Kiloniella laminariae gen. nov., sp. nov., an alphaproteobacterium from the marine macroalga Laminaria saccharina

Jutta Wiese, Vera Thiel, Andrea Gärtner, Rolf Schmaljohann and Johannes F. Imhoff

Kieler Wirkstoff-Zentrum am Leibniz-Institut für Meereswissenschaften IFM-GEOMAR, Düsternbrooker Weg 20, 24105 Kiel, Germany

A novel alphaproteobacterium, strain LD81T, was isolated from the marine macroalga Laminaria saccharina. The bacterium is mesophilic and shows a typical marine growth response. It is a chemoheterotrophic aerobe with the potential for denitrification. Growth optima are 25 °C, pH 5.5 and 3 % NaCl. Strain LD81T has a unique phylogenetic position, not fitting any of the known families of the Alphaproteobacteria. The 16S rRNA gene sequence revealed a distant relationship to species of several orders of the Alphaproteobacteria, with less than 90 % sequence similarity. Phylogenetically, strain LD81T is related to the type strains of Terasakiella pusilla (88.4 % 16S rRNA gene sequence similarity) and the three Thalassospira species (88.9–89.2 %). It forms a cluster with these bacteria and a novel as-yet undescribed isolate (KOPRI 13522; 96.6 % sequence similarity). Strain LD81T has a relatively low DNA G+C content (51.1 mol%) and, due to its distant phylogenetic position from all other alphaproteobacteria, strain LD81T (=NCIMB 14374T =JCM 14845T) is considered as the type strain of a novel species within a new genus, for which the name Kiloniella laminariae gen. nov., sp. nov. is proposed. The genus Kiloniella represents the type of the new family Kiloniellaceae fam. nov. and order Kiloniellales ord. nov.

The Alphaproteobacteria is one of the most well-represented bacterial groups observed in marine habitats (Giovannoni & Rappé, 2000), with members of the orders Caulobacterales, Sphingomonadales, Rhizobiales, Rickettsiales, Rhodobacterales, Rhodospirillales, Kordiimonadales and ‘Parvularculales’ being reported (Garrity et al., 2005; Kwon et al., 2005). In a study concerning the phylogenetic analysis of bacteria that are associated with the marine brown alga Laminaria saccharina from the Baltic Sea, strain LD81T was isolated.

Pieces of Laminaria saccharina tissue were suspended in sterile seawater and homogenized using an Ultraturrax T25 (IKA Werke). The suspension was diluted in sterile seawater and plated on TSB medium (1 %: 3 g Difco tryptic soy broth, 7 g NaCl, 15 g Bacto agar; pH 7.2). The plates were incubated at 22 °C in the dark for 20 days. After good growth was obtained, an overlay containing TSB medium (with 8 g l⁻¹ Bacto agar) and 10 % (v/v) overnight culture of Candida glabrata DSM 6425 was poured onto the plates and incubated for 24 h at 22 °C in order to detect inhibition zones against C. glabrata by individual colonies. Antibiotically active colonies were repeatedly streaked on agar plates with TSB medium to obtain pure cultures. One of the pure cultures obtained was strain LD81T, which was stored at −80 °C using the Cryobank System (Mast Diagnostica GmbH) for maintenance.

Cell morphology was examined by scanning electron microscopy. Strain LD81T was cultivated for 24 h in marine broth (MB; Difco 2216) at 28 °C on a rotary shaker with shaking at 95 r.p.m., followed by fixation with a final concentration of 1 % formol and filtration through 0.2 μm polycarbonate filters (Sarstedt). The filters were applied in a subsequent ethanol series for dehydration (50, 70 and 90 % and three times in 100 % for 10 min each) (Boyde & Wood, 1969), critical-point dried with CO2 and sputter-coated with Au/Pb and examined with a Zeiss DSM 940 scanning electron microscope. Light microscopy was used for determination of the cell size and to study motility.

