**Thalassobaculum litoreum** gen. nov., sp. nov., a member of the family **Rhodospirillaceae** isolated from coastal seawater

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A Gram-negative, facultatively anaerobic strain with slightly curved and straight rod-shaped cells, strain CL-GR58\(^T\), was isolated from coastal seawater (near Gori, Korea). Analyses of the 16S rRNA gene sequence revealed that strain CL-GR58\(^T\) belonged to the family **Rhodospirillaceae** with **Azospirillum lipoforum** as its closest relative (gene sequence similarity of 90.9%). Phylogenetic analyses of the 16S rRNA gene sequences showed that strain CL-GR58\(^T\) was not associated with any known genera in the family **Rhodospirillaceae**. The novel strain grew in the presence of 1–10% sea salts, optimally at 30–35 °C and pH 8. The major cellular fatty acids consisted of C\(_{18:1}\)ω7c (48.5%), C\(_{16:0}\) (14.8%), C\(_{17:0}\) (12.2%), C\(_{19:0}\) cyclo ω8c (6.3%) and summed feature 3 (C\(_{16:1}\)ω7c and/or iso-C\(_{15:0}\)2-OH, 6.0%). Among the phylogenetically related genera, the fatty acid C\(_{17:0}\) was found only in strain CL-GR58\(^T\). The DNA G+C content of the novel strain was 68.0 mol%. According to phylogenetic analyses of the 16S rRNA gene sequence, fatty acid content and the physiological data, strain CL-GR58\(^T\) represents a novel species in a new genus of the family **Rhodospirillaceae**, for which the name **Thalassobaculum litoreum** gen. nov., sp. nov. is proposed. The type strain of the type species is CL-GR58\(^T\) (=KCCM 42674\(^T\)=DSM 18899\(^T\)).

The family **Rhodospirillaceae**, belonging to subgroup 1 (Woese et al., 1984) of the class Alphaproteobacteria, currently comprises 14 genera (http://www.bacterio.cict.fr). Members of the family **Rhodospirillaceae** exhibit a variety of modes of growth: the genera **Rhodovibrio** and **Phaeospirillum** and some species in three other genera (i.e. **Rhodocista centenaria**, **Rhodospirillum photometricum** and **Roseospira marina**) are capable of both photo- and chemoheterotrophic growth under anoxic conditions in the light and under microoxic to oxic conditions in the dark, respectively (Nissen & Dundas, 1984; Mack et al., 1993; Garrity et al., 2005). The other species in the genera **Rhodospirillum** and **Roseospira** (i.e. **Rhodospirillum rubrum**, **Roseospira mediosalina** and **Roseospira navarrensis**) are capable of photolithoautotrophic growth (with hydrogen or sulfide as an electron donor) as well as the above growth modes (Guyoneaud et al., 2002; Garrity et al., 2005). Other species in the genus **Rhodocista** (i.e. **Rhodocista pekingensis**) can grow photo- and chemolitho-heterotrophically (with hydrogen as an electron donor) under anoxic conditions in the light and under oxic conditions in the dark, respectively (Zhang et al., 2003). The genus **Rhospira** is capable of photolitho- (with sulfide as an electron donor) and chemoheterotrophic growth under anoxic conditions in the light and under microoxic conditions in the dark, respectively (Pfenning et al., 1997). The genus **Telmatospirillum** is capable of chemoheterotrophic growth under anoxic to microoxic conditions and both chemolithoautotrophic and lithoautotrophic growth (with hydrogen as an electron donor), under microoxic conditions (Sizova et al., 2007). Furthermore, chemoheterotrophic genera, **Azospirillum** (except **Azospirillum oryzae** which can grow chemolitho-heterotrophically utilizing hydrogen as an electron donor; Xie & Yokota, 2005), **Skermanella**, **Inquilius**, **Tistrella**, **Thalassospira**, **Defluvicoccus** and **Magnetospirillum** have been reported (Sly & Stackebrandt, 1999; Coenye et al., 2002; López-López et al., 2002; Shi et al., 2002; Garrity et al., 2005; Maszenan et al., 2005).

