Description of Three New Species of the Genus *Peptostreptococcus* from Human Clinical Specimens: *Peptostreptococcus harei* sp. nov., *Peptostreptococcus ivorii* sp. nov., and *Peptostreptococcus octavius* sp. nov.

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In a previous investigation of the laboratory identification of clinical strains of the genus *Peptostreptococcus*, several isolates were found to be atypical. In this study, we further examined these strains by using both phenotypic and genotypic methods. Based on our findings, we describe the following three new species of the genus *Peptostreptococcus* from human clinical specimens: *Peptostreptococcus harei*, whose type strain is DSM 10020 (isolated from a sacral sore); *Peptostreptococcus ivorii*, whose type strain is DSM 10022 (isolated from a leg ulcer); and *Peptostreptococcus octavius*, whose type strain is NCTC 9810 (isolated from nasal flora). An analysis of their 16S rRNA gene sequences indicated that all three species are related to *Clostridium* cluster XIII, which includes most species of the genus *Peptostreptococcus*. The phenotypic characteristics of the new species are described.

The genus *Peptostreptococcus* as currently constituted consists of a group of obligately anaerobic gram-positive cocci which is phenotypically very diverse (2, 10, 19). In addition to considerable metabolic diversity, members of the genus have been shown by nucleic acid analysis to be phylogenetically heterogeneous (2, 11, 15, 22). In particular, *Peptostreptococcus anaerobius*, the type species of the genus *Peptostreptococcus*, is phylogenetically far removed from other *peptostreptococci* (11, 22) and exhibits a close affinity with certain *clostridial* species (*Clostridium* rRNA cluster XI, as described by Collins et al. [2]). *Peptostreptococcus productus* has been shown to be a close phylogenetic relative of *Clostridium cocoides* and *Streptococcus hansenii* (*Clostridium* rRNA cluster XIVa [2]), whereas the majority of *peptostreptococcal* species form a phylogenetically distinct group closely related to *Helcococcus kunzii* (*Clostridium* rRNA cluster XIII [2]). At present, the genus *Peptostreptococcus* comprises 13 species (5), but unnamed groups of strains which may constitute additional species have been described (15, 19); the species *Peptostreptococcus acaciaeoliformis* and *Peptostreptococcus prevotii* are recognized as genetically heterogeneous taxa (5, 9, 10, 14, 19, 25).

In a study of more than 250 human clinical and reference strains of *peptostreptococci*, approximately 20% of the organisms could not be identified to the species level (19). When the whole-cell compositions of 127 *peptostreptococci*, most of which were from this collection, were investigated by pyrolysis mass spectrometry (PyMS), the results confirmed the presence of several unrecognized taxa (18). One group corresponded to Hare group VIII (24), which has not to date been validly named. In this study, PyMS was used to select seven representative strains from Hare group VIII and two other previously undescribed groups. We performed additional biochemical investigations on these strains, compared their phenotypic characteristics with the phenotypic characteristics of appropriate type strains of species of the genus *Peptostreptococcus*, and determined their phylogenetic relationships by performing a 16S rRNA gene sequence analysis. On the basis of phenotypic and genotypic criteria, the following three new species are proposed: *Peptostreptococcus harei*, *Peptostreptococcus ivorii*, and *Peptostreptococcus octavius*.