The temperature (4–50 °C) and pH (pH 3.5–10) ranges as well as the optima for growth of strain LD81T were examined by cultivation in MB. The temperature and pH...

**Abbreviations:** ME, minimum evolution; ML, maximum-likelihood; NJ, neighbour-joining; PHB, poly-β-hydroxybutyrate.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain LD81T is AM749667.

16S rRNA gene sequence similarities between strain LD81T and related type strains are available as supplementary material in IJSEM Online.
optima were assessed after incubation for 3 days. Ranges were ascertained after prolonged incubation for 3 weeks. Growth was measured photometrically at OD$_{600}$. Salt relations (0–10% NaCl, w/v) were determined after incubation at 25 °C for 10 days on a basal medium (l$^{-1}$: 1 g Bacto peptone, 5 g yeast extract, 15 g Bacto agar, pH 7.0) supplemented with NaCl.

Well-grown fresh colonies of overnight cultures [grown on half-strength MB agar (l$^{-1}$: 17 g Difco 2216, 15 g Bacto agar) at 28 °C] were used for the Gram reaction using KOH according to Gregersen (1978), for poly-$\beta$-hydroxybutyrate (PHB) staining with Sudan black following Smibert & Krieg (1994) and for the catalase reaction (detected with 5% H$_2$O$_2$). The presence of PHB was confirmed by phase-contrast microscopy (Axiophot; Zeiss). Luminescence was tested in liquid and on solid half-strength MB supplemented with 3% glycerol. The adsorption spectrum of disrupted cells was measured using a UV–Vis spectrophotometer Lambda 2 (Perkin Elmer) to determine the presence of photosynthetic pigments.

The aerobic oxidation of organic carbon compounds was tested using the Biolog GN2 system. Strain LD81$^T$ was inoculated in half-strength MB (17 g Difco 2216 l$^{-1}$) and incubated overnight. Cells were centrifuged at 8000 g for 10 min, resuspended in 1% NaCl solution and adjusted to an OD$_{600}$ of 0.8–1.3. Three microplates were inoculated with this suspension and incubated at 22 °C for 48 h. Utilization of compounds was scored as positive when three positive reactions were observed. In addition, further physiological characteristics including enzyme activities were tested using API 20E strips for Gram-negative bacteria (bioMérieux) and API ZYM strips (bioMérieux) according to the manufacturer’s instructions. The inoculum was prepared as described above and the test systems were inoculated at 32 °C for 3 days. Both tests were run in triplicate.

The DNA base composition (G+C content) of strain LD81$^T$ was determined by the HPLC method of Mesbah et al. (1989). The profile of cellular fatty acids was studied using GC analysis according to the Microbial Identification System (MIDI Inc.) (Sasser, 1990). Both determinations were carried out by the German Collection of Microorganisms and Cell Cultures (DSMZ GmbH, Braunschweig, Germany). Extraction of genomic DNA and amplification and sequencing of the 16S rRNA gene were performed according to Gärtner et al. (2008).

Phylogenetic classification was performed with the Naive Bayesian rRNA Classifier (Wang et al., 2007) version 2.0 of the Ribosomal Database Project (RDP) release 9.56 (http://rdp.cme.msu.edu/index.jsp).

For phylogenetic study, the nearest bacterial relatives of strain LD81$^T$ were determined by comparison to 16S rRNA gene sequences in the NCBI GenBank and EMBL databases using BLAST (Altschul et al., 1997) and the Seqmatch program of the RDP II (http://rdp.cme.msu.edu/seqmatch/seqmatch_intro.jsp), restricted to type strains. Sequences were aligned using the FASTALIGN function of the alignment editor implemented in the ARB software package (http://www.arb-home.de) (Ludwig et al., 2004) and refined manually employing secondary structure information. For phylogenetic calculations, PhyML Online (Guindon et al., 2005) and MEGA version 3.1 (Kumar et al., 2004) were used. Trees were calculated by the maximum-likelihood (ML) (Felsenstein, 1981), neighbour-joining (NJ) (Saitou & Nei, 1987) and minimum-evolution (ME) (Rzhetsky & Nei, 1993) methods. The ML tree was calculated using the GTR model and estimated proportion of invariable sites as well as the gamma distribution parameter. The NJ and ME trees were calculated based on distances corrected by Kimura’s two-parameter nucleotide substitution model, using sites corresponding to the ‘pairwise deletion’ option, respectively including transition and transversion substitutions and uniform substitution rates. Sequence similarity values were determined using the BLAST 2 SEQUENCES tool of the NCBI database (http://www.ncbi.nlm.nih.gov/BLAST/bl2seq/wblast2.cgi; Tatusova & Madden, 1999).