Most species in the family **Rhodospirillaceae** have been isolated from various non-marine habitats such as freshwater, activated sludge biomass, soil and roots of plants and cystic fibrosis patients (Coenye et al., 2002; Garrity et al., 2005). Only limited numbers of members in the family **Rhodospirillaceae** have been discovered in marine environments (López-López et al., 2002): only five species affiliated with the genera **Rhodovibrio** (**Rhodovibrio salinarum** and **Rhodovibrio sodomensis**; Nissen & Dundas, 1984; Mack et al., 1993) and **Thalassospira** (**Thalassospira lucentensis**, **Thalassospira profundimaris** and **Thalassospira xiamenensis**, López-López et al., 2002; Liu et al., 2007) in
the family \textit{Rhodospirillaceae} have been isolated from seawater samples.

Here, we describe a chemoheterotrophic bacterium, strain CL-GR58\textsuperscript{T}, isolated from coastal seawater in Gori, Korea. In August 2005, coastal seawater and sediment samples were brought back to the laboratory and incubated in a 150 mm diameter glass Petri dish for around 15 months at room temperature. Without disturbing the sediment, a 150 mm diameter glass Petri dish for around 15 months at room temperature. Without disturbing the sediment, a 100 µl sample of seawater was removed from the surface and spread on a marine agar 2216 (MA; Difco) plate, which was then incubated at 30 °C for 1 week. Strain CL-GR58\textsuperscript{T} was isolated and subsequently purified on MA at 30 °C four times. The strain was maintained both on MA at 30 °C and in marine broth 2216 (MB; Difco) supplemented with 30 % (v/v) glycerol at −80 °C.

The 16S rRNA gene was amplified from a single colony by using PCR with \textit{Taq} DNA polymerase (Bioneer) and primers 27F and 1492R (Lane, 1991). The PCR product was purified by using the Accuprep PCR purification kit (Bioneer) and direct sequence determination of the purified 16S rRNA gene was performed with an Applied Biosystems automated sequencer (ABI3730XL) at Macrogen, Seoul, Korea. The almost-complete 16S rRNA gene sequence of strain CL-GR58\textsuperscript{T} (1336 nucleotides) was obtained and compared with available 16S rRNA gene sequences in GenBank using \textit{BLASTN} searches (Altschul et al., 1990). The sequence of strain CL-GR58\textsuperscript{T} was manually aligned with all available 16S rRNA gene sequences of recognized species in the family \textit{Rhodospirillaceae} obtained from GenBank and Ribosomal Database Project (Cole et al., 2003) databases using known 16S rRNA secondary structure information. Phylogenetic trees were constructed by neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods. An evolutionary distance matrix for the neighbour-joining method was generated according to the model of Jukes & Cantor (1969). The robustness of the tree topologies was assessed by bootstrap analyses based on 1000 replications for the neighbour-joining and maximum-parsimony methods and 100 replications for the maximum-likelihood method. Alignment analysis was carried out using the \textit{jPHYDIT} program (Jeon et al., 2005) and phylogenetic analyses were carried out using \textit{MEGA} 3 (Kumar et al., 2004) and \textit{PAUP} 4.0 (Swofford, 1998). Likelihood parameters were estimated by using the hierarchical ratio test in \textsc{MODELTREE}, version 3.04 (Posada & Crandall, 1998).

The fatty acid methyl esters in whole cells of strain CL-GR58\textsuperscript{T} grown on MA at 30 °C for 5 days were analysed with gas chromatography according to the instructions of the Microbial Identification System (MIDI) at the Korean Culture Center of Microorganisms (KCCM) in Seoul, Korea. The DNA G+C content was analysed by HPLC (HP 100; Hewlett Packard) analysis of deoxyribonucleosides as described by Mesbah \textit{et al.} (1989), after DNA extraction according to the method of Marmur (1961). Lambda DNA was used as a standard. The quinone system was determined according to Minnikin \textit{et al.} (1984) and analysed by HPLC as described by Collins (1985).

