Reclassification of *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae* as *Parabacteroides distasonis* gen. nov., comb. nov., *Parabacteroides goldsteinii* comb. nov. and *Parabacteroides merdae* comb. nov.

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The characteristics of three *Bacteroides* species, *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae*, were examined. 16S rRNA gene sequence analysis showed that *B. distasonis*, *B. goldsteinii* and *B. merdae* should not be classified as species within the genus *Bacteroides*. Although *B. distasonis*, *B. goldsteinii* and *B. merdae* were phylogenetically related to *Tannerella forsythensis*, the ratios of anteiso-$C_{15:0}$ to iso-$C_{15:0}$ in whole-cell methanolysates of the three species were different from that of *T. forsythensis*. In addition, whereas the major menaquinones of *T. forsythensis* were MK-10 and MK-11, the major menaquinones of *B. distasonis*, *B. goldsteinii* and *B. merdae* were MK-9 and MK-10. The three species were phenotypically similar to *Bacteroides sensu stricto*, but phylogenetically distinct. Furthermore, *B. distasonis*, *B. goldsteinii* and *B. merdae* could be differentiated from *Bacteroides sensu stricto* (predominant menaquinones: MK-10 and MK-11) by the menaquinone composition. This is an important chemotaxonomic characteristic of the three species. On the basis of these data, a novel genus, *Parabacteroides* gen. nov., is proposed for *B. distasonis*, *B. goldsteinii* and *B. merdae*, with three species, *Parabacteroides distasonis* gen. nov., comb. nov. (the type species), *Parabacteroides goldsteinii* comb. nov. and *Parabacteroides merdae* comb. nov. The type strains of *P. distasonis*, *P. goldsteinii* and *P. merdae* are JCM 5825^T (=CCUG 4941^T=DSM 20701^T=ATCC 8503^T), JCM 13446^T (=CCUG 48944^T) and JCM 9497^T (=CCUG 38734^T=ATCC 43184^T), respectively.

Cells of *Bacteroides* species are obligately anaerobic, non-spore-forming, non-motile, Gram-negative rods. In the past, because of poor definition of the genus, more than 50 species of *Bacteroides* were included in *Bergey's Manual of Systematic Bacteriology* (Holdeman *et al.*, 1984) and the Approved Lists of Bacterial Names (Moore *et al.*, 1985). Later, Shah & Collins (1989) formally proposed that the genus *Bacteroides* should be restricted to *Bacteroides fragilis* and related taxa and the description of the genus was emended accordingly. Consequently, several novel genera, such as *Alistipes* (Rautio *et al.*, 2003), *Dialister* (Moore & Moore, 1994), *Dichelobacter* (Dewhirst *et al.*, 1990) and *Tannerella* (Sakamoto *et al.*, 2002), have been proposed for 'outmembers' of the genus *Bacteroides*. However, the taxonomic status of *Bacteroides distasonis* and *Bacteroides merdae* is still uncertain. 16S rRNA gene sequence analysis (Paster *et al.*, 1994; Sakamoto *et al.*, 2002) led to the suggestion that *B. distasonis* and *B. merdae* were not species within the genus *Bacteroides*. *B. distasonis* and *B. merdae* were related to members of the first subcluster of the *Porphyromonas* cluster, with a mean 16S rRNA gene sequence similarity of about 84 %. In addition, the two species were related to *Tannerella forsythensis* (Sakamoto *et al.*, 2002) with about 90 % similarity. More recently, Song *et al.* (2005) proposed a novel species of the genus *Bacteroides*, *Bacteroides goldsteinii*. This species was related to *B. distasonis* and *B. merdae*, with a mean 16S rRNA gene sequence similarity of

Abbreviations: G6PDH, glucose-6-phosphate dehydrogenase; 6PGDH, 6-phosphogluconate dehydrogenase; ITS, internal transcribed spacer.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of *P. distasonis* strains JCM 5825^T, JCM 13400, JCM 13401, JCM 13402, JCM 13403 and JCM 13404 and *P. merdae* strains JCM 9497^T and JCM 13405 are AB238922–AB238929, respectively.

