**Micropepsi pineolensis** gen. nov., sp. nov., a mildly acidophilic alphaproteobacterium isolated from a poor fen, and proposal of **Micropepsaceae** fam. nov. within **Micropepsales** ord. nov.

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**Abstract**

An obligately anaerobic, mildly acidophilic, fermentative alphaproteobacterium, designated strain CS4\(^T\), was isolated from an acidic, oligotrophic (nutrient poor) poor fen located near Pineola, NC, USA. Cultures contained Gram-negative, slightly curved, non-motile, non-spore-forming, non-prosthecate rods (0.1–0.4 μm in diameter and 0.4–4 μm long, depending, in part, on the growth substrate). Growth optima were 35 °C (range 15–35 °C), pH 5.6 (range of 5.0–6.8), and with 0–50 mM added NaCl (range, 0–100 mM added NaCl). The culture fermented cellobiose, α-glucose, α-mannose, fructose, galactose, glycerol, lactose, maltose, peptone, sucrose, trehalose and xylose. Respiratory growth was not detected. Major fatty acids were C\(_{18:1}\)\(\omega 7\), C\(_{19:0}\) cyclo \(\omega 8\), C\(_{14:0}\) and C\(_{16:0}\). The G+C content of the DNA was 61.9±0.3 mol%. The two most closely related species phylogenetically, *Rhizomicrobium palustre* A48\(^T\) (AB081581) and *Rhizomicrobium electricum* Mtc52\(^T\) (AB365487) shared 94 and 93 % SSU rRNA gene sequence identity, respectively, to that of strain CS4\(^T\). Lower SSU rRNA gene sequence identities resulted from pairwise comparisons with members of the order ‘Rhizobiales’ (85–88 %) or *Sphingomonadales* (85–86 %). These findings all support the classification of strain CS4\(^T\) as representative of a novel genus, family and order of Alphaproteobacteria. The type strain of the species *pineolensis* within the genus *Micropepsi*, family *Micropepsaceae* and order *Micropepsales* is CS4\(^T\) (=KUM 307111\(^T\)=ATCC BAA-2724\(^T\)).

Peatlands are unique environments that contain acidic soils, low redox potentials and associated low decomposition rates [1], and they serve as the largest natural source of atmospheric methane, releasing approximately 0.4 Gt CH\(_4\) annually [2]. Numerous studies have shown that *Proteobacteria*, specifically *Alphaproteobacteria*, are prevalent in peatlands and thought to be involved in methane oxidation, as well as sugar fermentation and anaerobic respiration [3–5]. Herein, we describe the characteristics and phylogenetic placement of a novel alphaproteobacterium strain CS4\(^T\) isolated from a poor fen (more minerotrophic and less acidic than a true bog), Pineola Bog, in the southern Appalachian mountains, Pineola, NC, USA. Cultured and uncultured strains related to strain CS4\(^T\) form a novel family and order within *Alphaproteobacteria*.

Peat samples were collected on 12 September 2013, from Pineola Bog, at three locations within the bog, at a depth of 25–30 cm, in airtight jars and taken directly to an anaerobic (N\(_2\) and H\(_2\)) glove box. Inoculum was prepared by homogenization with deionized water using an immersion blender and then pressed through a series of filters, with a final filter size of 0.45 μm. Enrichment was performed in Balch tubes, with 5 ml of a basal medium, peat medium 1 (PM1), prepared anaerobically as described by Bräuer *et al.* [6]. Prior to inoculation, the tubes were flushed with ultra-high-purity N\(_2\) gas and sterilized. Post-sterilization, the following additions were made (final concentrations): ca. 0.5 mM Ti(III) nitrilotriacetate (TiNTA) (preparation described by Bräuer *et al.* [6]), 20 mM MES (pH 5.7), vitamin solution (0.2, 1.0, 0.5 or 0.01 μg l\(^{-1}\) of each vitamin as described by Bräuer *et al.* [6] and Balch *et al.* [7]), 40 mg yeast extract l\(^{-1}\), 1 g glycerol l\(^{-1}\) and 10 mg rifampicin l\(^{-1}\). Tubes inoculated with 0.5 ml peat filtrate were incubated in the dark at 28 ºC without shaking, and growth was monitored by visual inspection and by use of a spectrophotometer at OD\(_{600}\).

