Reclassification of *Bacteroides termitidis* Sebald (Holdeman and Moore) in a New Genus *Sebaldella*, as *Sebaldella termitidis* comb. nov.

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*Bacteroides termitidis* (Sebald) differs so much from the type species of the genus *Bacteroides*, *Bacteroides fragilis* (Castellani and Chalmers), that it should not be retained within this genus. On the basis of biochemical, chemical, and genetic criteria, we propose that *Bacteroides termitidis* be reclassified in a new genus, *Sebaldella*, as *Sebaldella termitidis* comb. nov., the type species of the genus. The type strain of *S. termitidis* is strain NCTC 11300 (= ATCC 33386).

*Bacteroides termitidis* was originally isolated from the posterior intestinal contents of termites (*Reticulitermes lucifugus*), where it is part of the predominant bacterial flora (7). However, the taxonomic position of *B. termitidis* is controversial (9). In Bergey's Manual of Systematic Bacteriology, 39 species of *Bacteroides* are recognized (2). These species are biochemically and chemically very diverse, and their guanine-plus-cytosine (G+C) contents range from 28 to 61 mol% (2, 9).

We have indicated previously (9) that the genus *Bacteroides* should be restricted to *Bacteroides fragilis* and related species (e.g., *Bacteroides egerthii*, *Bacteroides distasonis*, *Bacteroides ovatus*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis* and *Bacteroides vulgatus*). The *B. fragilis* group of organisms exhibits a relatively small G+C content range (ca. 40 to 48 mol%) (3) and has relatively homogeneous biochemical and chemical properties (9). For example, *B. fragilis* and related species produce succinic and acetic acids as the major end products of glucose metabolism (2) and possess enzymes of the hexas monophosphate shunt-pentose phosphate pathway (viz., glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase), and glutamate and malate dehydrogenases (9, 10). *B. termitidis* differs from the *B. fragilis* group by exhibiting a lower G+C content (32 to 36 mol%), by producing acetic and lactic acids as major end products of glucose fermentation, and by lacking hexose monophosphate shunt enzymes and glutamate and malate dehydrogenases (7, 9; Collins and Shah, unpublished data). *B. termitidis* also differs markedly from the *B. fragilis* group in lipid composition. The long-chain fatty acids of *B. fragilis* and related species are predominantly of the straight-chain saturated, anteiso- and iso-methyl branched-chain types, with mono-unsaturated acids either absent or present in only trace amounts (4, 8). In contrast, *B. termitidis* primarily synthesizes acids of the straight-chain saturated and monounsaturated types, and methyl branched acids are absent. For example, in strain NCTC 11300T (T = type strain) the following acids are found: C₁₂:₀ (2.5%), C₁₄:₀ (8.5%), C₁₆:₀ (37.0%), C₁₆:₁ (3.0%), C₁₈:₀ (0.5%), C₁₈:₁ (41.0%), 30H-C₁₄:₀ (7.0%) and 30H-C₁₆:₀ (0.5%). Similarly, the *B. fragilis* group and *B. termitidis* differ in their isoprenoid quinone compositions; *B. fragilis* and related species possess menaquinones (vitamin K₂), whereas *B. termitidis* lacks respiratory quinones (1, 8). On the basis of 16S ribosomal ribonucleic acid oligonucleotide cataloging studies, Paster and associates recently demonstrated that *B. termitidis* is phylogenetically distinct from other *Bacteroides* species (including the type species, *B. fragilis*) and that this species does not cluster with any of the previously defined eubacterial phyla (5). The latter studies reinforce the major phenotypic differences between *B. termitidis* and the *B. fragilis* group of organisms and support our previous suggestion that *B. termitidis* should be removed from the genus *Bacteroides* (9). Therefore, in view of the overwhelming phenotypic and phylogenetic evidence, we formally propose that bacteria presently designated *B. termitidis* be reclassified in a new genus, *Sebaldella*, as *Sebaldella termitidis* comb. nov. Characteristics that are useful in distinguishing the genus *Sebaldella* from *B. fragilis* and other *Bacteroides* spp. with low G+C contents are summarized in Table 1.