The cellular fatty acid content and biochemical characteristics of *Parabacteroides distasonis* gen. nov., comb. nov. and *Parabacteroides merdae* comb. nov. and a phylogenetic tree based on sequences of 16S–23S rRNA gene ITS regions are available as supplementary material in IJSEM Online.

about 93 %. Furthermore, *B. goldsteinii* was related to *T. forsythensis*, with about 90 % similarity. *B. goldsteinii* was classified as a novel *Bacteroides* species as, using current phenotypic tests, the bacterium could not be separated from *Bacteroides sensu stricto*. In this study, we attempted to determine the taxonomic status of *B. distasonis*, *B. goldsteinii* and *B. merdae*. Based on the results presented, a novel genus is proposed to accommodate *B. distasonis*, *B. goldsteinii* and *B. merdae*.

The strains used in this study were maintained on Eggerth Gagnon (EG) agar (Merck), supplemented with 5 % (v/v) horse blood, for 2 days at 37 °C in an atmosphere of 100 % CO_2. Strains JCM 13400, JCM 13401, JCM 13402, JCM 13403, JCM 13404 and JCM 13405 were isolated from human faeces. Bacteroides bile aesculin agar (Shah, 1992) was used to check whether the growth of the isolates was inhibited on this medium. A multiplex-PCR technique using species-specific primers (Liu *et al.*, 2003) was used to identify *B. distasonis* and *B. merdae*. Physiological reactions were determined in duplicate with an API 20A anaerobe test kit, as recommended by the manufacturer (bioMérieux). Fatty acid methyl esters (FAMEs) were obtained from about 40 mg wet cells by saponification, methylation and extraction, using minor modifications (Kuykendall *et al.*, 1988) of the method of Miller (1982). Cellular fatty acid profiles were determined by using the MIDI microbial identification system (Microbial ID). Isoprenoid quinones were extracted as described by Komagata & Suzuki (1987) and were analysed as described previously (Sakamoto *et al.*, 2002). Biochemical reactions were determined in duplicate with a Rapid ID 32A anaerobe identification kit, as recommended by the manufacturer (bioMérieux). The 16S rRNA gene was analysed as described previously (Sakamoto *et al.*, 2002). Related sequences were aligned using the CLUSTAL W program (Thompson *et al.*, 1994) and corrected by manual inspection. Nucleotide substitution rates (K_{nuc} values) were calculated (Kimura, 1980) after gaps and unknown bases had been eliminated. A phylogenetic tree was constructed by using the neighbour-joining method (Saitou & Nei, 1987). Bootstrap resampling analysis (Felsenstein, 1985) was performed to estimate the confidence of tree topologies.

Cells of strains JCM 13400–13405 were obligately anaerobic, non-spore-forming, non-motile, Gram-negative rods. Strains JCM 13400–13404 were identified as representing *B. distasonis* by using a multiplex-PCR assay; likewise, strain JCM 13405 was identified as representing *B. merdae*. The growth of these six clinical isolates and *B. distasonis* JCM 5825^T, *B. goldsteinii* JCM 13446^T and *B. merdae* JCM 9497^T was not inhibited on medium containing 20 % bile. Cells on EG agar were 0·8–1·6 × 1·2–12 μm in size and occurred singly. Colonies on EG agar plates were 1–2 mm in diameter, grey to off-white–grey, circular, entire, slightly convex and smooth. Phenotypic characteristics are given in the species descriptions.

