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Proposal of the genera *Anaerococcus* gen. nov., *Peptoniphilus* gen. nov. and *Gallicola* gen. nov. for members of the genus *Peptostreptococcus*

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Members of genus *Peptostreptococcus* have previously been found to be distantly related to the type species, *Peptostreptococcus anaerobius*, on the basis of 16S rDNA sequence similarities. They were divided into three major phylogenetic groups, and their peptidoglycan structure and biochemical traits differed between groups. The reclassification of the species of these three groups into three new genera, *Peptoniphilus* gen. nov., *Anaerococcus* gen. nov. and *Gallicola* gen. nov., is proposed. The genus *Peptoniphilus* gen. nov. includes the following butyrate-producing, non-saccharolytic species that use peptone and amino acids as major energy sources: *Peptoniphilus asaccharolyticus* comb. nov. (type species), *Peptoniphilus lacrimaris* comb. nov., *Peptoniphilus harei* comb. nov., *Peptoniphilus indolicus* comb. nov. and *Peptoniphilus ivorii* comb. nov. The genus *Anaerococcus* gen. nov. contains the saccharolytic, butyrate-producing species *Anaerococcus prevotii* comb. nov. (type species), *Anaerococcus tetradius* comb. nov., *Anaerococcus lactolyticus* comb. nov., *Anaerococcus hydrogenalis* comb. nov., *Anaerococcus vaginalis* comb. nov. and *Anaerococcus octavius* sp. nov. The genus *Gallicola* gen. nov. contains a single species, *Gallicola barnesae* comb. nov.

Keywords: *Peptostreptococcus*, taxonomy, *Anaerococcus*, *Peptoniphilus*, *Gallicola*

INTRODUCTION

In a previous study, we determined the 16S rDNA sequences of all members of the genus *Peptostreptococcus* and reported that the members of genus were divided into five phylogenetic groups (Li *et al*., 1994). This observation was later confirmed by Collins *et al*. (1994). These authors examined a large number of clostridial 16S rRNA sequences and reported that the genus *Clostridium* contained phylogenetically distinct species. They proposed that these organisms be classified into 19 phylogenetic groups. The peptostreptococci were scattered over different groups of the clostridia. In particular, no other member of the genus *Peptostreptococcus* clustered together with the type species, *Peptostreptococcus anaerobius*. The phylogenetic groups of peptostreptococci correlated well with groups based on peptidoglycan structure. Biochemical tests and peptidoglycan structure could differentiate each of the groups. The new genera *Micromonas* and *Finegoldia* were proposed for the species of one group (Murdoch & Shah, 1999). In this study, we propose three new genera for the members of the remaining three groups.

Abbreviation: PYG, peptone/yeast extract/glucose.

The GenBank/EMBL/DDBJ accession numbers for the 16S rDNA sequences determined in this study are D14145, D14152, D14153 and AB038359–AB038361.

METHODS

Bacterial strains and 16S rDNA sequences. The strains and 16S rDNA accession numbers of the peptostreptococci and reference species used in this study are listed in Table 1.

Analysis of sequence data. About 1440 bp spanning positions 50–1490 of 16S rDNA sequences were used for multiple alignment. rDNA sequences were aligned by using CLUSTAL W (Thompson *et al*., 1994). Phylogenetic distances were calculated by the neighbour-joining method (Saitou & Nei, 1986) with and without gaps. Bootstrap analysis was performed 1000 times and the results are indicated in Fig. 1.

Table 1. Organisms used in this study

Accession numbers in bold indicate sequences determined in this study.

