Reclassification of *Bacteroides praecacutus* Tissier (Holdeman and Moore) in a New Genus, *Tissierella*, as *Tissierella praecacuta* comb. nov.

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The placement of *Bacteroides praecacutus* (Tissier) in the genus *Bacteroides* is controversial. Recent biochemical and chemical data clearly demonstrate that *B. praecacutus* is sufficiently unrelated to the type species of *Bacteroides*, *B. fragilis* (Castellani and Chalmers), that it should not be retained within this genus. It is therefore formally proposed that *B. praecacutus* be removed from the genus *Bacteroides* and reclassified in a new genus, *Tissierella*, as *T. praecacuta* comb. nov. The type strain of *T. praecacuta* is ATCC 25539 (NCTC 11158).

The species *Bacteroides praecacutus* was originally isolated from infant feces and described by Tissier in 1908 (16). In addition to being found in infant and adult feces, the organism has been, albeit infrequently, isolated from lung abscesses, gangrenous lesions, and blood (1, 2, 6). Although *B. praecacutus* is well characterized (1, 2, 11), its placement within the genus *Bacteroides* is controversial (13). The genus *Bacteroides* as described in Bergey’s Manual of Systematic Bacteriology (7) comprises a heterogeneous collection of obligately anaerobic, gram-negative, non-sporeforming, rod-shaped bacteria. Over 40 species are currently recognized. These species are phenotypically diverse and possess a DNA base composition range of 28 to 61 mol% G+C, although it is now generally accepted that a difference of >10% indicates that species are unrelated at the generic level. In addition to this wide range of DNA base composition, members of the genus exhibit a variety of cellular morphologies and are biochemically and physiologically extremely heterogeneous. We have indicated previously (13) that the genus *Bacteroides* should be restricted to *B. fragilis* and related species (i.e., *B. eggerthii*, *B. distasonis*, *B. ovatus*, *B. thetaiotaomicron*, *B. uniformis*, and *B. vulgatus*). The *B. fragilis* group of organisms possesses the relatively small G+C range of 40 to 48 mol% (8) and is biochemically and physiologically relatively homogeneous (7, 13, 14). For example, *B. fragilis* and related species are saccharolytic, produce succinic and acetic acids as the major end products of glucose metabolism (7), contain menaquinones as sole respiratory quinones (12), and possess enzymes of the hexose monophosphate shunt-pentose phosphate pathway (viz., glucose-6-phosphate dehydrogenase and 6-phosphogluconate dehydrogenase) and glutamate and malate dehydrogenases (13, 14). *B. praecacutus*, however, possesses a significantly lower DNA base composition (28 mol% G+C) and differs markedly from the *B. fragilis* group in being non- or weakly fermentative (2, 7). Butyric, isovaleric, and acetic acids are the predominant metabolic end products together with low levels of other acids (2). *B. praecacutus* also differs from *B. fragilis* and related species in lacking menaquinones and the enzymes glucose-6-phosphate dehydrogenase, glutamate dehydrogenase, and malate dehydrogenase (13). The long-chain fatty acids of *B. praecacutus* are also incompatible with that of the *B. fragilis* group. *B. fragilis* and related species synthesize primarily methyl branched-chain acids, with 12-methyltetradecanoic acid (anteiso-C15:0) predominating (10, 12). *B. praecacutus* also synthesizes major amounts of methyl branched-chain acids but with that of the iso series predominating (e.g., NCTC 11158: iso-C14:0, 2.5%; C14:0, 8.0%; iso-C15:0, 4.5%; C15:0, 0.5%; iso-C16:0, 0.5%; C16:1, 3.0%; C16:0, 20.0%; iso-C17:0, 7.0%; C18:1, 2.5%; C18:0, 1.5%; 30H-C14:0, 0.5%; 30H-C16:0, 9.0%; 30H-iso-C16:0, 0.5%). *B. praecacutus* can also be readily distinguished from other asaccharolytic *Bacteroides* species. For example, *B. praecacutus* resembles the asaccharolytic pigmenting species *B. asaccharolyticus*, *B. endodontalis*, and *B. gingivalis* in being nonfermentative, producing major levels of butyric acid (in combination with acetic, isovaleric, and other acids) and in possessing primarily iso-methyl, branched, long-chain fatty acids, with 13-methyltetradecanoic acid predominating. The production of an NAD-dependent 6-phosphogluconate dehydrogenase by *B. praecacutus*, together with the absence of malate dehydrogenase and glutamate dehydrogenase, however, distinguishes these taxa. The presence of substantially different DNA base compositions (i.e., 28 mol% G+C [2] for *B. praecacutus* compared with 44 to 54 mol% G+C [3, 15, 17] for the asaccharolytic, pigmented species) further emphasizes this lack of relatedness. Johnson and Harich (9), on the basis of ribosomal ribonucleic acid studies, recently demonstrated that *B. praecacutus* is phylogenetically distinct from the *B. fragilis* group and other *Bacteroides* species (including asaccharolytic taxa), thereby reinforcing these major phenotypic differences.