The cellular fatty acid composition of *Bacteroides* species has been determined (Mayberry *et al.*, 1982; Miyagawa *et al.*, 1979; Shah & Collins, 1980) and reviewed for the classification of the genus *Bacteroides* (Shah & Collins, 1983). In this study, the cellular fatty acid compositions of the clinical isolates and *B. distasonis* JCM 5825^T and *B. merdae* JCM 9497^T were almost the same. The major cellular fatty acids of the above strains were anteiso-$C_{15:0}$ and iso 3-OH-$C_{17:0}$ (25–32 and 23–26 %, respectively). A significant amount of $C_{18:1}\omega9c$ (14–16 %) was also present (Supplementary Table S1 in IJSEM Online). These findings are in agreement with that reported for *B. goldsteinii*, except for anteiso 3-OH-$C_{17:0}$ (Song *et al.*, 2005). Song *et al.* (2005) reported that the ratio iso 3-OH-$C_{17:0}$/anteiso 3-OH-$C_{17:0}$ in whole-cell methanolysates of *B. goldsteinii* was lower than that for *B. merdae* (ratio ranging from 1·4 to 2·2 for *B. goldsteinii* and 6·1 to 8·3 for *B. merdae*). In this study, the ratio iso 3-OH-$C_{17:0}$/anteiso 3-OH-$C_{17:0}$ in whole-cell methanolysates of *B. distasonis* and *B. merdae* was 5·7–9·4 and 5·2–7·6, respectively.

The major menaquinones of the clinical isolates and *B. distasonis* JCM 5825^T, *B. goldsteinii* JCM 13446^T and *B. merdae* JCM 9497^T were MK-9 and MK-10 (Table 1). The menaquinone compositions of *B. distasonis* JCM 5825^T and *B. goldsteinii* JCM 13446^T were almost the same. On the other hand, the major menaquinones of other *Bacteroides* species were MK-10 and MK-11, except for *Bacteroides vulgatus* JCM 5826^T, which contained a small amount of MK-11 (Sakamoto *et al.*, 2002).

API ZYM and API An-Ident have been reported to be useful in the identification of oral and non-oral Gram-negative bacteria (Laughon *et al.*, 1982; Slots, 1981; Tanner *et al.*, 1985). In addition, the RapID-ANA system (Innovative Diagnostics Systems) has been reported to be helpful in the identification of some phenotypically similar bile-inhibited *Bacteroides* species (Dellinger & Moore, 1986). The biochemical characteristics of the clinical isolates and *B. distasonis* JCM 5825^T and *B. merdae* JCM 9497^T are available in Supplementary Table S2 in IJSEM Online. In this study, all strains were tested using Rapid ID 32A. The biochemical characteristics of strains JCM 13400–13404 were similar to those of *B. distasonis* JCM 5825^T. Furthermore, the biochemical characteristics of strain JCM 13405 and *B. merdae* JCM 9497^T resembled each other.

Approximately 1500 bases of the 16S rRNA gene sequence were determined for the clinical isolates and *B. distasonis* JCM 5825^T and *B. merdae* JCM 9497^T. Strains JCM 13400–13404 were closely related to *B. distasonis* JCM 5825^T, with about 99 % similarity (>98·7 %). In addition, strain JCM 13405 was closely related to *B. merdae* JCM 9497^T, with 99·9 % similarity. For the phylogenetic analysis, 1340 bp (positions 61–1375; *Escherichia coli* numbering system) sequences of each strain were used. 16S rRNA gene sequence analysis showed that *B. distasonis* JCM 5825^T, *B. goldsteinii* JCM 13446^T and *B. merdae* JCM 9497^T were not species within the genus *Bacteroides* (Fig. 1). These three species were phylogenetically closely related to each other (>92·3 %) and were related to *T. forsythensis* with about

Table 1. Menaquinone composition of *Parabacteroides* gen. nov. and related taxa

Values are percentages of total menaquinones. tr, Trace amount (<1 %).

Strain	MK-7	MK-8	MK-9	MK-10	MK-11	MK-12
Parabacteroides distasonis JCM 5825^T	tr	4	24	67	4	
Parabacteroides distasonis JCM 13400	1	7	42	47	1	
Parabacteroides distasonis JCM 13401	1	8	44	45	1	
Parabacteroides distasonis JCM 13402	1	7	41	49	1	
Parabacteroides distasonis JCM 13403	1	7	41	49	1	
Parabacteroides distasonis JCM 13404	1	7	41	49	1	
Parabacteroides goldsteinii JCM 13446^T	tr	3	24	67	4	
Parabacteroides merdae JCM 9497^T	2	5	52	37	tr	
Parabacteroides merdae JCM 13405	2	6	50	40	tr	
Bacteroides acidifaciens JCM 10556^T				47	50	
Bacteroides caccae JCM 9498^T				48	51	
Bacteroides ovatus JCM 5824^T				49	43	
Bacteroides stercoris JCM 9496^T			2	66	29	
Bacteroides thetaiotaomicron JCM 5827^T				49	48	
Bacteroides uniformis JCM 5828^T				48	49	
Bacteroides vulgatus JCM 5826^T			6	80	7	
Tannerella forsythensis JCM 10827^T			13	48	33	6