Colonies from anaerobic enrichment cultures were isolated on 1.5 % agar plates (PM1 plates) supplemented with the PM1 additions, excluding TiNTA, streaked aerobically and incubated anaerobically in a mason jar with an N\(_2\) head-space. After approximately 1 week of growth, single colonies were transferred to new plates. Colonies were re-streaked three times to ensure purity, and axenic colonies were

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**Abbreviation:** TiNTA, Ti(III) nitrilotriacetate.

The GenBank/EMBL/DDBJ accession number for the SSU rRNA gene sequence of strain CS4\(^T\) is KU738893.
transferred back to liquid medium in the anaerobic glovebox. Purity was visually inspected using fluorescence microscopy on an Olympus BX51 using acridine orange with a FITC filter. The SSU rRNA gene was PCR amplified from extracted DNA and sent to Beckman Coulter Genomics for Sanger sequencing. Once isolated, strain CS4 was also grown in PM1 medium containing the addition of 500 mg l\(^{-1}\) peptone and/or with 1 g l\(^{-1}\) of either sucrose or dextrose substituted for glycerol.

Effects of pH, salinity and temperature on growth were examined in PM1 supplemented with glucose (1 g l\(^{-1}\)). For physiological studies, the isolate was grown in PM1 in at least duplicate or triplicate trials. Aerobic growth was tested by addition of 25, 50 or 100 % air in the N\(_2\) headspace in Balch tubes with and without the reductant, TiNTA, or by incubating plates streaked with bacteria aerobically at 28 and 35 °C. Gram-staining, oxidase and catalase tests were completed according to previously described procedures [8]. Presence or absence of cell motility was examined visually under a phase-contrast microscope and by culturing anaerobically in swarm plates (0.8 % nutrient broth with 0.3 % agar), supplemented with 1 g l\(^{-1}\) sucrose. Heat tolerance was examined by submerging inoculated PM1 in 80 °C (10 min) and determining subsequent bacterial viability. Cell morphology was observed by transmission electron microscopy of negatively stained [1 % phosphotungstic acid] cells fixed on a 100 square formvar coated grid. Cells were imaged using a JEM-1400 transmission electron microscope.

Fermentative growth was examined in PM1 supplemented with sterile, anaerobic substrates (ca. 20 mM). Utilization of electron acceptors was tested in PM1 supplemented with 1 g l\(^{-1}\) glucose as the sole carbon source and either sodium sulfate, ferric ammonium citrate, sodium fumarate, sodium malate (20 mM each) or O\(_2\) (headspace replaced with O\(_2\)) as the sole electron acceptor. The Fe(III)-reducing capability of strain CS4 was tested in PM1 supplemented with 1 g glucose l\(^{-1}\) (with and without TiNTA) and with ferric ammonium citrate added to a final concentration of 2, 4 and 8 mM. FerroZine Iron Reagent Solution Pillows (Hach) were used at pH 7.0 to determine the presence of Fe(II) colorimetrically. The Fe(III)-reducing ability was additionally tested with the addition of acetate, ethanol, formate, glycerol, lactate, pyruvate or succinate (20 mM) as the sole electron donor. Nitrate or sulfate reduction was determined using previously described methods [8, 9]. The G+C content of the genomic DNA (in triplicate) was calculated as described by Shelobolina et al. [10] using linear regression analyses of a standard curve of melting temperatures (\(T_m\)) for standard DNA (in triplicate) from the following species: Clostridium acetobutylicum, Flavobacterium capsulatum, Bacillus subtilis, Methanoregula boonei, Micrococcus luteus and Escherichia coli. Phospholipid-derived fatty acids from freeze-dried cells harvested in stationary phase after growth in PM1 supplemented with 1 g glucose l\(^{-1}\) were analysed via fatty acid methyl ester analysis at MIDI Labs. HPLC was utilized to determine the production of organic acids on a Dionex platform operated isocratically (mobile phase, 0.085 M H\(_2\)SO\(_4\); flow rate, 0.4 ml min\(^{-1}\)). Separation was completed with a Bio-Rad Aminex HPX-87H ion exchange column (50 °C); eluted compounds were detected with a refractive index detector and UV detector, in tandem.