**Description of *Sebaldella gen. nov.*** *Sebaldella* (Se. bal' de la. M.L. dim. ending -ella; M.L. fem. N. *Sebaldella* named after the French microbiologist Madeleine Sebald, who first described the organism) cells are gram-negative, nonspore-forming, nonmotile rods. Obligately anaerobic. Acid produced from glucose and some other sugars. The major end products of glucose fermentation are acetic and lactic acids; formic acid may also be produced. Hexose monophosphate shunt enzymes, glucose-6-phosphate dehydrogenase, and 6-phosphogluconate dehydrogenase are absent. Glutamate dehydrogenase and malate dehydrogenase are absent. Nonhydroxylated and 3-hydroxylated long-chain fatty acids are present. The fatty acids are primarily of the straight-chain saturated and monounsaturated types. Menaquinones are absent. The deoxyribonucleic acid base composition is 32 to 36 mol% G+C, as determined by chromatographic (7) and buoyant density (6) methods. The type species is *Sebaldella termitidis*.

**Description of *Sebaldella termitidis* comb. nov.** The gram-negative, obligately anaerobic, nonmotile, rod-shaped cells are 0.3 to 0.5 by 2 to 12 μm with central swellings and occur singly, in pairs, and in filaments. Surface colonies are 1 to 2 mm in diameter, circular, and transparent to opaque. Colonies in deep agar are lenticular and nonpigmented. Acetic and lactic acids are the major end products of glucose metabolism; formic acid may also be produced. Acid is produced from glucose, fructose, maltose, mannitol, mannose, rhamnose, sucrose, trehalose, and xylose. Acid is not produced from arabinose, melezitose, or starch; low levels
TABLE 1. Biochemical and chemical characteristics useful in distinguishing the genus *Sebaldella* from *Megamonas*, *B. fragilis*, and other *Bacteroides* species with low G+C contents

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Major end products from PYG&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Mode of metabolism&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Malate dehydrogenase</th>
<th>Glutamate dehydrogenase</th>
<th>Glucose-6-phosphate dehydrogenase</th>
<th>6-Phosphogluconate dehydrogenase</th>
<th>Menaquinones</th>
<th>Major long-chain fatty acids</th>
<th>G+C content (mol %)&lt;sup&gt;c&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Sebaldella</em></td>
<td>A, L</td>
<td>F</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;, C&lt;sub&gt;18:1&lt;/sub&gt;</td>
<td>C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>32–36</td>
</tr>
<tr>
<td><em>Megamonas</em></td>
<td>P, A, I</td>
<td>F</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td></td>
<td>32–35</td>
</tr>
<tr>
<td><em>B. fragilis</em></td>
<td>S, A</td>
<td>F</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Bacteroides coagulans</em></td>
<td>a</td>
<td>NF</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>MK-10, MK-11</td>
<td>antiseo-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>41–44</td>
</tr>
<tr>
<td><em>Bacteroides furoeus</em></td>
<td>L, a</td>
<td>NF</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td></td>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;, C&lt;sub&gt;18:1&lt;/sub&gt;</td>
<td>37</td>
</tr>
<tr>
<td><em>Bacteroides praecacus</em></td>
<td>A, B, IV</td>
<td>NF</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td></td>
<td>C&lt;sub&gt;18:0&lt;/sub&gt;</td>
<td>28</td>
</tr>
<tr>
<td><em>Bacteroides putridinoid</em></td>
<td>S, IV, P</td>
<td>NF</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td></td>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>ND</td>
</tr>
</tbody>
</table>

<sup>a</sup> A and a, Acetic acid; B, butyric acid; L and l, lactic acid; P, propionic acid; S, succinic acid; IV, isovaleric acid. Upper-case letters indicate major products, and lower-case letters indicate minor products. Data from reference 2.<br><br><sup>b</sup> F, Fermentative; NF, nonfermentative or weakly fermentative.<br><br><sup>c</sup> Data from references 2, 3, and 9.<br><br><sup>d</sup> ND, Not determined.<br><br>Collins, unpublished data.

of acid may be produced from lactose (delayed reaction). Most strains produce H<sub>2</sub>S. Gelatin is not liquefied; coagulated proteins are not attacked. Urease, chitinase, and indole are not produced. Nitrate is not reduced. Uric acid is degraded to CO<sub>2</sub>, acetate, and ammonia. Malate dehydrogenase and glutamate dehydrogenase are not produced.

Nonhydroxylated and 3-hydroxylated long-chain fatty acids are present. The fatty acids are of the straight-chain saturated and monounsaturated types, with hexadecanoic and octadecenoic acids predominating. Menaquinones are not produced. The G+C content of the deoxyribonucleic acid is 32 to 36 mol% (6, 7). Isolated from posterior intestinal contents of termites, where these organisms are part of the predominant bacterial flora. The type strain is strain NCTC 11300 (= ATCC 33386).

Description of the type strain. The description of the type strain corresponds to that of the species, except that glycerol and lactose are not fermented and H<sub>2</sub>S is produced.

LITERATURE CITED