Celeribacter neptunius gen. nov., sp. nov., a new member of the class Alphaproteobacteria

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A whitish Gram-negative, motile, aerobic bacterium, designated strain H 14T, was isolated from seawater collected at St Kilda beach in Port Phillip Bay, Melbourne, Australia. Analysis of 16S rRNA gene sequences revealed that the organism belonged to the Roseobacter lineage of the class Alphaproteobacteria, forming a distinct evolutionary lineage at the genus level. Strain H 14T was distantly related to the genera Nautila, Ruegeria and Pseudoruegeria (family Rhodobacteraceae). Strain H 14T was unable to degrade gelatin, casein, chitin, agar and starch, did not produce any carotenoids, did not possess bacteriochlorophyll a and had a limited ability to utilize carbon sources. Strain H 14T grew with concentrations of 1–8 % (w/v) NaCl and over a temperature range of 5–35 °C. Phosphatidylglycerol was the major phospholipid (90 %); phosphatidylethanolamine (7.0 %) and phosphatidylethanolamine (2.0 %) were present in minor quantities. The predominant fatty acids were C18:1ω7c (82.4 %), C18:1ω9c (5.1 %) and C18:0 (3.8 %). The DNA G+C composition for strain H 14T was 59.1 mol%. Based on the results of physiological, biochemical, chemotaxonomic and phylogenetic investigations, a new genus, Celeribacter gen. nov., with the type species Celeribacter neptunius sp. nov. is proposed. The type strain of the type species is H 14T (=KMM 6012T=CIP 109922T).

The phylogenetically diverse class Alphaproteobacteria has undergone intensive reclassifications (Uchino et al., 1998; Soller et al., 2000; Martens et al., 2006) and the list of new members is constantly growing (e.g. Yoon et al., 2008). This study aims to describe another novel representative of the class Alphaproteobacteria.

Strain H 14T was isolated from seawater collected from Port Phillip Bay, Melbourne, Australia, at St Kilda beach on 12 December 2007. A seawater sample was taken from the first metre below the surface. The sample handling and isolation procedure used was as previously described (Ivanova et al., 1996, 2004; Webb et al., 2009). Determination of the phenotypic properties, used for the characterization of new isolates, was performed by using standard procedures (Smibert & Krieg, 1994) and as described by Ivanova et al. (1996, 1998).

Cell size and morphology (see Supplementary Fig. S1 in IJSEM Online) were examined using electron microscopy as previously described (Ivanova et al., 2005). To study physiological properties, bacteria were grown on marine agar (MA) 2216 (BD) at 22–24 °C. Motility was studied using hanging drop preparations. The following physiological and biochemical properties were examined: oxidation/fermentation of glucose (Hugh & Leifson, 1953), Gram staining, reduction of nitrate and nitrite, catalase [with 5 % (v/v) H2O2], and oxidase (Kovacs, 1956) activities, gelatin liquefaction, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase activities, poly-β-hydroxybutyrate and acetoin production (Voges–Proskauer test), sodium requirement [0, 1, 3, 6, 8, 10, 12, 15 % (w/v) NaCl], indole and H2S production, and the...
ability to hydrolyse starch, Tween 80, casein, DNA and agar. The temperature range for growth was examined on MA incubated at 2, 5, 10, 30, 35, 37 and 42 °C. Other physiological and biochemical tests were performed with the API 20E, API 50 and API ZYM systems (BioMérieux).

Susceptibility to antibiotics was tested by the conventional diffusion plate technique, using MA and discs impregnated with following antibiotics (μg per disc unless otherwise stated): chloramphenicol (30), benzylpenicillin (10 U), carbenicillin (100), nalidixic acid (30), lincomycin (15), rifampicin (5), ofloxacin (5), ampicillin (10), cephalixin (30), oleandomycin (15), cephalozin (30), tetracycline (30), kanamycin (30), oxacillin (10), streptomycin (30), gentamicin (10), erythromycin (15), polymyxin (300 U) and neomycin (30). The morphological, growth, physiological and biochemical characteristics of the novel strain are given in Table 1 and in the genus and species descriptions.

To enable bacteriochlorophyll a (BChl a) isolation and characterization, strain H 14T was grown at 28 °C on MA over 48 h and the bacterial mass was collected from five Petri plates as described earlier by Ivanova et al. (2005). The bacterial cells were disrupted using a homogenizer (MPW-324; Mechanika Precyzjna) and the entire homogenate was extracted twice using methanol. The combined organic extract phases were evaporated to dryness. The resulting extract was used to determine the presence of BChl a as previously described (Ivanova et al., 2005).