**MATERIALS AND METHODS**

**Investigation of whole-cell compositions by PyMS.** The 127 strains investigated by PyMS comprised 101 clinical strains and 26 reference strains included for comparison. Ninety clinical strains were selected from a previously described collection (19, 20) of 256 strains from St. Bartholomew's Hospital in London, United Kingdom; these strains were chosen to represent the full range from biochemically typical strains to highly atypical strains. They were supplemented with 11 strains isolated at Southmead Hospital in Bristol, United Kingdom; 7 of these strains resembled *Peptostreptococcus tetradius*, 1 resembled *Peptostreptococcus indicolus*, and 3 resembled *Peptostreptococcus hydrogenalis*. The reference strains were acquired recently from appropriate reference collections and included the type strains of *Peptococcus niger* and all recognized species of the genus *Peptostreptococcus*. The methods used for PyMS have been described elsewhere (8, 16, 17). Briefly, growth from blind-coded cultures of the 127 strains was sampled in quadruplicate and placed on pyrolysis foils (Horizon Instruments, Heathfield, United Kingdom). Each foil was processed in a PyMS model 200X pyrolysis mass spectrometer (Horizon Instruments), in which the foil and specimen were heated in a vacuum to 530°C for 4 s. Volatile products were subjected to low-energy electron impact ionization (35 eV), and the ions produced were separated and quantified with a quadrupole mass spectrometer. The spectra produced were recorded, and mean strain spectra were compared statistically by using the Discriminant Analysis procedure of the SPSS-PC suite (1). The resulting dissimilarity matrix was visualized as a dendrogram by using the Clustan 2-PC suite (25).

**Biochemical and physiological characterization.** Seven strains were selected for further biochemical and genetic analysis (Table 1). The strains were first characterized by previously described methods (19). Briefly, we determined the cellular and colonial morphology, the preformed enzyme profile (PEP) with the ATB 32A commercial system (API-Biomerieux, Basingstoke, United Kingdom), and the volatile fatty acid (VFA) profile by using gas-liquid chromatography (10, 19). The ATB 32A kit was used to detect production of indole, urease, alkaline phosphatase (ALP), and arginine dihydrolase (ADH). Tests for carbohydrate fermentation (acid production) were then performed in 3-ml volumes of Fastid-
P. asaccharolyticus
P. indolicus
P. prevosii
P. tetrasii
P. hydrogenalis
P. lactifaci
P. vaginale
Peptostreptococcus sp.
Peptostreptococcus sp.
Peptostreptococcus sp.
Peptostreptococcus sp.
Peptostreptococcus sp.
Hare group VIII
Hare group VIII
Peptostreptococcus sp.

Species or group Strain* Source
P. asaccharolyticus NCTC 11461T Not recorded
P. indolicus NCTC 11088T Bovine summer mastitis
P. prevosii NCTC 11086T Human, umbilical cord
P. tetrasii DSM 2951T Vaginal discharge
P. hydrogenalis DSM 7454T Vaginal discharge
P. lactifaci DSM 7455T Discharge from eye
P. vaginale DSM 7457T Ovarian abscess
Peptostreptococcus sp. DSM 10020T Pus from sacral soro
Peptostreptococcus sp. DSM 10021T Pus from peritoneal cavity
Peptostreptococcus sp. DSM 10022T Leg ulcer
Peptostreptococcus sp. DSM 10023 T Swab from abdominal cavity
Hare group VIII NCTC 9810T Nasal flora
Hare group VIII NCTC 9820T Nasal flora
Peptostreptococcus sp. DSM 10024T Antral washout, maxillary sinusitis

* NCTC, National Collection of Type Cultures, London, United Kingdom; DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany.

RESULTS AND DISCUSSION

In a study of peptostreptococci isolated at St. Bartholomew’s Hospital in London, United Kingdom (19), 256 strains from human clinical material were investigated, of which 22% could not be assigned to previously recognized species. Therefore, 127 strains (101 clinical strains and 26 reference strains), most of which were from this study, were selected for an analysis of their whole-cell compositions by PyMS. Figure 1 shows the clustering of these strains. A group of nine strains formed a distinct cluster (designated PyMS cluster 18) which was separate from other peptostreptococci, including *P. asaccharolyticus* (Fig. 1, cluster 1). These nine strains exhibited biochemical similarities with typical strains of *P. asaccharolyticus* but were readily distinguished from all of the other peptostreptococcal strains studied. On the basis of the PyMS data, two representative strains from this cluster (strains DSM 10020T and DSM 10021T) were selected for further study. A group of three strains, cluster 22, was readily separable from all other PyMS clusters, including the type strain of *P. anaerobius*, NCTC 11460 (cluster 25), to which it exhibited some phenotypic resemblance. However, the strains of cluster 22 produced a distinctive PEP (Table 2) and were unique in forming isovaleric acid as their terminal VFA. Strains DSM 10022T and DSM 10023 of cluster 22 were selected for further characterization. Four strains formed a homogeneous group, designated cluster 9, which was distinct but was part of a compositionally similar