Colonies grown on MB agar for 7 days at 22 °C are cream-coloured, smooth and soft, 1–2 mm in diameter. Cells grown in MB for 24 h at 22 °C are motile with one polar flagellum. The cells are slender, slightly curved spirilla, and their size measured in the light microscope is 0.5–0.6 μm. Short rod-like cells and also longer filamentous cells were occasionally observed (Fig. 1).

Strain LD81$^T$ grows as a chemoheterotrophic, aerobic bacterium in complex media. It can use nitrate as an alternative electron acceptor, which is reduced to gaseous products (N$_2$O is the major product; the gene for N$_2$O reductase, nosZ, is lacking). The temperature for growth is 4–40 °C with an optimum at 25 °C. The pH for growth of

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**Fig. 1.** Scanning electron photomicrograph of cells of strain LD81$^T$ after cultivation in MB for 48 h at 28 °C. Bar, 2 μm.
the isolate is pH 3.5–9.5, with an optimum at pH 5.5. Growth is observed in media containing 0.3–8.0 % NaCl (optimum 3.0 %) or 0.3–10 % artificial sea salts (optimum 4.0 %), indicating a typical marine growth response. Catalase and oxidase reactions are positive and PHB is accumulated. Luminescence is negative.

Details concerning the physiological characteristics of strain LD81T including substrate utilization (according to Biolog GN2) and enzyme activities are given in the species description. Pigments are not produced under any growth conditions applied in this study.

The components of the fatty acid profile are listed in Table 1; the major cellular fatty acids are C18 : 1 (49 %), C16 : 1ω7c (31 %), C16 : 0 (9 %), C18 : 0 (3 %) and C19 : 0 cyclo ω8c (1 %). The DNA G+C content of strain LD81T was 51.1 mol%.

Phylogenetic classification using the Naive Bayesian rRNA Classifier led to the assignment of strain LD81T to the class Alphaproteobacteria (100 % confidence). Sequence similarity values are below 91 % to any of the 20 closest sequences of type strains of species with validly published names (Supplementary Table S1, available in IJSEM Online). BLAST searches revealed strain KOPRI 13522 as the closest strain LD81T including substrate utilization (according to Biolog GN2) and enzyme activities are given in the species description. Pigments are not produced under any growth conditions applied in this study.

Table 1. Fatty acid profile of strain LD81T

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Proportion (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>C12 : 0 ALDE</td>
<td>1.7</td>
</tr>
<tr>
<td>C13 : 0 AT 12–13</td>
<td>0.1</td>
</tr>
<tr>
<td>Unknown (ECL 14.502)</td>
<td>0.7</td>
</tr>
<tr>
<td>C15 : 0ω8c</td>
<td>0.3</td>
</tr>
<tr>
<td>Unknown (ECL 14.959)</td>
<td>1.2</td>
</tr>
<tr>
<td>C14 : 0 3-OH/iso-C16 : 1</td>
<td>1.2</td>
</tr>
<tr>
<td>C16 : 1ω7c</td>
<td>30.7</td>
</tr>
<tr>
<td>C16 : 0</td>
<td>8.5</td>
</tr>
<tr>
<td>C17 : 0ω8c</td>
<td>0.3</td>
</tr>
<tr>
<td>C17 : 0ω6c</td>
<td>0.1</td>
</tr>
<tr>
<td>C17 : 0</td>
<td>0.9</td>
</tr>
<tr>
<td>C18 : 0ω7c</td>
<td>48.6</td>
</tr>
<tr>
<td>C18 : 0</td>
<td>3.0</td>
</tr>
<tr>
<td>C17 : 0 3-OH</td>
<td>0.2</td>
</tr>
<tr>
<td>Unknown (ECL 18.814)</td>
<td>0.4</td>
</tr>
<tr>
<td>C19 : 0 Cyclo ω8c</td>
<td>1.4</td>
</tr>
<tr>
<td>C18 : 0 3-OH</td>
<td>0.5</td>
</tr>
<tr>
<td>C20 : 0ω9c</td>
<td>0.3</td>
</tr>
</tbody>
</table>