Strain	16S rDNA sequence accession no.
Clostridium coccoides DSM 2088^T	M59057
Clostridium difficile DSM 11209	X73450
Clostridium ghonii DSM 10636^T	X73451
Clostridium oroticum ATCC 13619^T	M59109
Clostridium perfringens ATCC 13124^T	M59103
Clostridium sordellii ATCC 9714^T	M59105
Coprococcus catus VPI C6-61^T	**AB038359**
Coprococcus eutactus ATCC 27759^T	D14148
Eubacterium cellulosolvens ATCC 43171^{NT}	L34613
Finegoldia magna ATCC 15794^T	D14149
Micromonas micros GIFU 7701	D14143
Peptococcus niger ATCC 27731^T	X55797
Peptostreptococcus anaerobius ATCC 27337^T	L04168
Peptostreptococcus asaccharolyticus ATCC 14963^T	D14138
Peptostreptococcus barnesae DSM 3244^T	**AB038361**
Peptostreptococcus harei DSM 10020^T	Y07839
Peptostreptococcus hydrogenalis GIFU 7662^T	D14140
Peptostreptococcus indolicus ATCC 29427^T	D14147
Peptostreptococcus ivorii DSM 10022^T	Y07840
Peptostreptococcus lacrimalis GIFU 7667^T	D14141
Peptostreptococcus lactolyticus GIFU 8586^T	D14154
Peptostreptococcus octavius NCTC 9810^T	Y07841
Peptostreptococcus prevotii ATCC 9321^T	D14139
Peptostreptococcus tetradius GIFU 7672^T	D14142
Peptostreptococcus vaginalis GIFU 12669^T	D14146
Peptostreptococcus genospecies 1 GIFU 7717	**D14145**
Peptostreptococcus genospecies 2 GIFU 7946	**D14152**
Peptostreptococcus genospecies 3 GIFU 8124	**D14153**
Peptostreptococcus genospecies 4 GIFU 7729	**AB038360**
Ruminococcus albus ATCC 27210^T	X85098
Ruminococcus bromii ATCC 27255^T	X85099
Ruminococcus callidus VPI 57-31^T	X85100
Ruminococcus flavefaciens NCFB 2213^T	X83430
Ruminococcus gnavus ATCC 29149^T	D14136
Ruminococcus hansenii ATCC 27752^T	D14155
Ruminococcus lactaris ATCC 29176^T	L76602
Ruminococcus obeum ATCC 29174^T	X85101
Ruminococcus productus ATCC 27340^T	D14144
Ruminococcus torques ATCC 27756^T	L76604
Sarcina maxima DSM 316^T	X76650
Sarcina ventriculi GIFU 7886^T	D14151

Other methods. Peptidoglycan structure and biochemical traits were determined by methods described before (Li *et al*., 1992).

RESULTS AND DISCUSSION

Peptostreptococcus anaerobius, the type species of the genus *Peptostreptococcus*, clustered with *Clostridium sordellii* and *Clostridium difficile* in Fig. 1 in a phylogenetic analysis based on 16S rDNA sequences. The other current members of the genus *Peptostreptococcus* were grouped in three different groups. These results were consistent when phylogenetic distances were calculated with and without gaps. Therefore, only the result with gaps is shown in Fig. 1. The species in group 1 were non-saccharolytic and had ornithine as the diamino acid in their peptidoglycan. Their rRNA sequence similarities ranged from 90 to 100 %. The species of group 2 were saccharolytic organisms and the diamino acid in their peptidoglycan was lysine. Their rRNA sequence similarities ranged from 87·42 to 100 %. Group 3 organisms were butyrate-negative and