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**TABLE 1.** Peptostreptococcus strains used in this study

<table>
<thead>
<tr>
<th>Species or group</th>
<th>Strain*</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>P. asaccharolyticus</em></td>
<td>NCTC 11461T</td>
<td>Not recorded</td>
</tr>
<tr>
<td><em>P. indolicus</em></td>
<td>NCTC 11088T</td>
<td>Bovine summer mastitis</td>
</tr>
<tr>
<td><em>P. prevosii</em></td>
<td>NCTC 11086T</td>
<td>Human, umbilical cord</td>
</tr>
<tr>
<td><em>P. tetrasii</em></td>
<td>DSM 2951T</td>
<td>Vaginal discharge</td>
</tr>
<tr>
<td><em>P. hydrogenalis</em></td>
<td>DSM 7454T</td>
<td>Vaginal discharge</td>
</tr>
<tr>
<td><em>P. lactifaci</em></td>
<td>DSM 7455T</td>
<td>Discharge from eye</td>
</tr>
<tr>
<td><em>P. vaginale</em></td>
<td>DSM 7457T</td>
<td>Ovarian abscess</td>
</tr>
<tr>
<td>Peptostreptococcus sp.</td>
<td>DSM 10020T</td>
<td>Pus from sacral soro</td>
</tr>
<tr>
<td>Peptostreptococcus sp.</td>
<td>DSM 10021T</td>
<td>Pus from peritoneal cavity</td>
</tr>
<tr>
<td>Peptostreptococcus sp.</td>
<td>DSM 10022T</td>
<td>Leg ulcer</td>
</tr>
<tr>
<td>Peptostreptococcus sp.</td>
<td>DSM 10023T</td>
<td>Swab from abdominal cavity</td>
</tr>
<tr>
<td>Hare group VIII</td>
<td>NCTC 9810T</td>
<td>Nasal flora</td>
</tr>
<tr>
<td>Hare group VIII</td>
<td>NCTC 9820T</td>
<td>Nasal flora</td>
</tr>
<tr>
<td>Peptostreptococcus sp.</td>
<td>DSM 10024T</td>
<td>Antral washout, maxillary sinusitis</td>
</tr>
</tbody>
</table>

* NCTC, National Collection of Type Cultures, London, United Kingdom; DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany.

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**FIG. 1.** Clustering of 26 reference and 101 clinical strains of gram-positive anaerobic cocci on the basis of whole-cell composition as assessed by PyMS. Numbered but unnamed clusters did not contain recognized type strains. Abbreviations: *P.*, Peptostreptococcus; *Pc.*, Peptococcus.
A detailed phylogenetic analysis was therefore performed with all members of this cluster together with representatives of Clostridium rRNA clusters XI and XIVa, which include P. anaerobius and P. productus, respectively. Figure 2 is a tree which shows the phylogenetic affinities of strains NCTC 9810T, DSM 10020T, and DSM 10022T based on a comparison of approximately 1,330 bases. It was evident from the treeing analysis and the sequence divergence values (Table 3) that the three representative strains of PyMS clusters 18, 22, and 9 constitute three separate sublines within Clostridium rRNA cluster XIII.

