Planctobacterium marinum gen. nov., sp. nov., a new member of the family Alteromonadaceae isolated from seawater

Der-Shyan Sheu, Shih-Yi Sheu, Kai-Rou Lin, Yuh-ling Lee Chen and Wen-Ming Chen*

Abstract

A bacterial strain designated K7T was isolated from the South China Sea and characterized using a polyphasic taxonomic approach. Cells of strain K7T were Gram-stain-negative, aerobic, poly-β-hydroxybutyrate-accumulating, motile by means of a monopolar flagellum, non-spore forming rods surrounded by a thick capsule and forming yellow colonies. Growth occurred at 4–35°C (optimum, 25–30°C), at pH 5.0–9.0 (optimum, pH 7.0) and with 0.5–10% (w/v) NaCl [optimum, 1–4% (w/v)]. The predominant fatty acids were summed feature 3 (comprising C16:1ω7c and/or C16:1ω6c), C16:0 and C18:1ω7c. The major isoprenoid quinone was Q-8 and the DNA G+C content was 46.5 mol%. The polar lipid profile consisted of a mixture of phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinomonomethylethanolamine, one uncharacterized phospholipid, two uncharacterized aminophospholipids and five uncharacterized lipids. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain K7T formed a distinct lineage with respect to closely related genera in the family Alteromonadaceae. Strain K7T was most closely related to Aestuariibacter, Aliglacicola, Paraglaciecola and Glaciecola, and the levels of 16S rRNA gene sequence similarity with respect to the type species of related genera were less than 95%. On the basis of the genotypic and phenotypic data, strain K7T represents a novel species of a new genus of the family Alteromonadaceae, for which the name Planctobacterium marinum gen. nov., sp. nov. is proposed. The type strain of Planctobacterium marinum is K7T (=BCRC 80901T=LMG 28835T=KCTC 42657T).

The family Alteromonadaceae, belonging to the order Alteromonadales of the class Gammaproteobacteria, is a morphologically, metabolically and ecologically diverse group. Members of this family are motile or non-motile, rod-shaped, aerobic or facultatively anaerobic chemoheterotrophs [1–5]. In most species, the major isoprenoid quinone is ubiquinone Q-8. The major fatty acids are C16:0, C16:1ω7c and C18:1ω7c. This family has 22 identified genera so far (www.bacterio.net/alteromonadaceae.html; http://bjs.sgmjournals.org/), which were isolated from various habitats, such as coastal, open and deep-sea waters, sediment and invertebrates from marine environments.

During the characterization of micro-organisms from a seawater sample collected from the South China Sea (GPS location: 21°25′3″ N 119° 28′ 42″ E), a bacterial strain, designated K7T, was isolated on marine agar 2216 (MA; BD Difco) and subjected to detailed taxonomic analyses. Subcultivation was performed on MA at 25°C for 48–72 h. The isolate was preserved at −80°C in marine broth 2216 (MB; BD Difco) with 20% (v/v) glycerol or by lyophilization.

Genomic DNA was isolated using a bacterial genomic kit (DP02-150; GeneMark Technology) and the 16S rRNA gene sequence was analysed as described by Chen et al. [6]. Primers fD1 (5′-AGAGTTTGATCCTGGCTCAG-3′) and rP2 (5′-ACGGCTACCTTGTTACGACTT-3′) were used for PCR amplification of bacterial 16S rRNA genes [7, 8]. These primers correspond to nucleotide positions 8–27 and 1472–1492, respectively, of the Escherichia coli 16S rRNA gene and can be used for amplifying the nearly full-length 16S rRNA gene. The PCR product was purified and cloned into the pGEM-T vector (Promega), and direct sequencing was performed by using fD1, rP2, SP6 promoter and T7 promoter primers with a DNA sequencer (ABI Prism 3730; Applied Biosystems). The sequenced length of the 16S rRNA gene was 1497 bp for strain K7T, and this gene sequence was compared with those available from the EzTaxon-e [9], the Ribosomal Database Project [10] and GenBank (http://blast.ncbi.nlm.nih.gov/Blast.cgi) databases. Analysis of the sequence data was performed by using the software package BioEdit [11] and MEGA 7 [12], after...
multiple alignments of the data by CLUSTAL X version 2.0 [13]. The resulting multiple sequence alignment was corrected manually and gaps at the 5’ and 3’ ends of the alignment were omitted for further analyses. Distances (corrected according to Kimura’s two-parameter model; [14]) were calculated and clustering was performed with the neighbour-joining method [15]. Maximum-likelihood [16], maximum-parsimony [17] and minimum-evolution [18] trees were generated by using the treeing algorithms contained in the PHYLIP software package [19]. In each case, bootstrap values were calculated based on 1000 replications.