Morphological and physiological characteristics were determined. Gram-staining was performed as described by Smibert & Krieg (1994). Cell motility was observed by the hanging drop method (Suzuki \textit{et al.}, 2001). Cell morphology and presence of flagella was observed using transmission electron microscopy (EX2; JEOL). Anaerobic growth was checked on MA using the GasPak anaerobic system (BBL). Poly-β-hydroxybutyrate granules were observed by epifluorescence microscopy (BX60; Olympus) after Nile blue A staining (Ostle & Holt, 1982). Bacteriochlorophyll \textit{a} production was determined in 90 % acetone extracts using a spectrophotometer (Ultraspex 2000; Pharmacia Biotech) for cells that had been grown either in the light or in the dark for 7 days. The temperature range for growth was examined on the basis of colony formation on MA incubated at temperatures ranging from 5 to 40 °C, using increments of 5 °C. The pH range (pH 3–10, using increments of 1 pH unit) for growth was determined by assessing changes in OD\textsubscript{600} over the incubation period (up to 7 days) in MB. The final pH was adjusted using 1 M NaOH and 1 M HCl solutions. The tolerance of strain CL-GR58\textsuperscript{T} to sea salts was determined both on the basis of colony formation on synthetic Zobell agar (5 g Bacto peptone, 1 g yeast extract, 0.1 g ferric citrate, 15 g Bacto agar, 1 l distilled water) and assessing changes in OD\textsubscript{600} in Zobell broth with different concentrations (0–10 % increments of 1 % and 15 %, w/v) of sea salts (Sigma). Growth in a medium containing NaCl as the sole salt was determined both on the basis of colony formation on synthetic Zobell agar and by assessing changes in OD\textsubscript{600} in Zobell broth with different concentrations of NaCl (0–10 % increments of 1 % and 15 %, w/v). The ability to fix dinitrogen was tested, under anoxic conditions, on NFB medium (5.0 g malate, 0.5 g K\textsubscript{2}HPO\textsubscript{4}, 0.2 g MgSO\textsubscript{4}\cdot7H\textsubscript{2}O, 0.1 g NaCl, 0.02 g CaCl\textsubscript{2}, 2H\textsubscript{2}O, 2 ml 0.5 % bromothymol blue in 0.2 M KOH, 1 ml sterile filtered vitamin solution, 2 ml sterile filtered micronutrient solution, 4 ml 1.64 % FeEDTA solution, 4.5 g KOH, 1 l distilled water and 15 g l\textsuperscript{−1} Bacto agar, at pH 6.8; Eckert \textit{et al.}, 2001), using \textit{Azospirillum doebereinerae} KCTC 12904\textsuperscript{T} as the reference strain. Further, the presence of the \textit{nifH} gene fragment was determined by using PCR amplification with specific primers (PolF/PolR; Poly \textit{et al.}, 2001) for both strain CL-GR58\textsuperscript{T} and \textit{A. doebereinerae} KCTC 12904\textsuperscript{T}. The oxidase and catalase tests were performed according to the protocols described by Smibert & Krieg (1994). Gelatinase, amylase and nitrate reductase activities and degradation of Tween 80 were determined according to Hansen & Sørheim (1991). In addition, other enzyme activities were assayed using the API ZYM kit (bioMérieux) according to the manufacturer’s instructions, except that the cell suspension was prepared using artificial seawater (24 g NaCl, 5.1 g MgCl\textsubscript{2}, 4 g Na\textsubscript{2}SO\textsubscript{4}, 1.1 g CaCl\textsubscript{2}, 0.7 g KCl, 0.2 g NaHCO\textsubscript{3}, 0.1 g
KBr, 0.027 g H$_3$BO$_3$, 0.024 g SrCl$_2$, 0.003 g NaF, 1 l distilled water; Lyman & Fleming, 1940).