Two strains of PyMS cluster 18 (DSM 10020T and DSM 10021) exhibited considerable phylogenetic divergence (approximately 11%) (Table 3) from the phenotypically similar organism P. asaccharolyticus. The nearest relative of PyMS cluster 18 is Peptostreptococcus lacrimalis, but a sequence divergence value of more than 8% clearly demonstrates that strains DSM 10020T and DSM 10021 represent a species different from P. lacrimalis. The two representative strains of PyMS cluster 22 (DSM 10022T and DSM 10023) were phylogenetically distinct and exhibited more than 10% sequence divergence from previously recognized species of peptostreptococci. These data, in conjunction with the biochemical distinctiveness of the organisms (Table 4), demonstrate that the PyMS cluster 22 strains represent a new peptostreptococcal lineage. Strain NCTC 9810T and NCTC 9820T correspond to what was previously designated Hare group VIII. In addition, strain DSM 10024 was also found to be a member of this group. The phylogenetic analysis demonstrated that these strains (PyMS cluster 9) are members of a small peptostreptococcal rRNA subcluster which also includes P. hydrogenalis, P. lactolyticus, P. prevotii, P. tetradius, and P. vaginalis (Fig. 2). Although the association of PyMS cluster 9 strains with these peptostreptococcal species was statistically significant, sequence divergence values of 5.2 to 8.3% (Table 3) clearly show that this group represents a new species.

Based on the results of the present study, we believe that strains belonging to PyMS clusters 18, 22, and 9 form three phylogenetically distinct lineages that are worthy of species status. The names Peptostreptococcus harei (for strains of PyMS cluster 18), Peptostreptococcus ivorii (for strains of PyMS cluster 22), and Peptostreptococcus ovatus (for strains of PyMS cluster 9) are therefore proposed. The species descriptions below are based on characteristics of the strains selected for genetic analysis (Table 1). We recognize that the new taxa, along with all other species of peptostreptococci, are phylogenetically far removed from the type species of the genus, P. anaerobius. However, we feel that at present it would be premature to recommend a major taxonomic restructuring of the genus. Assignment of the three new species to the genus Peptostreptococcus is, in our opinion, phenotypically the most appropriate at present. However, we recognize that this assignment is a placement of convenience which in the future may require emendation as the taxonomy of the group is revised.

**Description of Peptostreptococcus harei sp. nov. Peptostreptococcus harei** (ha’re.i., M. L. gen. n. harei, of Hare, a British microbiologist). Cells are strictly anaerobic, gram-positive cocci that vary considerably in size (diameter, 0.5 to 1.5 μm) and shape (circular, oval, or elliptical). Colonies on sheep blood agar are less than 1 mm in diameter after incubation for 48 h; after 5 days, they are approximately 1 mm in diameter, entire, flat, translucent, and nonhemolytic. Urease, ALP, coagulase, and ADH are not produced. Nitrate is not reduced. Indole and catalase production are variable. Acid is not formed from glucose, lactose, maltose, sucrose, raffinose, trehalose, sorbitol, cellobiose, arabinose, ribose, mannose, or mannitol. Acid formation from fructose is variable (one of the

**VOL. 47, 1997 THREE NEW PEPTOSTREPTOCOCCUS SPECIES 783**
<table>
<thead>
<tr>
<th>Species</th>
<th>Strain</th>
<th>G+C content (mol%)</th>
<th>Terminal major VFA</th>
<th>Production of:</th>
<th>Nitrification</th>
<th>Carbohydrate fermentation reactions</th>
<th>Saccharolytic enzymes</th>
<th>Proteolytic enzymes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Indole</td>
<td>Urease</td>
<td>ALP</td>
<td>Glucose, Lactose, Maltose, Sucrose, Fructose, Raffinose, Riboose, Mannose</td>
<td>Alpha-galactosidase</td>
<td>Beta-galactosidase-6-phosphate</td>
</tr>
<tr>
<td><em>P. asaccharolyticus</em></td>
<td>NCTC 11461T</td>
<td>ND</td>
<td>B</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td><em>P. harei</em> sp. nov.</td>
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<td>25</td>
<td>B</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
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</tr>
<tr>
<td><em>P. harei</em> sp. nov.</td>
<td>DSM 10021</td>
<td>ND</td>
<td>B</td>
<td>w</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. indolicus</em></td>
<td>NCTC 11088T</td>
<td>ND</td>
<td>B</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. hydrogenalis</em></td>
<td>DSM 7454T</td>
<td>ND</td>
<td>B</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. lactofermentans</em></td>
<td>DSM 7455T</td>
<td>ND</td>
<td>B</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
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<tr>
<td><em>P. vaginatis</em></td>
<td>DSM 7457T</td>
<td>ND</td>
<td>B</td>
<td>-</td>
<td>w</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. prevotii</em></td>
<td>NCTC 11806T</td>
<td>ND</td>
<td>B</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. tetradis</em></td>
<td>DSM 2951T</td>
<td>ND</td>
<td>B</td>
<td>-</td>
<td>w</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. ivorii</em></td>
<td>DSM 10022T</td>
<td>29</td>
<td>IV</td>
<td>-</td>
<td>-</td>
<td>w</td>
<td>-</td>
<td>-</td>
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<tr>
<td><em>P. ivorii</em> sp. nov.</td>
<td>DSM 10025</td>
<td>ND</td>
<td>IV</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
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<tr>
<td><em>P. anaerobius</em></td>
<td>NCTC 11460T</td>
<td>ND</td>
<td>IC</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
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<tr>
<td><em>P. octavius</em> sp. nov.</td>
<td>NCTC 9810T</td>
<td>28</td>
<td>C</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><em>P. octavius</em> sp. nov.</td>
<td>NCTC 9820</td>
<td>26</td>
<td>C</td>
<td>-</td>
<td>w</td>
<td>+</td>
<td>-</td>
<td>-</td>
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<tr>
<td><em>P. octavius</em> sp. nov.</td>
<td>DSM 10024</td>
<td>31</td>
<td>C</td>
<td>-</td>
<td>w</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