90 % similarity. Other remotely related taxa included the genera *Bacteroides* (83·5–88·8 % sequence similarity), *Dysgonomonas* (85·9–89·4 %), *Paludibacter* (86·9–88·5 %; Ueki *et al.*, 2006), *Porphyromonas* (82·2–86·9 %), *Prevotella* (77·2–81·9 %) and *Proteiniphilum* (85·9–87·3 %; Chen & Dong, 2005). In addition, a preliminary analysis of the 16S–23S rRNA gene internal transcribed spacer (ITS) regions also showed that *B. distasonis* and *B. merdae* were phylogenetically distinct from species of the genus *Bacteroides* and were related to *T. forsythensis* (Supplementary Fig. S1 in IJSEM Online). The ITS regions have been used as an important tool for classification and differentiation of bacterial species (Conrads *et al.*, 2005).

Although *B. distasonis*, *B. goldsteinii* and *B. merdae* were phylogenetically related to *T. forsythensis*, the ratios of anteiso-$C_{15:0}$ to iso-$C_{15:0}$ in whole-cell methanolysates of the three species were different from that of *T. forsythensis*.

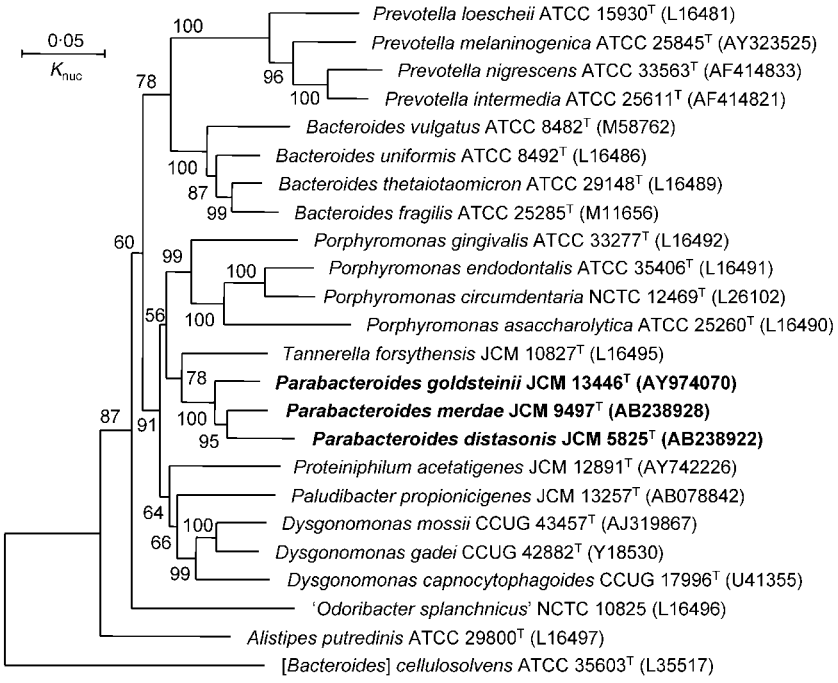

Fig. 1. Phylogenetic tree showing the relationship between members of *Parabacteroides* gen. nov. and some related taxa. The tree was constructed by using the neighbour-joining method based on 16S rRNA gene sequences. Numbers at nodes indicate percentage bootstrap values of 1000 replicates. Bar, 0·05 substitutions per nucleotide position. GenBank accession numbers are given in parentheses.