For the analysis of phospholipids and fatty acids, the novel strain was grown at 28 °C on MA and cells were harvested after an incubation period of 48 h. The lipids were extracted by a method modified from that of Bligh & Dyer (1959). The detection and identification of lipids and fatty acids was performed according to a previously described method (Ivanova et al., 2005). Polar lipids were separated using two-dimensional micro-thin layer chromatography with the solvent systems described by Vaskovsky & Terekhova (1979). Phosphatidylglycerol was found to be the major phospholipid (90%) and phosphatidylcholine (7.9%) and phosphatidylethanolamine (2%) were found to be present in minor quantities. An unidentified aminolipid and traces of lysophosphatidyl ethanolamine were also detected (see Supplementary Fig. S2 in IJSEM Online). The predominant fatty acids were found to be C18:1ω7c (82.4%), C18:1ω9c (5.1%) and C18:0 (3.8%). The presence of fatty acid C18:1ω9c in the novel strain, a feature that is not found in the fatty acid profiles of members of the genera Nautila and Pseudorugeria (Yoon et al., 2007; Vandecandelaere et al., 2009), and a higher proportion of the principal fatty acids, i.e. C18:1ω7c, were found to be characteristic features of the fatty acid profile of the new isolate. The polar lipids and the major cellular fatty acids for strain H 14T are presented in Supplementary Table S1 (available in IJSEM Online).

DNA was isolated from the novel strain according to the method described by Marmur (1961). The G+C content of the DNA was found to be 59.1 mol% as determined by the thermal denaturation method (Marmur & Doty, 1962).

The 16S rRNA gene sequence was amplified and sequenced by the Australian Genome Research Facility (AGRF) Laboratories (Brisbane, Australia). The 16S rRNA gene sequence of strain H 14T was compared against a database of cultured species via BLAST analysis (http://blast.ddbj.nig.ac.jp/top-e.html) and the EzTaxon database of type strains (Chun et al., 2007) in order to retrieve most similar sequences of recognized bacteria. The 150 sequences retrieved were aligned with CLUSTAL X 2.0 (Larkin et al., 2007). Alignments were then manually checked with SeaView (Galtier et al., 1996) and domains common to all sequences were used to derive a first phylogenetic tree using the most recent version of SeaView. A BIONJ analysis allowed the selection of the 37 sequences of the most closely related type strains. Alignments were checked again and a full phylogenetic analysis was undertaken using the BIONJ, parsimony (DNAPARS) and maximum-likelihood algorithms, excluding positions containing indels, to confirm the tree topology (see Supplementary Figs S3 and S4 in IJSEM Online). For the neighbour-joining (NJ) analysis, a matrix distance was calculated using a Kimura two-parameter correction. Bootstrap replicates were performed using 1000 replications. BIONJ was used according to the method described by Gascuel (1997) and maximum-likelihood was determined using PhyML (Guindon & Gascuel, 2003). The phylogenetic trees were drawn using TreeDyn (Chevenet et al., 2006) or SeaView. Among type strains, Nautila italica LMG 24365T, Pseudorugeria aquimaris SW-255T and Roseovarius crassostreae CV919-312T showed gene sequence similarity values between 96.7% and 96% (55, 46 and 56 differences in 1421 positions, respectively) with strain H 14T clustered with Nautila italica LMG 24365T, with only 77% bootstrap support. Notably, strain H 14T did not cluster with any other recognized species, clearly indicating that the new isolate belongs to a separate genus.

On the basis of the physiological, biochemical, chemotaxonomic and phylogenetic data (Fig. 1), strain H 14T represents a novel genus and species within the class Alphaproteobacteria. A summary of the phenotypic differential characteristics of strain H 14T and its closest phylogenetic neighbors is presented in Table 1. Comparative analysis of phenotypic traits indicated that strain H 14T exhibited a characteristic phenotypic and chemotaxonomic profile. For example, strain H 14T could be distinguished from other related species identified by the phylogenetic analysis by the negative oxidase reaction and by different utilization of D-glucose, citrate, D-xylose and L-arabinose. The proportion of three major fatty acids, C18:0, C18:1ω9c and C18:1ω7c, and three major phospholipids, phosphatidylglycerol, phosphatidylcholine and phosphatidylethanolamine, can be regarded as taxonomic markers for the new genus. Based on these results, a new
Table 1. Characteristics that differentiate strain H 14T from other phylogenetically related species