**Abbreviations:** B, butyrate; IV, isovalerate; IC, isocaproate; C, n-caproate; aGAL, alpha-galactosidase; bGAL, beta-galactosidase; aGLU, alpha-glucosidase; bGUR, beta-glucuronidase; ArgA, arginine AMD; ProA, proline AMD; LeuA, leucine AMD; PyrA, pyroglutamate AMD; TyrA, tyrosine AMD; HisA, histidine AMD.

**ND:** not determined.

*+, positive (pH < 5.5); -, negative (pH > 6.0); w, weakly positive (pH 5.5 to 6.0).
two strains examined is positive). When the ATB 32A pre-
formed enzyme system (API-BioMerieux) is used, the proteo-
ytic enzyme arginine arylamidase (AMD) is present, but sac-
charolytic enzymes are not detected; production of the
enzymes leucine AMD, tyrosine AMD, and histidine AMD is
variable. The major VFAs produced in Robertson’s cooked
meat broth are acetic acid and butyric acid, and smaller quan-
tities of propionic, isovaleric, and n-valeric acids are sometimes
produced. P. harei has been isolated from antral washout spec-
imens, pus from the peritoneal cavity, infected sacral sores, and
abscesses of the face, neck, breast, and thigh, occasionally in
premature infants, pus from an infected sacral sore of a diabetic patient; it
was cocultured with P. micros, E. coli, and other
Peptococcus species belonging to Clostridium rRNA clusters XI, XIII, and XIVa (2). Significant bootstrap values (90% or more), expressed as
percentages based on 500 replications, are indicated at the branch points.

Description of Peptostreptococcus ivorii sp. nov. Peptostrepto-
coccus ivorii (i.vo’ri.i. M. L. gen. n. ivori, of Ivor, a British
microbiologist who first isolated the organism). Cells are
strictly anaerobic, gram-positive cocci which vary in size (di-
ameter, 0.4 to 1.5 μm) and occur in clumps. Colonies on sheep
blood agar are tiny after incubation for 48 h; after 5 days they are 1 to 2 mm in diameter, yellow-white, low convex, entire, cir-
cular, and nonhemolytic. Indole, urease, ALP, coagulase, and
ADH are not produced. Nitrate is not reduced. Catalase pro-
duction is variable. Acid is not produced from glucose, lactose,
maltose, sucrose, fructose, raffinose, trehalose, sorbitol, cel-
biose, arabinose, ribose, mannose, or mannitol. When the ATB
32A preformed enzyme system (API-BioMerieux) is used, sac-
charolytic enzymes are not detected, and proline AMD is the
only proteolytic enzyme formed. The major VFAs produced in
Robertson’s cooked meat broth are butyric and isovaleric ac-
ids, and smaller, variable quantities of acetic, propionic, isoba-
rytic, and n-valeric acids are also produced. P. ivorii has been
isolated from a leg ulcer, a preputial sac, and an intrauterine
contraceptive device (20). The type strain, DSM 10022, was
isolated from a leg ulcer; it was cocultured with P. magna, Klebsiella oxytoca, and Bacteroides ureolyticus. Strain DSM
10022T does not form catalase. The G+C content of the DNA
of strain DSM 10022T is 29 mol%.