Whereas the ratios of anteiso-$C_{15:0}$ to iso-$C_{15:0}$ ranged from 3·1 to 10·3 in *B. distasonis*, *B. goldsteinii* and *B. merdae* strains, those of *T. forsythensis* strains ranged from 22·8 to 95·2 (Sakamoto *et al.*, 2002). In addition, although the major menaquinones of *T. forsythensis* were MK-10 and MK-11, the major menaquinones of *B. distasonis*, *B. goldsteinii* and *B. merdae* were MK-9 and MK-10. The three species were phenotypically similar to *Bacteroides sensu stricto*, but phylogenetically distinct. Furthermore, *B. distasonis*, *B. goldsteinii* and *B. merdae* could be differentiated from *Bacteroides sensu stricto* (predominant menaquinones: MK-10 and MK-11) by the menaquinone composition. This is an important chemotaxonomic characteristic of these species. These results suggest that a novel genus should be established to accommodate *B. distasonis*, *B. goldsteinii* and *B. merdae*.

Based on the above-mentioned findings and the 16S rRNA gene sequence analysis, we propose a novel genus, *Parabacteroides* gen. nov. *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae* are reclassified as *Parabacteroides distasonis* gen. nov., comb. nov., *Parabacteroides goldsteinii* comb. nov. and *Parabacteroides merdae* comb. nov., respectively. Differential characteristics of *Parabacteroides* gen. nov. and some related taxa are shown in Table 2.

Description of *Parabacteroides* gen. nov.

Parabacteroides (Pa′ra.bac.te.ro′i.des. Gr. prep. *para* beside; N.L. masc. n. *Bacteroides* a genus name; N.L. masc. n. *Parabacteroides* resembling the genus *Bacteroides*).

Cells are Gram-negative, obligately anaerobic, non-spore-forming, non-motile and rod-shaped, and 0·8–1·6 × 1·2–12 μm in size. Colonies on EG agar plates are 1–2 mm in diameter, grey to off-white–grey, circular, entire, slightly convex and smooth. Saccharolytic. Major end-products are acetic and succinic acids; lower levels of other acids may be produced. Grow on medium containing 20 % bile. Aesculin is hydrolysed. Indole is not produced. Glucose-6-phosphate dehydrogenase (G6PDH), 6-phosphogluconate dehydrogenase (6PGDH), malate dehydrogenase and glutamate dehydrogenase are present. α-Fucosidase is negative. The principal respiratory quinones are menaquinones MK-9 and MK-10. Both non-hydroxylated and 3-hydroxylated long-chain fatty acids are present. The non-hydroxylated acids are predominantly of the saturated straight-chain and anteiso-methyl branched-chain types. The G + C content is 43–46 mol%. Member of the *Bacteroides* subgroup of the phylum *Bacteroidetes*. The type species is *Parabacteroides distasonis*.

Description of *Parabacteroides distasonis* (Eggerth and Gagnon 1933) comb. nov.

Parabacteroides distasonis (dis.ta.so′nis. N.L. gen. n. *distasonis* of Distaso, named after A. Distaso, a Romanian bacteriologist).

Basonym: *Bacteroides distasonis* Eggerth and Gagnon 1933.

The description of *Parabacteroides distasonis* is as those given by Eggerth & Gagnon (1933) and Holdeman *et al.* (1977, 1984). Urease is not produced. Catalase is produced. Gelatin is not liquefied. Acid is produced from D-cellobiose, glucose, lactose, D-mannose, D-melezitose, D-raffinose, L-rhamnose, salicin, sucrose, D-trehalose and D-xylose, but not from L-arabinose, glycerol, D-mannitol or D-sorbitol. Positive reactions are obtained using Rapid ID 32A for α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, glutamic acid decarboxylase, alkaline phosphatase, arginine arylamidase, leucyl glycine arylamidase, phenylalanine arylamidase, leucine arylamidase, tyrosine arylamidase, alanine arylamidase, glycine arylamidase, histidine arylamidase and glutamyl glutamic acid arylamidase. Variable for α-arabinosidase and serine arylamidase. Mannose and raffinose are fermented. All the other tests are negative. Major cellular fatty acids are anteiso-$C_{15:0}$ and iso 3-OH-$C_{17:0}$. A significant amount of $C_{18:1}\omega9c$ is also present. The G + C content of the type strain is 44 mol%.