Values are percentages of total fatty acids. ECL, Equivalent chain-length.

Included in any of the known alphaproteobacterial orders with 100 % bootstrap values. They are related distantly to the group consisting of Terasakiella pusilla IFO 13613T and the three strains of the three known Thalassospira species (Thalassospira xianensis M-5T, Thalassospira lucentensis DSM 14000T and Thalassospira profundimaris WP0211T). Though members of the genus Thalassospira were provisionally assigned to the family Rhodospirillaceae (López-López et al., 2002), the phylogenetic analysis of our study does not confirm this affiliation (Fig. 2). Thalassospira species together with Terasakiella pusilla, strain KOPRI 13522 and strain LD81T form a strongly supported cluster (>90 % bootstrap values) clearly separated from the Rhodospirillaceae and Acetobacteraceae (<90 % sequence similarity). However, isolate LD81T and species of the genera Thalassospira and Terasakiella share 16S rRNA gene sequence similarities below 90 % (Supplementary Table S1). Therefore, strain LD81T is supposed to represent the type of a novel species within a new genus, which is the type of a new family and order.

Strain LD81T was also different morphologically, chemotaxonomically and physiologically from other members of the class Alphaproteobacteria. Strains belonging to the family Rhodospirillaceae and Acetobacteraceae exhibit significantly higher DNA G+C contents, generally well above 60 mol%, mostly between 62 and 67 mol% and, in some clusters of the Acetobacteraceae related to Craurococcus, above 70 and even up to 75 mol% (Shi et al., 2002). Representatives of the family Acetobacteraceae show ellipsoid, rod or coccoid cell morphology and usually do not require salt for growth. Many members of the Rhodospirillaceae produce photosynthetic pigments.

The nearest relatives of strain LD81T within the order Rhodobacterales are Pseudovibrio dentriﬁcans DN34T and Pseudovibrio ascidiaeicola NBRC 100514T (approx. 91 % 16S rRNA gene sequence similarity), which are rod-shaped and produce gelatinase (Shieh et al., 2004; Fukunaga et al., 2006). The nearest relatives within the order Rhizobiales, Mesorhizobium chacoense PR5T (90 % similarity), Ensifer terangae LMG 7834T (89.7 % similarity) and Pseudaminobacter salicylatoxidans BN12T (89.5 % similarity), exhibit DNA G+C contents of 62, 61.6 and 63.9 mol%, respectively (Velázquez et al., 2001; Young, 2003; de Lajudie et al., 1994; Kämpfer et al., 1999). To date, only one representative of the ‘Parvularculales’ has been described (Cho & Giovannoni, 2003). The production of pigments and the DNA G+C content of 60.8 mol% clearly distinguish Parvularcula bermudensis HTCC2503T from isolate LD81T. Kordiimonas gwangyangensis GW14-5T, the sole member of the order Kordiimonadales, is not able to reduce nitrate and, quite unusually for the Alphaproteobacteria, has a DNA G+C content of only 39.3 mol% and produces iso-C17 : 1ω as the predominant fatty acid (Kwon et al., 2005).