Sequences similar to the partial SSU rRNA gene sequence for strain CS4 (KU738893) as well as sequences for members of closely related alphaproteobacterial orders were collected from the GenBank database [11] using the BLAST tool (http://blast.ncbi.nlm.nih.gov/Blast.cgi) and were aligned using the SILVA aligner of the ARB program (www.arb-silva.de/aligner/). Aligned sequences were trimmed utilizing BioEdit software (Ibis Biosciences). Phylogenetic trees were reconstructed with neighbour-joining [12] and maximum-likelihood methods using DNADIST, SEQBOOT with CONSENSE for bootstrapping, NEIGHBOR and DNAML programs within the PHYLIP package (http://evolution.gs.washington.edu/phylip.html). Tree output files were visualized in Tree Explorer and exported to Adobe Illustrator to allow the addition of full organism names.

Colonies of strain CS4 grown anaerobically on PM1 plates, which had been poured and stored aerobically prior to inoculation, were smooth, translucent and ca. 2 mm in diameter. Strain CS4 grew when streaked aerobically and incubated anaerobically, indicating a tolerance to brief oxygen exposure. However, bacterial growth was not observed with the addition of any percentage of air in the headspace or on the PM1 plates incubated aerobically; therefore, strain CS4 is considered an obligate anaerobe. Cells stained Gram-negative. As observed thus far, cells averaged from 0.1 to 0.4 µm in diameter and were 0.4–4 µm long, as follows: when grown on glucose (1 g l\(^{-1}\)), cells were curved rods 0.2–0.3 µm in diameter and 1–3 µm long (Fig. 1); when grown on sucrose (1 g l\(^{-1}\)), cells were 0.2–0.4 µm in diameter and 2–4 µm long; and when grown on glycerol (1 g l\(^{-1}\)), cells were 0.1 µm in diameter and 0.4–0.5 µm long. Catalase and oxidase tests were negative. Division by binary fission was observed, but protease and motility were not. Heat-tolerant cells were not produced. Strain CS4 tolerate up to 100 mM NaCl and grew optimally with the addition of 0–50 mM NaCl to the medium. Optimal growth rates were observed at an initial pH of 5.6 (final pH 4.0; range, 5.0–6.8) and at 35 °C (range, 15–35 °C), unlike isolates of the phylogenetically closest related genus, Rhizobium, members of which displayed a higher NaCl tolerance of up to 1 % (171 mM) and a higher pH optimum of 6.7–6.8 (Table 1). Strain CS4 grew fermentatively on numerous substrates including disaccharides derived from decomposing organic matter, such as cellobiose and maltose, as detailed below in the species description. Fermentation products from glucose (1 g l\(^{-1}\)) were ethanol (1.1±0.1 mM), formate (3.1±0.5 mM), acetate (1.6±0.1 mM), H\(_2\) (2.1 mmole l\(^{-1}\) culture), CO\(_2\) (4.2 mmole l\(^{-1}\) culture) and trace amounts of lactate. Low fermentation yields were likely due to cell growth and/or acidification of the medium because the cessation of cell growth occurred at pH 4.0. Unlike members of the Rhizobium, strain
CS4<sup>T</sup> did not use sodium sulfate, ferric ammonium citrate, sodium fumarate, sodium malate or O<sub>2</sub> as electron acceptors (Table 1). Fe(III) was not reduced with either acetate, ethanol, formate, glucose, pyruvate or succinate as the sole electron donor.

The major fatty acids (>5 %) of strain CS4<sup>T</sup> were C<sub>18:1</sub>ω7c (36.7 %), C<sub>19:0</sub> cyclo ω8c (22 %), C<sub>14:0</sub> (17 %) and C<sub>16:0</sub> (13.2 %). Other fatty acids detected (>0.1 %) included C<sub>16:0</sub> 3-OH (4.6 %); C<sub>18:0</sub> (2.2 %), C<sub>14:0</sub> 3-OH and/or iso-C<sub>14:0</sub> I (1.2 %), C<sub>18:1</sub>ω7c 11-methyl (0.9 %), C<sub>16:1</sub>ω7c and/or C<sub>16:1</sub>ω6c (0.8 %), C<sub>20:2</sub>ω6,9c (0.6 %), C<sub>12:0</sub> (0.4 %), C<sub>19:1</sub>ω6c and/or C<sub>19:1</sub>ω7c (0.2 %) and C<sub>15:0</sub> (0.2 %) and C<sub>15:0</sub> 3-OH (0.1 %). Notably, the phospholipid-derived fatty acid profile demonstrates that strain CS4<sup>T</sup> can adapt to low pH environments by the significant presence of the saturated, cyclopropane-containing fatty acid C<sub>19:0</sub> cyclo ω8c [13], indicating a stiffer and more stress-tolerant membrane structure. Members of both the Rhizomicrobiaceae and strain CS4<sup>T</sup> also contain C<sub>18:1</sub>ω7c as their most abundant fatty acid. The genomic DNA G+C content of strain CS4<sup>T</sup> was estimated at 61.9±0.3 mol% using melt curve analysis.