The type strain is JCM 5825^T (=CCUG 4941^T=DSM 20701^T=ATCC 8503^T), which was isolated from human faeces, where it is one of the most common species. Strains have been isolated occasionally from human clinical specimens.

Description of *Parabacteroides goldsteinii* (Song *et al.* 2006) comb. nov.

Parabacteroides goldsteinii (gold.stei′ni.i. N.L. gen. n. *goldsteinii* of Ellie J. C. Goldstein, in honour of the outstanding infectious disease clinician who has done a lot of work with anaerobes).

Basonym: *Bacteroides goldsteinii* Song *et al.* 2006.

The description of *Parabacteroides goldsteinii* is as that given by Song *et al.* (2005). Urease is not produced. Nitrate is not reduced. Acid is produced from cellobiose, glucose, rhamnose, sucrose, trehalose and xylose, but not from arabinose or xylan. In peptone yeast broth and peptone yeast glucose broth, major amounts of acetic and succinic acids and minor amounts of isovaleric acid, propionic acid and formic acid are produced. Using API ZYM, Rapid ID 32A and RapID ANA II systems, strains have the same profile. Positive reactions are obtained for α-glucosidase, α-galactosidase, β-galactosidase, *N*-acetyl-β-glucosaminidase, naphthol-AS-BI-phosphohydrolase, acid phosphatase, alkaline phosphatase, leucine arylamidase, *p*-nitrophenylphosphatase, arginine arylamidase, leucyl glycine arylamidase, phenylalanine arylamidase, alanine arylamidase, glycine arylamidase, histidine arylamidase, glutamyl glutamic acid arylamidase, leucyl glycine aminopeptidase, glycine aminopeptidase, phenylalanine aminopeptidase, arginine aminopeptidase and serine aminopeptidase. All the other tests are negative. Mannose and raffinose are fermented (Rapid ID 32A). Using Rosco diagnostic tablets (Rosco), β-xylosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-galactosidase, β-galactosidase

Table 2. Differential characteristics of *Parabacteroides* gen. nov. and some related taxa

Genera: 1, *Parabacteroides*; 2, *Bacteroides*; 3, *Dysgonomonas*; 4, *Paludibacter*; 5, *Porphyromonas*; 6, *Prevotella*; 7, *Proteiniphilum*; 8, *Tannerella*. Data from Chen & Dong (2005), Hofstad *et al.* (2000), Lawson *et al.* (2002), Sakamoto *et al.* (2002), Song *et al.* (2005), Ueki *et al.* (2006) and this study. +, Positive; −, negative; F, fermentative; MF, moderately fermentative; NF, non-fermentative; NT, not tested; V, variable; NAM, *N*-acetylmuramic acid.

Characteristic	1	2	3	4	5	6	7	8
Growth in bile	+	+	+	−	−	−	−	−
Aerobic growth	−	−	+	−	−	−	−	−
NAM required	−	−	−	−	−	−	−	+*
Production of:								
α-Fucosidase	−	V	V	NT	−†	V	NT	+
Catalase	V	V	V	−	V	V	−	V
Indole	−	V	V	−	V	V	−	V
Hydrolysis of aesculin	+	V	V	+	−	V	+	+
Pigment	−	−	−	−	+‡	V	−	−
Metabolism	F	F	F	F	NF§	MF	NF	NF
Major end-products‖	A, S	A, S	P, L, S	A, P	A, B, IV, P, PA, S	A, S	A, P	A, B, IV, P, PA
Presence of:								
G6PDH	+	+	NT	NT	V	−	NT	+
6PGDH	+	+	NT	NT	V	−	NT	+
Proteolytic activity	−	−	V	NT	V	V	+	+
Major cellular fatty acids	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$	iso-$C_{14:0}$, anteiso-$C_{15:0}$ and iso 3-OH-$C_{16:0}$	anteiso-$C_{15:0}$, $C_{15:0}$ and anteiso 3-OH-$C_{17:0}$	iso-$C_{15:0}$¶	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$
Ratio of anteiso-$C_{15:0}$ to iso-$C_{15:0}$	3·1–10·3	1·9–8·2	6·0–8·8	28	<1	1·2–11·3	12·3	22·8–95·2
Predominant menaquinones	MK-9, MK-10	MK-10, MK-11	NT	MK-8	MK-9, MK-10	MK10, MK-11, MK-12, MK-13#	NT	MK-10, MK-11
Growth at 37 °C	+	+	+	−	+	+	+	+
DNA G+C content (mol%)	43–46	40–49	38–38·5	39·3	40–55	40–60	46·6	44–48
Principal habitat	Faeces	Faeces	Human clinical specimen	Irrigated rice-field soil	Oral cavities	Oral cavities	USBA sludge	Periodontal pockets