Common properties of strain LD81T and its closest neighbours in the phylogenetic tree, Terasakiella pusilla and the three Thalassospira species, are the salt requirement
Mesorhizobium chacoense PR5 (AJ278249)
Psuedomonasbaacter salicylatovorans BN12 (AF172042)
Mesorhizobium mediterraneum DSM 11557 (L38820)
Phyllobacterium leguminosarum ORS 1419 (AY788532)
Ensifer terangae LMG 7831 (X68388)
Roseobacter litoralis ATCC 49656 (X78912)
Ruegeria gelatinovorans IAM 12617 (D88523)
Roseovarius tolerans DSM 11457 (Y15151)
Silicibacter iwasakii DSM 13141 (UT77644)
Roseovarius halodurans Och 239 (DB6859)
Poracoccus dentiferians ATCC 17741 (Y16927)
Rhodobacter sphaeroides DSM 1568 (X38855)
Pseudomonas anatis NCPPB 10044 (AB002864)
Nesiobacter exalbescens LA338 (AB13441)
Stapnea aggregata IAM 12614 (D88520)
Symphyiella stellulata IAM 12615 (D88525)
Korondinos gwangyungensis GW 1465 (AY188384)
Parvularcula bermudensis HTCC2953 (AF544015)
Alistipes acidifaciens ATCC 15261 (AB016610)
Caulobacter vibrioides DSM 9893 (AJ277564)
Brevundimonas diminuta ATCC 11568 (M95064)
Sphingomonas paucimobilis ATCC 29637 (UJ7337)
Zymomonas mobilis ATCC 10886 (AB291031)
Blastomona urinaica KF-98 (Y15677)
Cruciferococcus roseus NS130 (D85628)
Paracoccus ruber NS80 (D85627)
Roseomonas aquatica TR5 (AM33587)
Roseococcus thiosulfatophilus RB-3 (X79206)
Aerocaldarchaeum entis (AB002706)
Kozakia burlingtonii Yo-3 (AB00321)
Gluconobacter oxydans NRRL 14391 (AB178433)
Tisselure mobiliis IAM 14872 (AB007166)
Rhodovibrio sodomensis DS1 (Y59072)
Azoarcinophilum lipophorum ATCC 29767 (M59061)
Magnetospirillum magneticum WISM 2008 (Y10109)
Rhodospirula turistica ATCC 700224 (AJ301276)
Roseospirillum gracei JA135 (AM25537)
Rhodopseudomonas palustris ATCC 17117 (CP0000230)
Thalassosspira xenoxoni DSM 14001 (AM294944)
Thalassospira profundimarum WP0217 (AY186199)
Terasakiella pusilla pFO 13613 (AB005768)
Strain KOPR1 13522 (GQ167245)
Kiloniella laminariae LD81 (A7494676)
Onorina butujugumari Karp (AF620074)
Rickettsia prowazekii Brenn® (M21789)
Wobocha pipiens (U23705)
Hyphomicrobium indicum NBP 24533 (AB195513)
Vibrio cholerae El-3712 (J031699)
Escherichia coli W3110 (AP009048)
Pseudomonas marina KMM 630® (AF140036)

and tolerance of up to approx. 8–10 % NaCl, the ability to reduce nitrate, the G+C content of the DNA (48–55 mol%) and the spiral to vibrioid cell shape (Table 2). Differences from these bacteria, in addition to clear differences in 16S rRNA gene sequences, are the proportions of fatty acids, the production of 3-hydroxyheptadecanoic acid by isolate LD81 and the reduction of nitrate to N2O by strain LD81 rather than nitrite, as produced by the other bacteria (Table 2). Also, Terasakiella pusilla possesses bipolar single flagella, in contrast to the single monopolar flagellum of LD81.

