase (C4) and lipase (C14) are weakly positive. Trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase are negative.

The DNA G + C content of the type strain is 45.9 mol%. The type strain, Q-192T (=NBRC 110095T = NCIMB 14932T), was isolated from the surface of a macroalga, Halimeda sp., collected from the coastal region of Ishigaki Island, Japan.

Acknowledgements

We thank Moriyuki Hamada for his advice on polar lipid analysis. This work was supported by the New Energy and Industrial Technology Development Organization of Japan (NEDO).

References