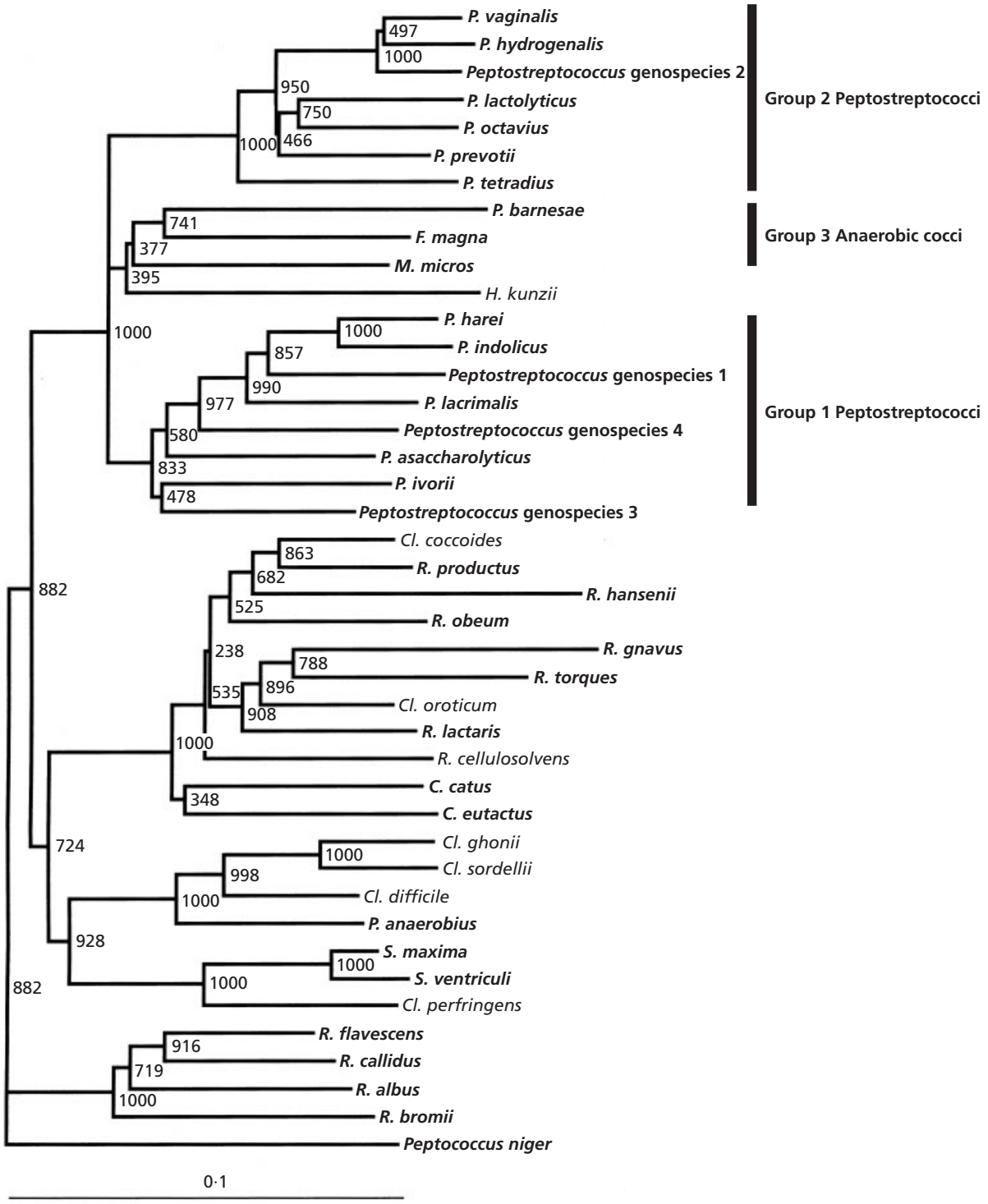

Fig. 1. Phylogenetic tree of anaerobic cocci based on 16S rDNA sequences. Bold type indicates obligately anaerobic cocci. Genera are abbreviated as: *P.*, *Peptostreptococcus*; *F.*, *Finegoldia*; *M.*, *Micromonas*; *H.*, *Helcococcus*; *Cl.*, *Clostridium*; *S.*, *Sarcina*; *C.*, *Coprococcus*; *R.*, *Ruminococcus*; *E.*, *Eubacterium*.