Thus, there is now overwhelming evidence that *B. praecacutus* should be excluded from the genus *Bacteroides*. Furthermore, on the basis of biochemical, chemical, and genetic criteria, we consider that *B. praecacutus* is sufficiently distinct to warrant a separate genus. We therefore formally propose that bacteria presently designated *B. praecacutus* be reclassified in a new genus, *Tissierella*, as *T. praecacuta* comb. nov. Characters useful in distinguishing *T.
TABLE 1. Biochemical and chemical characterization useful in distinguishing the genus *Tissierella* from *B. fragilis* group, pigmented asaccharolytic species and other *Bacteroides* species with low mol% G+C content

<table>
<thead>
<tr>
<th>Organism(s)</th>
<th>Major end products from PYG&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Metabolism&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Presence of:&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Major long-chain fatty acids</th>
<th>Menaquinones</th>
<th>Mol% G+C&lt;sup&gt;d&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Tissierella</em> spp.</td>
<td>B, A, iV</td>
<td>NF</td>
<td>+ + + +</td>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>F</td>
<td>28</td>
</tr>
<tr>
<td><em>B. fragilis</em> group</td>
<td>S, A</td>
<td>F</td>
<td>+ +</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Pigmented, asaccharolytic species&lt;sup&gt;e&lt;/sup&gt;</td>
<td>B, iV, A</td>
<td>NF</td>
<td>+ +</td>
<td>+ +</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>B. coagulans</em></td>
<td>a</td>
<td>NF</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>B. furcosus</em></td>
<td>L, a</td>
<td>NF</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>B. putredinis</em></td>
<td>S, iV, P</td>
<td>NF</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>B. termididis</em></td>
<td>A, L</td>
<td>F</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>B. ureolyticus</em></td>
<td>S, A</td>
<td>NF</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td><em>Megamonas</em> spp.</td>
<td>P, a, 1</td>
<td>F</td>
<td>+ + +</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

<sup>a</sup> Acids: A, acetic; B, butyric; L, lactic; P, propionic; S, succinic; iV, isovaleric. Lowercase letters indicate minor components. Data are from reference 7. PYG, Peptone-yeast extract-glucose broth.

<sup>b</sup> F, Fermentative; NF, non- or weakly fermentative.

<sup>c</sup> MDH, Malate dehydrogenase; GDH, glutamate dehydrogenase; G6PDH, glucose-6-phosphate dehydrogenase; 6PGDH, 6-phosphogluconate dehydrogenase.

<sup>d</sup> Data are from references 2, 3, 7, 8, 15, and 17.

<sup>e</sup> *B. asaccharolyticus, B. endodontalis,* and *B. gingivalis.*

<sup>f</sup> M. D. Collins, unpublished data.

<sup>g</sup> ND, Not determined.

*praeacuta* from other asaccharolytic species and other *Bacteroides* spp. containing a low mol% G+C content are summarized in Table 1.

**Description of *Tissierella* gen. nov.** M. L. dim. ending -ella; M. L. fem. N. *Tissierella* named after P. H. Tissier, who first described the organism. Obligately anaerobic, gram-negative, non-sporeforming rods. Weakly or nonfermentative. Major metabolic end products in peptone-yeast extract-glucose broth are acetic, butyric, and isovaleric acids together with low levels of other acids. 6-Phosphogluconate dehydrogenase is produced. Glucose-6-phosphate dehydrogenase, glutamate dehydrogenase, and malate dehydrogenase are absent. *meso*-Diaminopimelic acid is present in the cell wall peptidoglycan. Nonhydroxylated and 3-hydroxylated long-chain fatty acids are present. The fatty acids are primarily of the straight-chain saturated and iso-methyl branched-chain types. Menaquinones are absent. The DNA base composition of the type species is 28 mol% G+C (2).

The type species is *T. praeacuta.*

**Description of *T. praeacuta.*** Cells are motile by means of peritrichous flagella and occur singly or in pairs. Cells are 0.6 to 0.9 by 2 to 8 μm and have rounded or occasionally pointed ends; swelling toward the end of the cell is common. Filaments up to 20 μm long may occur. Colonies on blood agar are small, circular, low convex, grayish, and smooth. Glucose broth cultures are moderately turbid with a smooth sediment. Major metabolic end products in peptone-yeast extract-glucose broth are acetate, butyrate, and isovalerate; small amounts of propionate, isobutyrate, and other acids are produced. The optimum temperature for growth is 37°C. An NADP-dependent 6-phosphogluconate dehydrogenase is produced. Glucose-6-phosphate dehydrogenase, glutamate dehydrogenase, and malate dehydrogenase are absent. Urease and indole are not produced. Nitrate reduction, hippurate hydrolysis, and gelatin liquefaction are variable. Esculin is not hydrolyzed. H₂S is produced in SIM (Difco) broth. The cell wall peptidoglycan contains *meso*-diaminopimelic acid (4); no heptose or 2-keto-3-deoxyoctulosonic acid was detected in the wall (5). Nonhydroxylated and 3-hydroxylated long-chain fatty acids are produced. The fatty acids are primarily of the straight-chain saturated and iso-methyl branched-chain types, with 13-methyltetradecanoic (iso-C<sub>15:0</sub>) acid predominating. Menaquinones are not produced. The mol% G+C content of DNA from the type strain is 28 (2). Isolated from infant and adult feces, gangrenous lesions, lung abscesses, and blood. Type strain: ATCC 25539 (NCTC 11158).

**Description of the type strain.** The description of the type strain corresponds to that of the species except that gelatin is hydrolyzed and nitrate is reduced.

**LITERATURE CITED**