The phylogenetic analyses based on 16S rRNA gene sequences showed that strain K7T formed a distinct phylogenetic lineage in the family Alteromonadaceae of the order Alteromonadales within the class Gammaproteobacteria in the neighbour-joining tree (Fig. 1). The overall topologies of the phylogenetic trees obtained with the maximum-likelihood and maximum-parsimony methods were similar. These findings were confirmed by analysis based on the minimum evolution, maximum-likelihood and maximum-parsimony algorithms (see Figs S1–S3, available in the online Supplementary Material). Sequence similarity calculations (over 1400 bp) indicated that strain K7T was closely related to species of the genera Aestuariibacter (92.0–95.0 % 16S rRNA gene sequence similarity), Aleglaciecola (91.9–93.8 %), Paraglaciecola (91.5–92.1 %), Glaciecola (91.2–91.7 %), Alteromonas (89.0–93.5 %), Salinimonas (91.4–92.8 %), Bowmanella (91.8–92.1 %), Pseudobowmanella (92.3 %) and Agaribacter (90.0 %).

The morphology of bacterial cells was observed by phase-contrast microscopy (Leica DM 2000) and transmission electron microscopy (H-7500; Hitachi) (Fig. 2) using cells grown in MB at 25 °C for lag, exponential and stationary phases of growth. The Gram Stain Set 5 kit (BD Difco) and the Ryu non-staining KOH method [20] were used to perform the Gram reaction. Flagellar motility was tested using the hanging drop method, and the Spot Test flagella stain (BD Difco) was used for flagellum staining. The presence of the capsule was assessed using the Hiss staining method [21]. Colony morphology was observed on MA using a stereoscopic microscope (SMZ 800; Nikon). Poly-β-hydroxybutyrate granule accumulation was examined under light microscopy after staining the cells with Sudan black [22] and visualized by UV illumination after directly staining growing bacteria on plates containing Nile red [23].

The optimum pH range for growth was determined in MB using appropriate biological buffers such as glycine/HCl, citrate/Na₂HPO₄ phosphate buffer and glycine/NaOH to adjust the pH to 3.0–4.0, 4.0–8.0, 6.0–8.0 and 9.0–11.0 (at 0.5 pH unit intervals), respectively. Verification of the pH values after autoclaving revealed only minor changes. The temperature range for growth was determined in MB at 4–50 °C (4, 10, 15, 20, 25, 30, 35, 37, 40, 45 and 50 °C). To investigate the tolerance to NaCl, MB was prepared according to the formula of the BD Difco medium with NaCl concentration adjusted to 0, 0.5 and 1.0–12.0 % (w/v, at intervals of 1.0 %). Growth under anaerobic conditions was determined after incubating strain K7T on MA in the OxaperoGen system.

Strain K7T was examined for a broad range of phenotypic properties. Activities of catalase, oxidase, DNase, urease and lipase (corn oil), and hydrolysis of starch, casein, gelatin and Tweens 20, 40, 60 and 80 were determined using standard methods [24]. Hydrolysis of alginate (1 %, w/v, sodium alginate) was examined on MA. Chitin hydrolysis activity was determined on a chitinase-detection agar (CDA) plate. Chitin hydrolysis was visualized by the formation of a clear zone around the colonies in CDA plates. The CDA plate was prepared as described by Wen et al. [25]. Hydrolysis of CM-cellulose was tested according to the method described by Bowman [26] using MA as the basal medium. Additional biochemical tests were performed using API ZYM and API 20NE kits (both from bioMérieux) and carbon source utilization was evaluated using the GN2 microplate (Biolog). All commercial phenotypic tests were performed according to the manufacturers’ recommendations.