their peptidoglycan structures were variable. Their rRNA sequence similarities ranged from 87·67 to 100%. Two species of group 3 were recently reclassified in new monospecific genera as *Finegoldia magna* and *Micromonas micros* (Murdoch & Shah, 1999, 2000), although the genus name *Micromonas* is illegitimate under Rule 51b(4) of the Bacteriological Code because it is already the name of a genus of fungi

Table 2. Characteristics that differentiate members of the three new genera from other strictly anaerobic, Gram-positive cocci

Taxa are identified as: 1, *Anaerococcus prevotii* (type species); 2, *Anaerococcus tetradius*; 3, *Anaerococcus lactolyticus*; 4, *Anaerococcus hydrogenalis*; 5, *Anaerococcus octavius*; 6, *Anaerococcus vaginalis*; 7, *Peptoniphilus asaccharolyticus* (type species); 8, *Peptoniphilus lacrimalis*; 9, *Peptoniphilus harei*; 10, *Peptoniphilus ivorii*; 11, *Peptoniphilus indolicus*; 12, *Gallicola barnesae* (type species); 13, *Finegoldia magna* (type species); 14, *Micromonas micros* (type species); 15, *Peptostreptococcus anaerobius* (type species); 16, *Peptococcus niger* (type species); 17, *Ruminococcus flavefaciens* (type species); 18, *Coprococcus eutactus* (type species); 19, *Sarcina ventriculi* (type species); 20, *Sarcina maxima*. All taxa stain Gram-positive. Abbreviations: Dap, diaminopimelic acid; Orn, ornithine.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
DNA G+C content (mol%)*	29–33	30–32	30–34	30–34	26–31	30–34	31–32	30–34	25	29	32–35	32–34	32–34	28–30	34–36	50–51	39–45	39–42	28–31	28–31
Peptidoglycan†	Lys, D-Glu	Lys, D-Glu	Lys, D-Glu	Lys, D-Glu	Lys, D-Asp	Lys, D-Glu	Orn, D-Glu	Orn, D-Glu	Orn, D-Glu	Orn, D-Glu	Orn, D-Glu	Orn, D-Asp	Lys, Gly	Lys, D-Asp	Lys, D-Asp	Lys, D-Asp	mDap, none	mDap, none	LLDap, Gly	LLDap, Gly
Production of:																				
Butyrate	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	−	+	−	+
Caproate	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−
Peptone as major energy source	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−
Sugar fermented	+	+	+	+	+	+	−	−	−	−	−	−	−	−	+	−	+	+	+	+
Sugar required for growth	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	+	+

* Values in columns 16–20 are ranges for the particular genera.

† Position 3 (diamino acid) and the interpeptide bridge are listed.

(see http://www.bacterio.cict.fr/m/micromonas.html). *Peptostreptococcus barnesae* remained in the genus *Peptostreptococcus*.

The obligately anaerobic, Gram-positive cocci were once classified in the family *Peptococcaceae* Kluyver and van Niel 1936 (Rogosa, 1974). This family included the genera *Ruminococcus*, *Coprococcus*, *Sarcina*, *Peptococcus* and *Peptostreptococcus*. Most members of these genera were found in the phylum *Firmicutes*. *Sarcina ventriculi* has 95% sequence similarity to *Clostridium perfringens* and is related to clostridial group I (Li *et al*., 1994; Collins *et al*., 1994). *Peptostreptococcus anaerobius* was related to *Clostridium sordellii* of clostridial group XI (Collins *et al*., 1994). The ruminococci were separated into two major different phyla (Rainey & Janssen, 1995) and the coprococci were also related to clostridial group XVI. Thus, all of the type species of the members of the family *Peptococcaceae* were reclassified into different clostridial groups. This means that the family *Peptococcaceae* is no longer a legitimate classification.

The members of the genus *Peptostreptococcus* were also scattered into different clostridial groups. *Peptostreptococcus anaerobius*, the type species of the genus, was related to group XI of the clostridia. This group also contains *Clostridium difficile* and *Clostridium sordellii*. The other peptostreptococci were clustered into three different groups. No published clostridial species were clustered within each of these groups. As indicated in Table 2, the cell wall structures of these organisms support this grouping, with the exception of group 3.