Because of its isolated phylogenetic position, its low G+C content of 51 mol%, the absence of pigments, the salt requirement and other distinguishing properties as outline above and in Table 2, strain LD81 is considered as the representative of a novel species and genus within a new family and order of the Alphaproteobacteria. The name Kiloniella laminariae gen. nov., sp. nov. is proposed, and Kiloniella is defined as the type genus of the new family Kiloniellaceae fam. nov. and new order Kiloniellales ord. nov.

Due to their distant relationship to Kiloniella, the species of Terasakiella and Thalassospira are not considered members of the family Kiloniellaceae. They may be included in the order Kiloniellales as members of a separate family or families. However, determination of their exact taxonomic standing requires further studies with a larger number of representatives, and their taxonomic position should be defined when more data are available.

**Description of Kiloniella gen. nov.**

Kiloniella [Ki.l0’ni.e’ll.a. L. n. Kilonium Latin name of the northern German city of Kiel; N.L. fem. dim. n. Kiloniella arbitrary name for a bacterium found in marine waters close to Kiel, the place of an important institution of marine research (the IFM-GEOMAR), in which the first strain of the genus was discovered].

Mesophilic, chemoheterotrophic bacteria with typical marine and moderately halotolerant growth response. Metabolism is aerobic and facultatively anaerobic with nitrate as electron acceptor. Major fatty acids are mono-
unsaturated, even-numbered, straight-chain C18 and C16 fatty acids, with C18:1ω7c as the dominant component. Cells have spiral to vibrioid cell shape, occasionally rod-like or filamentous, and are motile by means of flagella. Gram-negative, oxidase- and catalase-positive. PHB is accumulated. The G+C content of the DNA of the type strain of the type species is 51.1 mol%. The type species is Kiloniella laminariae.

**Description of Kiloniella laminariae sp. nov.**

Kiloniella laminariae (la.mi.na’ri.ae. N.L. fem. n. Laminaria botanical name of a genus of macroalgae; N.L. gen. fem. n. laminariae pertaining to the alga Laminaria, from which the type strain was isolated).

Displays the following properties in addition to those described above for the genus. Cells are slender, slightly curved spirilla, 0.5–0.6 μm wide and 2.5–5.0 μm long. Cells carry monopolar flagella. Pigments are not produced. Colonies are cream in colour and grow up to 1–2 mm in diameter on MB agar. Grows at 4–40 °C, pH 3.5–9.5 and from 0.3–10% artificial sea salts. Salt is required for growth. Optimal growth at 25 °C, pH 5.5 and 3% NaCl. Growth occurs chemoheterotrophically under oxic conditions. Nitrate is used as an alternative electron acceptor under anoxic conditions. Nitrate is reduced to N2O. Carbon sources (Biolog GN2) used are glycogen, α-D-glucose, monomethyl succinate, acetic acid, β-hydroxybutyrate, DL-lactate, succinamate, alaninamide, D-alanine, L-alanine, L-alanyl glycine, L-asparagine, L-aspartate, L-glutamate, glycyl L-aspartate, glycyl L-glutamate, L-histidine, hydroxy-L-proline, L-leucine, L-proline, L-pyroglutamate, L-serine, L-threonine, urocanate, inosine, uridine and glycerol. Enzyme activities are observed for alkaline phosphatase, leucine arylamidase, valine arylamidase, trypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase. Negative reactions are obtained in tests for esterase, esterase lipase, lipase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, β-mannosidase and α-fucosidase.

Furthermore, the API 20NE test system shows strong activities of arginine dihydrolase, citrate utilization and

Table 2. Differential characteristics of strain LD81T and phylogenetically related species of the genera Terasakiella and Thalassospira