Sensitivity of strain K7T to antibiotics was tested by the disc diffusion method after spreading cell suspensions (0.5 McFarland) on MA. The discs (Oxoid) contained the following antibiotics: ampicillin (10 µg), chloramphenicol (30 µg), gentamicin (10 µg), kanamycin (30 µg), nalidixic acid (30 µg), novobioicin (30 µg), rifampicin (5 µg), penicillin G (10 U), streptomycin (10 µg), sulfamethoxazole (23.75 µg) plus trimethoprim (1.25 µg) and tetracycline (30 µg). The effect of antibiotics on cell growth was assessed after 2 days at 25 °C. The diameter of the antibiotic disc was 8 mm. The strain was considered susceptible when the diameter of the inhibition zone was <12 mm, intermediate at 10–12 mm and resistant at >10 mm as described by Nokhal and Schlegel [27]. Strain K7T was sensitive to penicillin G, ampicillin, chloramphenicol, gentamicin, rifampicin, kanamycin, tetracycline, novobiocin, streptomycin, nalidixic acid and sulfamethoxazole plus trimethoprim. Detailed results of physiological, biochemical and morphological characterization of strain K7T are provided in the genus and species descriptions and Table 1.

To analyse the whole-cell fatty acid composition, strain K7T was grown on MA at 25 °C for 2 days, when bacterial cultures reached the stationary stage of growth. We assessed growth of the novel strain and observed colony size at 1 day intervals before selecting the time point for generating biomass. Colony expansion could be clearly observed after 2 days of incubation compared with 3 and 4 days of incubation. Fatty acid methyl esters were prepared and separated according to the standard MIDI protocol (Sherlock Microbial Identification System, version 6.0), analysed by GC (Hewlett-Packard 5890 Series II) and identified by using the RTSBA6.00 database of the microbial identification system [28].

The detailed fatty acid composition of strain K7T was C₁₂:0 (1.7 %), C₁₂:0 3-0H (3.9 %), C₁₄:0 (2.4 %), C₁₅:0ω8c (2.8 %),
Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain K7T and the type strains of genera in the family Alteromonadaceae in the class Gammaproteobacteria. Numbers at nodes are bootstrap percentages <70% based on the neighbour-joining (above nodes) and maximum-parsimony (below nodes) tree-making algorithms. Filled circles indicate branches of the tree that were also recovered using the maximum-likelihood and maximum-parsimony tree-making algorithms. Open circles indicate that the corresponding nodes were also recovered in the tree generated with the maximum-parsimony algorithm. Bar, 0.01 substitutions per nucleotide position.
Strain K7 contained choline-containing lipids and glycolipids, respectively. Polar lipids were extracted and analysed by two-dimensional TLC according to Embley and Wait [29]. Molybdophosphoric acid, ninhydrin, Zinzadze reagent, Dragendorff reagent and α-naphthol reagent were used for the detection of total polar lipids, amino lipids, phospholipids, choline-containing lipids and glycolipids, respectively. Strain K7T exhibited a complex polar lipid profile consisting of phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylinomethylethanolamine, one uncharacterized phospholipid, two uncharacterized amino-phospholipids and five uncharacterized lipids (Fig. S4).

Like the phylogenetically related genera *Aestuariibacter*, *Aliiglaciecola*, *Paraglaciecola* and *Glaciecola*, strain K7T had PE and PG as major polar lipids (Table 1). PE and PG as major polar lipids have been previously described in *Aestuariibacter aggregatus* WH169T [30] and *Aliiglaciecola* species such as *Aliiglaciecola lipolytica* E3T [31], *Aliiglaciecola litoralis* KMM 3894T [32], *Aliiglaciecola coringensis* AK49T [33] and *Aliiglaciecola aliphaticivorans* GSD6T [5]. However, phosphatidylinomethylethanolamine was present in strain K7T (in this study) and *Glaciecola punicea* ACAM 611T [3]. Diphosphatidylglycerol was detected in *Paraglaciecola mesophila* KMM 241T [34] and *Paraglaciecola aquimarina* GGW-M5T [3], and phosphatidylcholine was present only in *G. punicea* ACAM 611T [3].

Isoprenoid quinones were extracted and purified according to the method of Collins [35] and were analysed by HPLC. Strain K7T had Q-8 as the major respiratory quinone. The DNA G+C content of strain K7T, determined by HPLC according to Mesbah et al. [36], was 46.5±1.0 mol%.