Members of group 1 use peptone as a major energy source and produce butyrate as their metabolic end-product. They are non-saccharolytic organisms. We propose a new genus, *Peptoniphilus* gen. nov., to contain *Peptostreptococcus asaccharolyticus*, *Peptostreptococcus indolicus*, *Peptostreptococcus lacrimalis*, *Peptostreptococcus harei* and *Peptostreptococcus ivorii*.

The group 2 organisms are saccharolytic and produce butyrate as a major metabolic end-product. We propose a new genus, *Anaerococcus* gen. nov., for the group 2 organisms *Peptostreptococcus prevotii*, *Peptostreptococcus hydrogenalis*, *Peptostreptococcus vaginalis*, *Peptostreptococcus lactolyticus*, *Peptostreptococcus tetradius* and *Peptostreptococcus octavius*.

Group 3 contained *Peptostreptococcus barnesae* and two newly reclassified species (Murdoch & Shah, 1999). *Finegoldia magna* and *Micromonas micros* were previously members of the genus *Peptostreptococcus*; they were validly reclassified in new monospecific genera (Murdoch & Shah, 2000), but *Peptostreptococcus barnesae* was left in the genus *Peptostreptococcus*. We propose to reclassify *Peptostreptococcus barnesae* as the type species of a new genus, *Gallicola* gen. nov., as *Gallicola barnesae* comb. nov.

Description of *Peptoniphilus* gen. nov.

Peptoniphilus (Pep.to.ni.phil′us. N.L. neut. n. *peptonum* peptone; Gr. adj. *philos* liking, friendly to; N.L. masc. n. *Peptoniphilus* friend of peptone, referring to the use of peptone as a major energy source).

Table 3. Biochemical differentiation of reclassified *Peptostreptococcus* species

Taxa are identified as: 1, *Anaerococcus prevotii* (type species); 2, *Anaerococcus tetradius*; 3, *Anaerococcus lactolyticus*; 4, *Anaerococcus hydrogenalis*; 5, *Anaerococcus octavius*; 6, *Anaerococcus vaginalis*; 7, *Peptoniphilus asaccharolyticus* (type species); 8, *Peptoniphilus lacrimalis*; 9, *Peptoniphilus harei*; 10, *Peptoniphilus ivorii*; 11, *Peptoniphilus indolicus*; 12, *Gallicola barnesae* (type species); 13, *Finegoldia magna* (type species); 14, *Micromonas micros* (type species); 15, *Peptostreptococcus anaerobius* (type species); 16, *Peptococcus niger* (type species). Characteristics are scored as: +, positive; −, negative; D, strain-dependent; W, weak.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Major terminal volatile fatty acid*	B	B	B	B	B, C	B	B	B	B	B	B	A, B	A	A	IC, IV	C
Production of:																
Indole	−	−	−	+	−	D	D	−	D	−	+	W	−	−	−	−
Urease	D	+	+	D	−	−	−	−	−	−	−	−	−	−	−	−
Alkaline phosphatase	−	−	−	D	−	D	−	−	−	−	+	−	D	+	−	−
Coagulase	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
Fermentation of:																
Glucose	D	D	+	+	+	+	−	−	−	−	−	−	−	−	+	−
Lactose	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−
Raffinose	+	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−
Mannose	+	+	+	+	+	D	−	−	−	−	−	−	−	−	+	−
Activity of:																
α-Galactosidase	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
β-Galactosidase	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−
α-Glucosidase	+	+	−	D	−	−	−	−	−	−	−	−	−	−	W	−
β-Glucosidase	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−
Arginine arylamidase	+	+	+	−	−	+	+	+	+	−	+	−	+	+	−	−
Proline arylamidase	−	−	−	−	+	−	−	−	−	+	−	−	−	+	+	−
Phenylalanine arylamidase	−	W	−	−	−	−	−	+	−	−	+	−	−	−	−	−
Leucine arylamidase	−	+	−	−	−	+	D	+	D	−	+	−	+	+	−	−
Pyroglutamyl arylamidase	+	W	−	−	W	−	−	−	−	−	−	−	+	+	−	−
Histidine arylamidase	+	W	−	−	−	+	W	+	+	−	+	−	D	+	−	−