Carbon utilization was tested using the basal broth medium supplemented with yeast extract (23.6 g NaCl, 0.64 g KCl, 4.53 g MgCl$_2$·6H$_2$O, 5.94 g MgSO$_4$·7H$_2$O, 1.3 g CaCl$_2$·2H$_2$O, 0.2 g NaNO$_3$, 0.2 g NH$_4$Cl, 0.05 g yeast extract, 1 l distilled water; Bruns et al., 2001) containing 0.4 % carbon source. Strain CL-GR58$^T$ was incubated for 4 weeks and carbon utilization was scored as negative when the growth rate was equal to, or less than, that in the negative control with no carbon source. Growth rate was measured by monitoring changes in OD$_{600}$. Resistance to antibiotics was determined by the disc diffusion plate method (Bauer et al., 1966).

The 16S rRNA gene sequence of strain CL-GR58$^T$ showed 90.9 % similarity to the type strains of *Azospirillum lipoferum*, 89.8 % to *Azospirillum oryzae*, 89.7 % to *Azospirillum canadense*, 89.5 % to *A. doebereinerae* and 79.3–89.5 % to the other type species of the family *Rhodospirillaceae*. Although strain CL-GR58$^T$ was closely related to species of the genus *Azospirillum* on the basis of 16S rRNA gene sequence similarity, the novel strain was not included in the clade of the genera *Azospirillum*, *Rhodocista* or *Skermanella* (Fig. 1). Further, the lineage of strain CL-GR58$^T$ was not associated with any other genera of the family *Rhodospirillaceae*. Therefore, phylogenetically, strain CL-GR58$^T$ should be recognized as representing a distinct genus in the family *Rhodospirillaceae*.

The fatty acid profile of strain CL-GR58$^T$ was composed of C$_{18:1\alpha7c}$ (48.5 %), C$_{16:0}$ (14.8 %), C$_{17:0}$ (12.2 %), C$_{19:0}$ cyclo 08c (6.3 %), summed feature 3 (iso-C$_{15:0}$ 2-OH and/or C$_{16:1\alpha7c}$, 6.0 %), 11-methyl C$_{18:1\alpha7c}$ (3.0 %), C$_{18:0}$ (2.0 %), C$_{15:0}$ (1.5 %) and an unknown fatty acid (ECL 18.814; 1.4 %) (Table 1). Fatty acid C$_{18:1\alpha7c}$ was commonly found as a major component in strain CL-GR58$^T$ and related genera (Table 1); a feature shared by members of the class *Alphaproteobacteria* (Labrenz et al., 2000). However, a significant amount of C$_{17:0}$ (12.2 %)