Several morphological, physiological and biochemical properties, such as colony pigmentation, cell shape, motility, aerobic growth, optimal growth at 25–30°C and pH 7.0, inability to reduce nitrate to nitrite, ability to hydrolyse ascenculin and gelatin, presence of C14 lipase, valine arylamidase, cystine arylamidase, α-chymotrypsin, acid phosphatase and α-glucosidase activities, and absence of α-galactosidase, β-galactosidase, β-glucosidase and N-acetyl-β-glucosaminidase activities, distinguish strain K7T from all members of the phylogenetically related genera in the family *Alteromonadaceae*, such as *Aestuariibacter*, *Aliiglaciecola*, *Paraglaciecola* and *Glaciecola* (Table 1). More importantly, strain K7T could be also differentiated from members of the family *Alteromonadaceae* based on chemotaxonomic characteristics, such as the major respiratory quinone and major polar lipids (Table 1). The fatty acid profile of strain K7T is compared with members of the most phylogenetically closely related genera in Table S1. Summed feature 3 (C16:0ω7c and/or C16:0ω6c), C18:1ω7c and C16:0 were commonly found as major components in the type strains of phylogenetically related type species of the family *Alteromonadaceae*. However, small amounts of iso-C18:0 and anteiso-C17:0ω9c were found in strain K7T only. Also, strain K7T contained a relatively high amount of C15:0ω8c when compared with other type strains. Strain K7T could be also differentiated from the type strains of the mostly closely related genus *Aestuariibacter* by the presence of minor amounts of C16:0 n alcohol and iso-C17:0 and by the absence of C12:1 3-OH and summed feature 2 (C12:0 aldehyde and/or iso-C16:1 I and/or C14:0 3-OH).

It is now generally accepted that 16S rRNA gene sequence similarities between two bacteria of less than 95% are an indication of affiliation to different genera [37]. Strain K7T thus probably represents a novel species of a new genus since the 16S rRNA gene sequence similarity to its closest relatives with validity published names, *Aestuariibacter halophilus* JC2043T, *Aestuariibacter salixigens* JC2042T and *Aliiglaciecola litoralis* KMM 3894T, was 95.0, 94.2 and 93.8%, respectively. Moreover, strain K7T can be readily distinguished from these closest phylogenetic neighbours by chemotaxonomic, physiological and biochemical characteristics. Also, the low levels of 16S rRNA gene sequence similarity between strain K7T and all other members of the family *Alteromonadaceae* together with differential phenotypic properties (Table 1) suggest that strain K7T represents a novel species of a new genus within the family.
Table 1. Characteristics that differentiate strain K7\textsuperscript{T} from other phylogenetically related genera in the family Alteromonadaceae

Taxa: 1, Strain K7\textsuperscript{T}; 2, Aestuariibacter [30, 38]; 3, Alilagiecola [2, 5, 31–33]; 4, Paraglaciecola [3, 4, 34, 39–43]; 5, Glaciecola [3, 44, 45]. +, Positive reaction; –, variable reaction; —, negative reaction; nd, no data available.

<table>
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<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<td>Source</td>
<td>Seawater</td>
<td>Seawater, sediment</td>
<td>Seawater, sediment, mangrove forest, sea-tidal flat</td>
<td>Marine invertebrate species, seawater, sediment</td>
<td>Sea ice, seawater</td>
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<tr>
<td>Colony pigmentation</td>
<td>Yellow</td>
<td>White, pale yellow</td>
<td>None, yellow, white-brown</td>
<td>None, yellowish brown, greyish yellow</td>
<td>Slightly cream, pink red, pale pink</td>
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<td>Cell shape</td>
<td>Rod</td>
<td>Short rod or rod</td>
<td>Rod</td>
<td>Ovoid or curved to short rod</td>
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<td>Motility</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<td>Relation to O\textsubscript{2}</td>
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<td>Aerobic, facultatively anaerobic</td>
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<td>pH range for growth (optimal)</td>
<td>5.0–9.0 (7.0)</td>
<td>5.5–8.0 (6.5–7.0)</td>
<td>5.5–10.0 (6.5–7.5)</td>
<td>4.0–9.0 (6.0–8.0)</td>
<td>4.0–8.5 (5.0–7.2)</td>
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<td>0.5–10</td>
<td>0.5–9</td>
<td>1–10</td>
<td>2–9</td>
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<td>Nitrate reduction</td>
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<td>V</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<td>+</td>
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<td>+</td>
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<td>Cystine arylamidase</td>
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<td>(\beta)-Glucosidase</td>
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<td>V</td>
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<tr>
<td>N-Acetyl-(\beta)-glucosaminidase</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>V</td>
<td>–</td>
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<tr>
<td>Major respiratory quinone(s)</td>
<td>Q-8</td>
<td>Q-8</td>
<td>Q-8*</td>
<td>MK7, Q-8</td>
<td>ND</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>46.5</td>
<td>48–54</td>
<td>41–44.6</td>
<td>40–47</td>
<td>40–46</td>
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</table>

\*Data from Jin et al. [5].
†PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidylmonomethylethanolamine; DPG, diphosphatidylglycerol; PC, phosphatidylcholine.