* B, Butyrate; C, caproate; IC, isocaproate; IV, isovalerate; A, acetate.

Non-spore-forming, Gram-positive, obligately anaerobic cocci. Cells may occur in pairs, short chains, tetrads or small clusters. Non-motile. The major cellular fatty acid is C18:1 (Ezaki *et al.*, 1983). Carbohydrates are not fermented. The major metabolic end-product from peptone/yeast extract/glucose (PYG) medium is butyric acid. The cell wall diamino acid is ornithine and the interpeptide bridge is D-glutamic acid. The G+C content of DNA of members of this genus is 30–34 mol% (Ezaki *et al.*, 1983). Characteristics that differentiate this genus from other genera are given in Table 2. The type species is *Peptoniphilus asaccharolyticus*.

Description of *Peptoniphilus asaccharolyticus* comb. nov.

Basonym: *Peptostreptococcus asaccharolyticus* (Distaso 1912) Ezaki *et al.* 1983.

Often isolated from various human clinical specimens such as vaginal discharges and ovarian and peritoneal abscesses. Most strains produce indole. Negative for urease, alkaline phosphatase, arginine dihydrolase and coagulase. Does not produce acid from carbohydrates. Major metabolic end-product from PYG is butyric acid. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Characteristics that differentiate this species from other members of the genus are given in Tables 2 and 3. The DNA G+C content is 31–32 mol%. The type strain is ATCC 14963^T.

Description of *Peptoniphilus indolicus* comb. nov.

Basonym: *Peptostreptococcus indolicus* (Christiansen 1934) Ezaki *et al.* 1983.

Isolated from summer mastitis of cattle. Most strains are coagulase-, alkaline phosphatase- and indole-positive. Negative for urease and arginine dihydrolase. No sugars are fermented. Major metabolic end-product from PYG is butyric acid. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Biochemical traits that differentiate this species from other species are given in Tables 2 and 3. The DNA G+C content is 32–34 mol%. The type strain is ATCC 29427^T.

Description of *Peptoniphilus lacrimalis* comb. nov.

Basonym: *Peptostreptococcus lacrimalis* Li *et al.* 1992.

Isolated from a human lachrymal gland abscess. Negative for indole, urease, arginine dihydrolase, alkaline phosphatase and coagulase. Carbohydrates are not fermented. Major metabolic end-product from PYG is butyric acid. Production of major saccharolytic and proteolytic enzymes is described by Murdoch (1998). A full description is given by Li *et al.* (1992). Differential characteristics are given in Tables 2 and 3. The DNA G+C content is 30–34 mol%. The type strain is GIFU 7667^T (= JCM 8139^T).

Description of *Peptoniphilus harei* comb. nov.

Basonym: *Peptostreptococcus harei* Murdoch *et al.* 1997.

The type strain was isolated from pus of a human sacral ulcer. Some strains produce indole. Negative for urease, arginine dihydrolase, alkaline phosphatase and coagulase. Carbohydrates are not fermented. Major metabolic end-product from PYG is butyric acid. Production of major saccharolytic and proteolytic enzymes is described by Murdoch (1998). Differential characteristics are given in Tables 2 and 3. The DNA G+C content is 25 mol%. The type strain is DSM 10020^T.

Description of *Peptoniphilus ivorii* comb. nov.

Basonym: *Peptostreptococcus ivorii* Murdoch *et al.* 1997.