![Fig. 1. Neighbour-joining tree derived from 16S rRNA gene sequences for strain CL-GR58$^T$ and members of the family Rhodospirillaceae with Escherichia coli as an outgroup. Only bootstrap values above 60 % are shown (1000 resamplings) at the branching points. Solid circles indicate that the corresponding nodes were also recovered in maximum-likelihood and maximum-parsimony trees. Bar, 0.02 nucleotide substitutions per site.](http://ijs.sgmjournals.org)
was only found in strain CL-GR58<sup>T</sup> and was not found at significant levels in the related genera *Azospirillum*, *Rhodovibrio*, *Tistrella* or *Inquilinus* (Table 1). Furthermore, the absence of fatty acids C<sub>16:0</sub> 2-OH, C<sub>16:0</sub> 3-OH, C<sub>17:0</sub> 2-OH and C<sub>18:1</sub> 2-OH clearly differentiated strain CL-GR58<sup>T</sup> from the genera *Azospirillum*, *Tistrella* and *Inquilinus* (Table 1). A significant concentration of C<sub>18:1</sub> 2-OH (15.5–16.1 %) observed in the genera *Tistrella* and *Inquilinus* was not detected in strain CL-GR58<sup>T</sup> or in the genus *Rhodovibrio*. Absence of fatty acid C<sub>19:0</sub> cyclo<sub>8</sub>C differentiated the genus *Rhodovibrio* from other related genera. Therefore, the fatty acid pattern of strain CL-GR58<sup>T</sup> differs distinctly from those of related genera in the family *Rhodospirillaceae*. The major quinone in strain CL-GR58<sup>T</sup> was ubiquinone 10 (Q-10), which is also found in the genera *Rhodocista* and *Rhodovibrio*, Q-9, and Q-10 and MK-10 were found, respectively (Table 2). The G+C content of the DNA was 68.0 mol% (Table 2). Cells of strain CL-GR58<sup>T</sup> were Gram-negative, slightly curved and straight rod-shaped and approximately 0.3–0.5 μm wide and 1.3–1.5 μm long. Cells were motile by means of a polar flagellum. Colonies were circular, convex and cream–yellow on MA plates. After 10 days on MA at 30 °C, colonies were approximately 1 mm in diameter. Strain CL-GR58<sup>T</sup> was heterotrophic and facultatively anaerobic. Cells contained poly-β-hydroxybutyrate granules. Bacteriochlorophyll α was not detected. The optimum growth temperature was 30–35 °C; the optimum pH was 8. Growth occurred at sea salts concentrations of 1–10 % (w/v; optimum 2–4 %), but no growth occurred in media containing only NaCl as a salt. Strain CL-GR58<sup>T</sup> was unable to fix dinitrogen and did not possess a *nifH* gene, whereas *A. doebereinerae* was able to grow on the NFb medium by fixing nitrogen and had a *nifH* gene (data not shown). Oxidase, catalase, gelatinase, nitrate reductase and amylase activities were positive. Tween 80 was not hydrolysed. According to API ZYM tests, alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α- and β-glucosidases and N-acetyl-β-glucosaminidase activities were positive and were weakly positive for esterase lipase (C8), lipase (C14), α- and β-galactosidases, α-mannosidase and α-fucosidase. No activities were found for cysteine arylamidase, trypsin, α-chymotrypsin and β-glucuronidase. Growth occurred on D-ribose, sucrose, L-arabinose and yeast extract. No growth occurred on acetate, α-ketobutyric acid, citrate, fructose, galactose, glucose, mannitol, raffinose, salicin, trehalose, ethanol, inositol, inulin, lactose, L-lysine, L-rhamnose, N-acetylglucosamine, oxalic acid, pyruvic acid, succinate or L-proline. Strain CL-GR58<sup>T</sup> was susceptible to streptomycin, gentamicin, vancomycin, kanamycin, penicillin, erythromycin, tetracycline, chloramphenicol, ciprofloxacin and ampicillin, but resistant to mitomycin C, nalidixic acid and polymyxin B.

Strain CL-GR58<sup>T</sup> could be differentiated phenotypically from the genus *Azospirillum* by its inability to perform nitrogen fixation and from the genera *Rhodocista* and *Rhodovibrio* by the absence of bacteriochlorophyll α (Table 2). Strain CL-GR58<sup>T</sup> could be differentiated from members of the genus *Defluviicoccus* by some phenotypic features (presence of flagella, positive activity for oxidase) and from the genus *Skermanella* by the positive activity for gelatinase. The growth temperature range distinguished strain CL-GR58<sup>T</sup> (10–35 °C) from members of the genus *Inquilinus* (25–42 °C). In addition, the salt tolerance range distinguished strain CL-GR58<sup>T</sup> (1–10 %) from the genera *Azospirillum* (<5 %), *Tistrella* (<1 %), *Skermanella* (<5 %) and *Inquilinus* (<6 %) (Table 2).