A database search of sequences closely related to strain CS4<sup>T</sup> revealed that it was most closely related (99 %) to two environmental clones 3C003352 (EU801969) and MUP3F11 (HQ178872) (Fig. 2). Two sequences from cultured strains Rhizomicrobium palustre A48<sup>T</sup> (ABO81581) and Rhizomicrobium electricum Mfc52<sup>T</sup> (AB365487) shared 94 and 93 % identity, respectively, to that of strain CS4<sup>T</sup>. R. palustre was isolated from the roots of rice plants in a flooded rice paddy and was originally phylogenetically placed in Alphaproteobacteria as a representative of a novel genus related to Sphingomonadales [14]. R. electricum was later isolated from a cellulose-fed microbial fuel cell and phylogenetically placed in the genus Rhizomicrobium as most closely related to the ‘Rhizobiales’, but not fully affiliated with any established order [15].

Overall, strain CS4<sup>T</sup> displays characteristics that clearly define it from previously characterized strains of the genus of closest relation, Rhizomicrobium (Table 1). The G+C content, growth optima (pH, salinity tolerance and O<sub>2</sub> requirement) and utilization of growth substrates (Table 1) support our consideration that strain CS4<sup>T</sup> is a member of a novel genus, Micropepsis, for which the proposed name is
**Micropepsis pineolensis.** Additionally, based on phylogenetic analyses of the SSU rRNA gene, comparisons of metabolic capabilities and assertions from previous work [15, 16], we propose that the genera *Micropepsis* and *Rhizomicrobium* form a new family, *Micropepsaceae*, within the new order *Micropepsales*.

**DESCRIPTION OF MICROPEPSIS GEN. NOV.**

*Micropepsis* (Mi.cro.pep’sis. Gr. adj. mikros small; Gr. fem. n. pepsis digestion; N.L. fem. n. Micropepsis small digester).

Cells are Gram-negative, non-spore-forming, curved rods without prosthecae that reproduce by binary fission. Growth occurs between 15 and 35 °C, without prosthecae that reproduce by binary fission. Cells are non-spore-forming, curved rods (0.1–0.4 μm in diameter and 0.4–4 μm long). The optimum growth temperature is 35 °C, and the optimum pH is 5.6. The optimum NaCl concentration for growth is 0–50 mM added NaCl (growth observed ≤100 mM NaCl). Grows fermentatively on cellobiose, d-glucose, d-mannose, fructose, galactose, glycerol, lactose, maltose, sucrose, trehalose, xylose and peptone. Does not utilize 2-butanol, acetate, alanine, arabinose, aspartic acid, cellulose, citrate, cysteine, aesculin, ethanol, fumarate, glycine, inulin, lactate, mannitol, methanol, propanol, protocatechuate, pyruvate, rhamnose, ribose, serine, sodium acetate, sodium formate, soluble starch, sorbitol, sorbose, succinate or xylan. Major fermentation products on glucose (1 g l⁻¹) are as follows: E (ca. 1 mM), F (ca. 3 mM), A (ca. 1.5 mM), H₂ (ca. 2 mmoles l⁻¹ culture) and CO₂ (ca. 4 mmoles l⁻¹ culture). Does not utilize acetate, ethanol, formate, lactate, pyruvate or succinate as an electron donor. Does not utilize Fe(III), Na₂SO₄, sodium fumarate, sodium malate or O₂ as an electron acceptor.