The type strain was isolated from a human leg ulcer. Negative for urease, arginine dihydrolase, alkaline phosphatase and coagulase. Carbohydrates are not fermented. Major metabolic end-product from PYG is butyric acid. Production of major saccharolytic and proteolytic enzymes is described by Murdoch (1998). Differential characteristics are given in Tables 2 and 3. The DNA G+C content is 29 mol%. The type strain is DSM 10022^T.

Description of *Anaerococcus* gen. nov.

Anaerococcus (An.ae.ro.coc′cus. Gr. prep. *an* without; Gr. n. *aer* air; L. masc. n. *coccus* berry, coccus; N.L. masc. n. *Anaerococcus* anaerobic coccus).

Strictly anaerobic, Gram-positive, non-motile cocci. Cells are found in pairs, tetrads, irregular masses or chains. Metabolize peptones and amino acids and the major metabolic end-products from PYG medium are butyric acid, lactic acid and small amounts of propionic and succinic acids. Most species are able to ferment several carbohydrates, but most are weakly fermentative. Glucose, fructose, sucrose and lactose are major fermentative sugars. Most species do not produce indole. The diamino acid of the cell wall is L-lysine. The interpeptide bridge is D-glutamic acid, except in the case of *Aerococcus octavius*. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Characteristics that differentiate members from other genera are given in Table 2. Members of the genus are typically isolated from the human vagina and various purulent secretions. The G+C content of the DNA is 25–33 mol% (T_m). The type species is *Anaerococcus prevotii*.

Description of *Anaerococcus prevotii* comb. nov.

Basonym: *Peptostreptococcus prevotii* (Foubert and Douglas 1948) Ezaki *et al.* 1983.

Often isolated from human clinical specimens such as vaginal discharges and ovarian, peritoneal and sacral abscesses. Negative for indole, alkaline phosphatase and coagulase. Some strains produce urease. Most strains ferment glucose and mannose. Acid is also produced from raffinose, ribose and mannose. No acid produced from lactose, cellobiose, maltose, sucrose or xylose. Major metabolic end-product from PYG is butyric acid. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The G+C content of the DNA is 29–33 mol%. The type strain is ATCC 9321^T.

Description of *Anaerococcus tetradius* comb. nov.

Basonym: *Peptostreptococcus tetradius* (*ex* Choukévitch 1911) Ezaki *et al.* 1983.

Isolated from vaginal discharges and ovarian abscesses. Urease-positive. Negative for indole, alkaline phosphatase, arginine dihydrolase and coagulase. Glucose and mannose are fermented. Acid is not produced from lactose, raffinose, ribose, cellulose, maltose, sucrose or xylose. Major metabolic end-product from PYG is butyric acid. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The DNA G+C content is 30–32 mol%. The type strain is GIFU 7672^T (= JCM 1964^T).

Description of *Anaerococcus hydrogenalis* comb. nov.

Basonym: *Peptostreptococcus hydrogenalis* Ezaki *et al.* 1990.

Organism is isolated from vaginal discharges and ovarian abscesses. Produces abundant hydrogen gas from PYG. Indole-positive. Some strains produce urease and alkaline phosphatase. Acid is produced from glucose, lactose, raffinose and mannose. Negative for arginine dihydrolase and coagulase. Major metabolic end-product from PYG is butyric acid. A full description is given by Ezaki *et al.* (1990). Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The DNA G+C content is 30–34 mol%. The type strain is GIFU 7662^T (= JCM 7635^T).

Description of *Anaerococcus vaginalis* comb. nov.

Basonym: *Peptostreptococcus vaginalis* Li *et al.* 1992.

Isolated from vaginal discharges and ovarian abscesses. Produces arginine dihydrolase. Some strains are positive for indole and alkaline phosphatase. Coagulase and urease are negative. Major metabolic end-product from PYG is butyric acid. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. A full description is given by Li *et al.* (1992). The DNA G+C content is 30–34 mol%. The type strain is GIFU 12669^T (= JCM 8138^T).