<table>
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<tr>
<th>Characteristic</th>
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<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>−</td>
<td>V</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
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<td>Motility</td>
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<td>V</td>
<td>V</td>
<td>−</td>
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<td>+</td>
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<td>Pigment</td>
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<td>V</td>
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<td>Red</td>
<td>Pink</td>
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<td>Growth at 37 °C</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>V</td>
<td>V</td>
<td>+</td>
<td>+</td>
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<td>Growth range with NaCl (%)</td>
<td>1–8</td>
<td>1–5</td>
<td>0.34–9</td>
<td>0–4</td>
<td>0–14</td>
<td>1.4–8</td>
<td>0–10</td>
<td>0–8</td>
<td>0–9</td>
<td>0.1–13</td>
<td>0–15</td>
<td>0.6–12</td>
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<td>−</td>
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<td>ND</td>
<td>V</td>
<td>−</td>
<td>W</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
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<td>−</td>
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<td>Lipase (Tween 80)</td>
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<td>+</td>
<td>ND</td>
<td>V</td>
<td>ND</td>
<td>+</td>
<td>V</td>
<td>−</td>
<td>+</td>
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<td>Gelatinase</td>
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<td>−</td>
<td>ND</td>
<td>ND</td>
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<td>D-Glucose</td>
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<td>V</td>
<td>+</td>
<td>−</td>
<td>W</td>
<td>V</td>
<td>−</td>
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<td>−</td>
<td>−</td>
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<td>Citrate</td>
<td>−</td>
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<td>+</td>
<td>ND</td>
<td>−</td>
<td>W</td>
<td>−</td>
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<td>D-Xylose</td>
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<td>−</td>
<td>ND</td>
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<td>−</td>
<td>+</td>
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<td>V</td>
<td>V</td>
<td>−</td>
<td>−</td>
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<tr>
<td>L-Arabinose</td>
<td>−</td>
<td>+</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>V</td>
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<tr>
<td>Major polar lipids</td>
<td>PE, PG, PC, LPE, AL</td>
<td>ND</td>
<td>PG, DPG, PC, PE, AL</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>PG, DPG, PE, PL, GL</td>
<td>DPG, PC</td>
<td>ND</td>
<td>PC, PG, DPG, PE, PL</td>
<td>PC, AL</td>
</tr>
</tbody>
</table>

All species are catalase-positive. +, Positive; −, negative; w, weakly positive reaction; v, variable reaction depending on strain; ND, no data available; NG, no growth; AL, unidentified aminolipid; LPE, lysophosphatidylethanolamine; DP, diphosphatidylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol.
genus and a novel species, *Celeribacter neptunius* gen. nov., sp. nov., is proposed.

**Description of Celeribacter gen. nov.**

*Celeribacter* (Ce.ler.i.bac’ter. L. adj. *celer* -eris -e quick, rapid; N.L. masc. n. *bacter* rod; N.L. masc. n. *Celeribacter* rapidly growing rod).

Rod-shaped cells. Gram-negative. Do not form endospores or resting stages. Aerobic. Anaerobic growth occurs by fermentation of D-glucose by anaerobic respiration of nitrate. Chemoorganotroph. Cytochrome oxidase-negative, catalase-positive. Reduce nitrate to nitrite. Three major fatty acids, C18:0, C18:1ω9c and C18:1ω7c, and three major phospholipids, phosphatidylglycerol, phosphatidylcholine and phosphatidylethanolamine, are characteristic of the genus. The type species of the genus is *Celeribacter neptunius*.

**Description of Celeribacter neptunius**

*Celeribacter neptunius* [nep.tu’ni.us. L. masc. adj. *neptunius* pertaining to Neptunius (Roman god of the sea), referring to the habitat of the bacteria].

Short rod-shaped cells with slightly irregular ends, approx. 0.8–1.8 μm long and 0.4–0.9 μm wide. Single polar or subpolar flagellum. Gram-negative. Chemoorganotroph with respiratory metabolism. Does not accumulate poly-β-hydroxybutyrate as an intracellular reserve product and does not have an arginine dihydrolase system. Does not decompose gelatin, agar, starch, casein, laminarin, chitin or DNA. Tween 80 is weakly utilized. Urease-positive. Negative for indole, H2S and acetoin production and for arginine dihydrolase, lysine decarboxylase and ornithine decarboxylase. Alkaline phosphatase, esterase (C4), esterase-lipase (C8), leucine arylamidase, α-glucosidase and β-glucosidase are produced. With the API 50 system, D-xylose, L-rhamnose, methyl α-D-glucopyranoside, D-lyxose, D-arabitol, D-glucose, D-fructose, arbutin, aesculin ferric citrate, salicin, cellobiose, maltose, D-lactose (bovine origin), sucrose and trehalose are utilized. Susceptible to (μg per disc unless otherwise stated): chloramphenicol (30), benzylpenicillin (10 U), carbenicillin (100), nalidixic acid.

![Fig. 1. Phylogenetic position of strain H 14T according to the 16S rRNA gene sequence analysis. Sequences in this tree were chosen from a larger tree obtained after a distance analysis was performed on a larger dataset. Percentages of bootstraps (1000 replications) are indicated for branches when higher than 50%. Bar, 0.01 nucleotide substitutions per site.](http://ijs.sgmjournals.org)
acid (30), rifampicin (5), ofloxacin (5), ampicillin (10), cephalaxin (30), cephaloridine (30), tetracycline (30), kanamycin (30), oxacillin (10), streptomycin (30), gentamicin (10), erythromycin (15) and neomycin (30). Resistant to: lincomycin (15), polymyxin (300 U) and oleandomycin (15). Phosphatidylglycerol, phosphatidylethanolamine and phosphatidylcholine are the major phospholipids. The main cellular fatty acid is C18:1ω7 (82.4%).

The type strain, H 14T (=KMM 6012T=CIP 109922T), was isolated from seawater collected in the Port Phillip Bay of the Tasman Sea of the Pacific Ocean. The DNA G+C content of the type strain is 59.1 mol%.

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References