Description of Peptostreptococcus octavius sp. nov. Peptostrepto-
coccus octavius (o.ca’ti.vi. M. L. adj. octavius, eighth, referring
to the fact that the organism was previously assigned to Hare
group VIII). Cells are strictly anaerobic, gram-positive cocci
(diameter, 0.7 to 0.9 μm) that occur in clumps. Colonies on
sheep blood agar are less than 1 mm in diameter after incu-
bation for 48 h; after 5 days, they are 1 to 2 mm in diameter,
yellow-white, glistening, circular, entire, and nonhemolytic.
Indole, urease, ALP, coagulase, and ADH are not produced.
Nitrate is not reduced. Catalase production is variable. Acid is
produced from glucose, fructose, ribose, and mannose, but not from lactose, raffinose, trehalose, cellobiose, or arabinose.
Acid production from maltose, sucrose, sorbitol, and mannitol is
variable. The proteolytic enzymes proline AMD and pyro-
glutamyl AMD are produced as determined with the ATB 32A

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TABLE 3. Levels of sequence divergence of 16S rRNA genes of Peptostreptococcus species

<table>
<thead>
<tr>
<th>Species*</th>
<th>% Sequence divergence</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>P. asaccharolyticus</td>
</tr>
<tr>
<td>P. asaccharolyticus</td>
<td>16.3</td>
</tr>
<tr>
<td>P. bamesae</td>
<td>12.4</td>
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<td>P. harei</td>
<td>14.8</td>
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<td>P. hydrogenalis</td>
<td>15.2</td>
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<td>P. indolicus</td>
<td>15.0</td>
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<tr>
<td>P. ivorii</td>
<td>12.3</td>
</tr>
<tr>
<td>P. lactimaris</td>
<td>12.3</td>
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<tr>
<td>P. magnus</td>
<td>15.6</td>
</tr>
<tr>
<td>P. micros</td>
<td>15.0</td>
</tr>
<tr>
<td>P. octavius</td>
<td>15.8</td>
</tr>
<tr>
<td>P. prevotii</td>
<td>15.2</td>
</tr>
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<td>P. tetradius</td>
<td>5.6</td>
</tr>
<tr>
<td>P. vaginalis</td>
<td>6.9</td>
</tr>
</tbody>
</table>

*P. Peptostreptococcus; H. Helcococcus.
preformed enzyme system (API-BioMerieux), but saccharolytic enzymes are not detected. The major VFAs produced in Robertson's cooked meat broth are butyric, isovaleric, and n-caproic acids. P. octavius has been isolated from intranasal specimens, skin, and normal vaginal flora (20, 24). The type strain, NCTC 9810, was isolated from normal nasal flora. Strain NCTC 9810\textsuperscript{T} does not form catalase; weak acid is produced from sorbitol but not from maltose, mannitol, or sucrose. The G+C content of the DNA of strain NCTC 9810\textsuperscript{T} is 28 mol%.

ACKNOWLEDGMENTS

We gratefully acknowledge the assistance of M. Corion of The London Hospital Medical College, the staff of the Department of Medical Microbiology, St. Bartholomew's Hospital, London, and the staff of the Department of Medical Microbiology, Southmead Hospital, Bristol. This work was supported by grants from the Showering Fund, Bristol, the Sir Jules Thorn Charitable Trust, and the European Community (grants Bio-2-CT93-019 and CHRX-CT93-0194).

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