Description of *Anaerococcus lactolyticus* comb. nov.

Basonym: *Peptostreptococcus lactolyticus* Li *et al.* 1992.

Isolated from vaginal discharges and ovarian abscesses. Urease-positive. Negative for indole, alkaline phosphatase, arginine dihydrolase and coagulase. Acid from glucose, lactose and mannose. Raffinose and ribose are not fermented. Major metabolic end-product from PYG is butyric acid. A full description is given by Li *et al.* (1992). Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The DNA G+C content is 30–34 mol%. The type strain is GIFU 8586^T (= JCM 8140^T).

Description of *Anaerococcus octavius* comb. nov.

Basonym: *Peptostreptococcus octavius* Murdoch *et al.* 1997.

The type strain was isolated from a human nasal cavity. Often isolated from skin, vagina and nasal cavity. Indole, urease, alkaline phosphatase, arginine dihydrolase and coagulase are negative. Glucose, ribose and mannose are fermented. Lactose and raffinose are not fermented. Major metabolic end-products from PYG are butyric acid and caproic acid. A full description is given by Murdoch *et al.* (1997). The cell wall diamino acid is lysine and the interpeptide bridge contains D-aspartic acid; this peptidoglycan structure is different from other members of the genus *Anaerococcus*. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The DNA G+C content is 26–31 mol%. The type strain is NCTC 9810^T.

Description of *Gallicola* gen. nov.

Gallicola (Gal.li′co.la. L. n. *gallus* rooster/chicken; L. masc. suffix *-cola* inhabitant.; N.L. masc. n. *Gallicola* inhabitant of chickens, referring to the isolation of the type species from chicken faeces).

Obligately anaerobic, Gram-positive, non-motile cocci that occur singly and in pairs. Carbohydrates are not fermented. Indole is negative. Peptidoglycan diamino acid is ornithine and the interpeptide bridge is D-aspartic acid. The metabolic end-products from PYG medium are acetic and lactic acids. The G+C content of the DNA is 27–34 mol% (T_m) (Ezaki *et al.*, 1983; Schiefer-Ullrich & Andreesen, 1985). The type and only species is *Gallicola barnesae*.

Description of *Gallicola barnesae* comb. nov.

Basonym: *Peptostreptococcus barnesae* Schiefer-Ullrich and Andreesen 1986.

Isolated from chicken faeces. Negative for the production of indole, urease, alkaline phosphatase, arginine dihydrolase and coagulase. A full description is given by Schiefer-Ullrich & Andreesen (1985). Glucose, lactose, raffinose, ribose and mannose are not fermented. The metabolic end-products from PYG medium are acetic and butyric acids. Descriptions of major saccharolytic and proteolytic enzymes are given by Murdoch (1998). Differential characteristics from other members of the genus are given in Table 3. The G+C content of the DNA is 32–34 mol%. The type strain is DSM 3244^T.

Emended description of *Peptostreptococcus* Kluyver and van Niel 1936

Obligately anaerobic, Gram-positive, non-motile cocci and coccobacilli. Cells are usually arranged in chains. Cell wall diamino acid is L-lysine and the interpeptide bridge is D-aspartate. The G+C content of the DNA is 33–34 mol% (T_m). Weakly saccharolytic. Negative for indole, urease, alkaline phosphatase, arginine dihydrolase and coagulase. Most strains produce acid from glucose. Some strains produce acid from mannose, maltose or sucrose. The metabolic end-products from PYG medium are acetic, butyric, isobutyric, isovaleric and isocaproic acids. Nitrate is not reduced to nitrite. Aesculin is not hydrolysed. The type species is *Peptostreptococcus anaerobius*, the only remaining member of the genus. *Peptostreptococcus anaerobius* is classified phylogenetically in clostridial group XI. The type strain of *Peptostreptococcus anaerobius* is NCTC 11460^T.

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