In conclusion, phylogenetic analyses based on 16S rRNA gene sequences, chemotaxonomic data (fatty acid profiles,
Table 2. Selected characteristics that differentiate strain CL-GR58T from other phylogenetically related genera in the family Rhodospirillaceae

Taxa: 1, strain CL-GR58T; 2, Azospirillum (Tarrand et al., 1978; Reinhold et al., 1987; Khammas et al., 1989; Sly & Stackebrandt, 1999; Eckert et al., 2001; Xie & Yokota, 2005; Peng et al., 2006; Meinaz et al., 2007); 3, Rhodocista (Favinger et al., 1989; Kawasaki et al., 1992; Imhoff et al., 1998; Zhang et al., 2003); 4, Rhodovibrio (Nissen & Dundas, 1984; Mack et al., 1993; Imhoff et al., 1998; Garrity et al., 2005); 5, Deflavivibio (Maszenan et al., 2005); 6, Tistrella (Shi et al., 2002); 7, Skermanella (Sly & Stackebrandt, 1999); 8, Inquilinus (Coene et al., 2002). +, Positive; w, weakly positive; −, negative; v, variable; MP, monopolar; BP, bipolar; NA, not available. All strains are Gram-negative and catalase-positive. Data for catalase were not available for the genera Rhodocista and Rhodovibrio.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony colour</td>
<td>Coastal seawater</td>
<td>Soil, root</td>
<td>Fresh water</td>
<td>Seawater, ponds of solar salt</td>
<td>Sludge</td>
<td>Wastewater</td>
<td>Lake water</td>
<td>Cystic fibrosis patients</td>
</tr>
<tr>
<td></td>
<td>Cream–yellow</td>
<td>Pink, white</td>
<td>Red, pink</td>
<td>Pink, red</td>
<td>Beige</td>
<td>NA</td>
<td>Apricot–coloured</td>
<td>Pink</td>
</tr>
<tr>
<td>Cell size (width × length; μm)</td>
<td>0.3–0.5 × 1.3–1.5</td>
<td>0.6–0.9 × 2–30</td>
<td>1–2 × 3.0</td>
<td>0.6–0.9 × 1.0–3.5</td>
<td>1.5–4.5</td>
<td>0.7–1.0 (width)</td>
<td>1–1.5 × 2–3</td>
<td>NA</td>
</tr>
<tr>
<td>Cell shape</td>
<td>Slightly curved and straight rod</td>
<td>Plump, vibrioid</td>
<td>Straight rod</td>
<td>Vibrioid, spiral</td>
<td>Vibrioid, spiral</td>
<td>Coccus</td>
<td>Rod</td>
<td>Rod</td>
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<td>Flagella</td>
<td>MP</td>
<td>V</td>
<td>MP</td>
<td>MP, BP</td>
<td>Absent</td>
<td>MP</td>
<td>MP</td>
<td>NA</td>
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<tr>
<td>Temperature range (°C)</td>
<td>10–35</td>
<td>4–41</td>
<td>25–47</td>
<td>20–47</td>
<td>20–30</td>
<td>20–40</td>
<td>10–37</td>
<td>25–42</td>
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<tr>
<td>Temperature optimum (°C)</td>
<td>30–35</td>
<td>20–41</td>
<td>31–45</td>
<td>35–42</td>
<td>25–30</td>
<td>30</td>
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<td>pH range</td>
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<td>7–8</td>
<td>5–8.5</td>
<td>5–9</td>
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<tr>
<td>pH optimum</td>
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<td>5–7.2</td>
<td>6.8–7</td>
<td>7–8</td>
<td>7.3–8</td>
<td>7.4</td>
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<td>Salt tolerance (%; w/v)</td>
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<td>3–24</td>
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<td>&lt;1</td>
<td>&lt;5</td>
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<td>Poly-β-hydroxybutyrate</td>
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<td>+</td>
<td>+</td>
<td>+</td>
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<td>Bacteriochlorophyll a</td>
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<td>+</td>
<td>NA</td>
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<td>Oxidase</td>
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<td>NA</td>
<td>NA</td>
<td>−</td>
<td>+</td>
<td>V</td>
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<td>Gelatinase</td>
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<td>NA</td>
<td>NA</td>
<td>W</td>
<td>−</td>
<td>V</td>
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<tr>
<td>Major quinone</td>
<td>Q-10</td>
<td>Q-10</td>
<td>Q-9</td>
<td>Q-10, MK-10</td>
<td>NA</td>
<td>Q-10</td>
<td>Q-10</td>
<td>NA</td>
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<tr>
<td>DNA G + C content (mol%)</td>
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<td>64–71</td>
<td>68.3–69.9</td>
<td>66.2–68.1</td>
<td>66</td>
<td>67.5</td>
<td>67.2</td>
<td>70.9</td>
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<tr>
<td>N-Acetylglucosamine</td>
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<td>V</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>+</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>L-Arabinose</td>
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<td>V</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>α-Glucose</td>
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<td>V</td>
<td>−</td>
<td>−</td>
<td>+</td>
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<td>−</td>
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<tr>
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<td>V</td>
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<tr>
<td>Inositol</td>
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<td>V</td>
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<td>−</td>
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<td>D-Mannitol</td>
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<td>L-Rhamnose</td>
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<td>D-Ribose</td>
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<td>NA</td>
<td>NA</td>
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<td>Sucrose</td>
<td>+</td>
<td>V</td>
<td>−</td>
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Thalassobaculum (Tha.las’so.ba.cu.lum. Gr. n. Thalassa the sea; L. neut. n. baculum stick; N.L. neut. n. Thalassobaculum rod-shaped bacterium from the sea).