The type strain CS4ᵀ (=JCM 30711ᵀ=ATCC BAA-2724ᵀ) was isolated from anoxic peat soil in a southern Appalachian peatland known as Pineola Bog, Pineola, NC, USA. The genomic DNA G+C content of the type strain is 61.9 ±0.3 mol%.

### Table 1. Select characteristics of strain CS4ᵀ, *Rhizomicrobium electricum* Mfc52ᵀ and *Rhizomicrobium palustre* A48ᵀ

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>CS4ᵀ</th>
<th><em>R. electricum</em> Mfc52ᵀ</th>
<th><em>R. palustre</em> A48ᵀ</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prosthecae</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cell division</td>
<td>Binary fission</td>
<td>Budding, binary fission</td>
<td>Budding, binary fission</td>
</tr>
<tr>
<td>pH optimum (range)</td>
<td>5.6 (5.0–6.8)</td>
<td>6.7 (5.0–7.5)</td>
<td>6.8 (5.5–7.3)</td>
</tr>
<tr>
<td>NaCl range (%)</td>
<td>0–0.3 %</td>
<td>0–1 %</td>
<td>0–1 %</td>
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<tr>
<td>O₂ requirement</td>
<td>Anaerobic</td>
<td>Facultatively anaerobic</td>
<td>Facultatively anaerobic</td>
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<tr>
<td>Anaerobic reduction of:</td>
<td></td>
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<tr>
<td>Nitrate</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Fumarate</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Fe(III)</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Fermentative growth on:</td>
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<tr>
<td>Cellobiose</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Glycerol</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Trehalose</td>
<td>+</td>
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<td>Mannose</td>
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<td>Ribose</td>
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<tr>
<td>Arabinose</td>
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<td>+</td>
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<tr>
<td>Xylan</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>61.9</td>
<td>64.7</td>
<td>55.4</td>
</tr>
<tr>
<td>Major fatty acids (%)</td>
<td>C₁₈:ω7c (36.7), C₁₉₀ cyclo ω8c (22.0), C₁₄₀ (17.0) and C₁₆₀ (13.2)</td>
<td>C₁₈:ω7c (47.3), anteiso-C₁₅₀ (14.0), C₁₆₀ (8.6)</td>
<td>C₁₈:ω7c (29.4), anteiso-C₁₅₀ (16.2), C₁₆₀ (13.2)</td>
</tr>
</tbody>
</table>

*Data collected by Kodama and Watanabe [15].
†Data collected by Ueki et al. [14].
Fig. 2. Neighbour-joining dendrogram, based on SSU rRNA gene sequences, showing the phylogenetic position of strain CS4\(^T\) (KU738893) in relation to the genus Rhizomicrobium. Members of Micropepsales ord. nov. are shown in comparison to other alphaproteobacterial orders including ‘Rhizobiales’ and Sphingomonadales. Nodal support was determined using bootstrapping values of 100 replicates in neighbour joining, and values are displayed only for those nodes with support values >50% that were also supported by maximum-likelihood analyses. Bar, 0.05 substitutions per nucleotide position.

DESCRIPTION OF MICROPEPSACEAE
FAM. NOV.

Micropepsaceae (Mi.cro.pep.sa.ceae. N.L. fem. n. Micropepsis the type genus of the family; -aceae to denote a family; N.L. fem. pl. n. Micropepsaceae the Micropepsis family).

Gram-negative, non-spore-forming rod-shaped bacteria that reproduce by binary fission or budding from prosthete mother cells. Obligately anaerobic, facultative or aerobic. Neutrophilic or mildly acidophilic. Grow fermentatively on mono-, di- and polysaccharides such as sucrose, dextrose, xylose, maltose, cellobiose and/or xylan. Ferric iron, nitrate, oxygen and/or fumarate may serve as electron acceptors. DNA G+C content is 55–64 mol%.

The nomenclatural type is the genus Micropepsis.

DESCRIPTION OF MICROPEPSALES ORD. NOV.

Micropepsales (Mi.cro.pep.sa.les. N.L. fem. n Micropepsis the type genus of the order; -ales ending denoting an order; N.L. fem. pl. n. Micropepsales the order of Micropepsis).

Description of the order is the same as that for the family.

The nomenclatural type is the genus Micropepsis.

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Conflicts of interest
The authors declare that there are no conflicts of interest.

References