*Bite wound isolates do not require NAM for growth.

†*Porphyromonas asaccharolytica* produces α-fucosidase.

‡*Porphyromonas catoniae* does not produce a black pigment on blood agar.

§Some species are weakly saccharolytic.

‖A, acetic acid; B, butyric acid; IV, isovaleric acid; L, lactic acid; P, propionic acid; PA, phenylacetic acid; S, succinic acid.

¶*Porphyromonas catoniae* contains approximately equal amounts of iso- and anteiso-$C_{15:0}$ as the predominant fatty acids.

#*Prevotella dentalis* lacks menaquinones.

(*o*-nitrophenol-β-D-galactopyranoside), *N*-acetyl-β-glucosaminidase, alkaline phosphatase and α-arabinosidase are present; α-arabinosidase is tested as positive only by Rosco tablets. Major cellular fatty acids are anteiso-$C_{15:0}$ and iso 3-OH-$C_{17:0}$ (25–28 and 18–23 %, respectively). Significant amounts of $C_{18:1}\omega9c$ and anteiso 3-OH-$C_{17:0}$ (11–16 and 9–15 %, respectively) are also present. Susceptible to metronidazole (MIC$\leqslant$2 μg ml^{-1}) and ertapenem (MIC$\leqslant$1 μg ml^{-1}). Some resistance is seen with clindamycin (MIC$\leqslant$8 μg ml^{-1}). Resistant to penicillin G (MIC$\geqslant$32 μg ml^{-1}), cefotetan (MIC$\leqslant$256 μg ml^{-1}) and vancomycin (MIC$\leqslant$32 μg ml^{-1}). β-Lactamase-positive. The G+C content of the type strain is 43 mol%.

The type strain is JCM 13446^{T} (=CCUG 48944^{T}), which was isolated from human clinical specimens of intestinal origin.

Description of *Parabacteroides merdae* (Johnson *et al.* 1986) comb. nov.

Parabacteroides merdae (mer′dae. L. gen. n. *merdae* of faeces, referring to the source of the type strain).

Basonym: *Bacteroides merdae* Johnson *et al.* 1986.

The description is the same as that given by Johnson *et al.* (1986). Urease and catalase are not produced. Gelatin is not liquefied. Acid is produced from glucose, lactose, maltose, D-mannose, D-raffinose, sucrose, D-trehalose and D-xylose, but not from L-arabinose, D-cellobiose, glycerol, D-mannitol, D-melezitose, L-rhamnose, salicin or D-sorbitol. Positive reactions are obtained using Rapid ID 32A for α-galactosidase, β-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, glutamic acid decarboxylase, alkaline phosphatase, arginine arylamidase, leucyl glycine arylamidase, phenylalanine arylamidase, leucine arylamidase, pyroglutamic acid arylamidase, tyrosine arylamidase, alanine arylamidase, glycine arylamidase, histidine arylamidase and glutamyl glutamic acid arylamidase. Variable for α-glucosidase, α-arabinosidase and serine arylamidase. Mannose and raffinose are fermented. All the other tests are negative. Major cellular fatty acids are anteiso-$C_{15:0}$ and iso 3-OH-$C_{17:0}$. A significant amount of $C_{18:1}\omega9c$ is also present. The G+C content of the type strain is 44 mol%.

The type strain is JCM 9497^{T} (=CCUG 38734^{T}=ATCC 43184^{T}), which was isolated from human faeces.

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