Cells are Gram-negative, slightly curved and straight rod-shaped and are motile by means of a polar flagellum. Growth is heterotrophic and facultatively anaerobic. Oxidase- and catalase-positive. Bacteriochlorophyll a is not detected. Unable to fix dinitrogen under anoxic conditions. Dominate cellular fatty acids are C₁₈:1ω7c, C₁₆:0, C₁₇:0, C₁₉:0 cyclo ω8c and summed feature 3 (C₁₆:1ω7c and/or iso-C₁₅:0 2-OH). The isoprenoid quinone is Q-10. The G+C content of the DNA is 68.0 mol%. Phylogenetically, the genus is a member of the family Rhodospirillaceae. The type species is Thalassobaculum litoreum.

Description of Thalassobaculum gen. nov.

Thalassobaculum (Tha.las’so.ba.cu.lum. L. neut. adj. littor-eum of the shore).
Displays the following properties in addition to those given in the genus description. Colonies are circular, convex and cream–yellow on marine agar plates. After 10 days on MA at 30 °C, colonies are approximately 1 mm in diameter. Cells are approximately 0.3–0.5 μm wide and 1.3–1.5 μm long. Grows at between 10 and 35 °C (optimum of 30–35 °C) and pH 7–9 (optimum of pH 8). Growth occurs at sea salts concentrations of 1–10 % (w/v) (optimum 2–4 %), but no growth occurs in media containing only NaCl as a salt. Cells contain poly-β-hydroxybutyrate granules. Gelatinase and amylase are produced. TWEEN 80 is not hydrolysed. Nitrate is reduced to nitrite. Positive for the following enzyme activities as tested with the API ZYM system: alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-Bl-phosphohydrolase, α- and β-glucosidases and N-acetyl-α-glucosaminidase; weakly positive for esterase lipase (C8), lipase (C14), α- and β-galactosidases, α-mannosidase and α-fucosidase. No activities for cystine arylamidase, trypsin, α-chymotrypsin and β-glucuronidase. D-ribose, sucrose, L-arabinose and yeast extract are utilized as carbon sources. Negative for utilization of the following: acetate, α-ketobutyric acid, citrate, fructose, galactose, glucose, mannitol, raffinose, salicin, trehalose, ethanol, inositol, inulin, lactose, L-lysine, L-rhamnose, N-acetylgalcosamine, oxalic acid, pyruvic acid, succinate and L-proline. Cells are sensitive to (μg per disc): streptomycin (10), gentamicin (10), vancomycin (30), kanamycin (30), penicillin (10), erythromycin (15), tetracycline (30), chloramphenicol (30), ciprofloxacin (5) and ampicillin (10).

The type strain, CL-GR58 T (=KCCM 42674 T=DSM 18839 T), was isolated from coastal seawater, Korea.

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References