Alteromonadaceae, for which the name Planctobacterium marinum gen. nov., sp. nov. is proposed.

DESCRIPTION OF PLANCTOBACTERIUM GEN. NOV.

Planctobacterium (Plancto.bac.te′ri.um. Gr. adj. planktos drifting, wandering; L. neut. n. bacterium rod; N.L. neut. n. Planctobacterium, a planktonic/drifting bacterium isolated from seawater).

Cells are Gram-stain-negative, aerobic, motile by means of a monopolar flagellum, non-spore forming rods surrounded by a thick capsule. Poly-\(\beta\)-hydroxybutyrate accumulation is observed. Oxidase and catalase are positive. The predominant quinone is Q-8. Major cellular fatty acids (<10\%) are summed feature 3 (comprising C\(_{16}:1\omega 7c\) and/or C\(_{16}:1\omega 6c\), C\(_{16}:0\) and C\(_{18}:1\omega 7c\). Predominant polar lipids are PE and PG. The DNA G+C content of the type strain of the type species is 46.5 mol\%. The type species is Planctobacterium marinum.

DESCRIPTION OF PLANCTOBACTERIUM MARINUM SP. NOV.

Planctobacterium marinum (ma.ri’n.um. L. neut. adj. mari.num of the sea, marine).

Displays the following properties in addition to those given in the genus description. Cells are approximately 0.8–1.0 \(\mu\)m in diameter and 2.5–4.5 \(\mu\)m in length after 48 h of incubation on MA at 25°C. Colonies are yellow, convex, round and smooth
with entire edges. Colonies are approximately 0.8–1.8 mm in diameter on MA after 48 h of incubation at 25 °C. Growth occurs at 4–35 °C (optimum, 25–30 °C), at pH 5.0–9.0 (optimum, pH 7.0) and with 0.5–10 % (w/v) NaCl [optimum, 1–4 % (w/v)]. Positive for hydrolysis of starch, casein, DNA, and Tweens 20, 40, 60 and 80. Negative for hydrolysis of chitin, CM-cellulose, alginate and corn oil. In API 20NE tests, positive reactions for aesculin and gelatin hydrolysis, and negative reactions for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and  β-galactosidase activities, and assimilation of glucose, arabinose, mannose, mannitol, N-acetyl-glucosamine, maltose, gluco- nate, caprate, adipate, malate, citrate and phenyl acetate. In the API ZYM kit, alkaline phosphatase, C4 esterase, C8 esterase lipase, C14 lipase, leucine arylamidase, valine arylamidase, aminopeptidase, naphthol-AS-BI-phosphohydrolase and alkaline phosphatase activities are present and α-galactosidase, β-galactosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. The following compounds are utilized as sole carbon sources in the GN2 microplate: α-cyclodextrin, dextrin, glycogen, Tweens 40 and 80, N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, adonitol, i-erythritol, D-fructose, D-galactose, gentiobiose, α-D-glucose, myo-inositol, α-D-lactose, lactulose, D-psicose, trehalose, xylitol, acetic acid, citric acid, D-glucuronic acid, α-hydroxybutyric acid, β-hydroxybutyric acid, p-hydroxyphenylactic acid, α-ketobutyric acid, α-ketoglutaric acid, DL-lactic acid, malonic acid, proionic acid, D-saccharic acid, succinic acid, D-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-aspartic acid, hydroxy-L-proline, L-ornithine, L-phenylalanine, L-proline, L-prolylglutamic acid, D-serine, L-serine, L-threonine, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butandiol, glycerol, DL-α-glycerol phosphate, α-D-glucose 1-phosphate and D-glucose 6-phosphate. All other substrates in the GN2 microplate are not utilized. The major fatty acids (<10 %) are summed feature 3 (comprising C16:1ω7c and/or C16:1ω6c), C16:0 and C18:1ω7c.

The type strain is K27T (=BCRC 80901T=LMG 28835T =KCTC 42657T), isolated from a seawater sample collected from the South China Sea.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


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