Data for reference taxa are derived from Sakane & Yokata (1994), Terasaki (1979), Satomi et al. (2002), López-López et al. (2002) and Liu et al. (2007). +, Positive; –, negative; w, weak; ND, no data available; BChl, bacteriochlorophyll. All taxa require salt for growth and are positive for oxidase and growth on carbohydrates.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain LD81T</th>
<th>Terasakiella pusilla</th>
<th>Thalassospira</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Spiral (occasionally rod or filamentous)</td>
<td>Spiral</td>
<td>Vibrioid to spiral</td>
</tr>
<tr>
<td>Flagella</td>
<td>+ (Single polar)</td>
<td>+ (Bipolar single)</td>
<td>+ (Single polar)/–</td>
</tr>
<tr>
<td>Pigment</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>BChl α</td>
<td>–</td>
<td>ND</td>
<td>–/ND*</td>
</tr>
<tr>
<td>Salt tolerance (%)</td>
<td>Up to 8</td>
<td>Up to 8</td>
<td>Up to 10</td>
</tr>
<tr>
<td>Catalase</td>
<td>+</td>
<td>w/–</td>
<td>+</td>
</tr>
<tr>
<td>Reduction of nitrate</td>
<td>+ (to N2O)</td>
<td>+ (to nitrite)</td>
<td>+ (to nitrite)/–</td>
</tr>
<tr>
<td>Quinone type</td>
<td>Not tested</td>
<td>Q10</td>
<td>ND</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>51.1</td>
<td>48/51†</td>
<td>47–54.7</td>
</tr>
<tr>
<td>Non-polar fatty acids (%)</td>
<td>49</td>
<td>58</td>
<td>43–45</td>
</tr>
<tr>
<td>C18:1</td>
<td>31</td>
<td>18</td>
<td>3–16</td>
</tr>
<tr>
<td>C16:0</td>
<td>9</td>
<td>15</td>
<td>15–18</td>
</tr>
<tr>
<td>C18:0</td>
<td>3</td>
<td>1</td>
<td>3–9</td>
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<tr>
<td>3-Hydroxy fatty acids (%)</td>
<td>64‖</td>
<td>87</td>
<td>25–41</td>
</tr>
<tr>
<td>C14:0 3-OH</td>
<td>0</td>
<td>2</td>
<td>51–61</td>
</tr>
<tr>
<td>C16:0 3-OH</td>
<td>11</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C18:0 3-OH</td>
<td>25</td>
<td>10</td>
<td>8–15</td>
</tr>
<tr>
<td>Oxygen requirement</td>
<td>Aerobe/anaerobe</td>
<td>Aerobe</td>
<td>Aerobe/anaerobe</td>
</tr>
<tr>
<td>Anaerobic phototrophic growth</td>
<td>–</td>
<td>ND</td>
<td>–/ND*</td>
</tr>
</tbody>
</table>

*Result for Thalassospira lucentensis. No data available for Thalassospira xiamenensis or Thalassospira profundimaris.†Sakane & Yokata (1994) reported 48 mol%; Terasaki (1979) reported 51 mol%.‡Percentages of total fatty acids.§Percentages of total 3-hydroxy fatty acids. Percentages shown for Thalassospira species are calculated from the data given by Liu et al. (2007).‖C14:0 3-OH and/or iso-C16:1 I.
Description of Kiloniellaceae fam. nov.

Kiloniellaceae (Ki.lo’ni.ell.a’ce.ae. N.L. fem. n. Kiloniella name of a bacterial genus; -aceae ending to denote the name of a family; N.L. fem. pl. n. Kiloniellaceae the Kiloniella family).

Bacteria of this family are Gram-negative and cells have spiral to vibrioid cell shape. Mesophilic, chemoheterotrophic bacteria with typical marine and moderately halotolerant growth response. Major fatty acids are monounsaturated, even-numbered, straight-chain C₁₈ and C₁₆ fatty acids. The G+C content of the DNA is approximately 50 mol%. The type genus is Kiloniella.

Description of Kiloniellales ord. nov.

Kiloniellales (Ki.lo’ni.ell.a’les. N.L. fem. n. Kiloniella name of a bacterial genus; -ales ending to denote an order; N.L. fem. n. Kiloniellales the order of Kiloniella).

The description is the same as for the family Kiloniellaceae. The type genus is Kiloniella.

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