Parasutterella excrementihominis gen. nov., sp. nov., a member of the family *Alcaligenaceae* isolated from human faeces

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A novel, strictly anaerobic, non-spore-forming, Gram-negative coccobacillus (strain YIT 11859^T) was isolated from human faeces. Biochemically, this strain was largely unreactive and was asaccharolytic. Growth of strain YIT 11859^T in peptone-yeast extract broth produced no visible turbidity, and a trace amount of propionate was detected as an end product of metabolism. 16S rRNA gene sequence analysis showed that strain YIT 11859^T was related most closely to the type strains of *Sutterella* species, with 90.8–88.0 % sequence similarity. Phylogenetic analysis of these and other related sequences confirmed that strain YIT 11859^T was phylogenetically most closely associated with *Sutterella* species, but formed a separate cluster, indicating that strain YIT 11859^T represents a novel member of the family *Alcaligenaceae*. Fatty acid analysis demonstrated the presence of a high concentration of C_{18:1}ω₉c (75 % of the total). The main respiratory quinones were menaquinone (MK-6) and methylated menaquinone (MMK-6). The G+C content of the DNA was 49.8 mol%. These results suggest that strain YIT 11859^T represents a novel species of a new genus, for which the name *Parasutterella excrementihominis* gen. nov., sp. nov. is proposed. The type strain of *Parasutterella excrementihominis* is YIT 11859^T (=DSM 21040^T =JCM 15078^T).

By using culture-independent approaches based on small-subunit (16S and 18S) rRNA gene sequence diversity, most bacterial phylotypes identified from the human intestinal microbiota have been assigned to seven phyla, of which members of the *Firmicutes* and *Bacteroidetes* are dominant (Rajilić-Stojanović *et al.*, 2007; Eckburg *et al.*, 2005; Hayashi *et al.*, 2002; Wang *et al.*, 2003). The proteobacteria are usually secondary to the above, and members of the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria* and *Epsilonproteobacteria* have been identified (Eckburg *et al.*, 2005). With conventional culture techniques, on the other hand, species of the *Proteobacteria* such as *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae* and some species of *Proteus* and *Citrobacter* have been identified from the human intestinal microbiota (Finegold *et al.*, 1974; Holdeman *et al.*, 1976; Moore & Holdeman, 1974), and

all of these species belong to the family *Enterobacteriaceae*, class *Gammaproteobacteria*, except for *Sutterella parvirubra* (Sakon *et al.*, 2008) and *Sutterella wadsworthensis* (Wexler *et al.*, 1996; Engberg *et al.*, 2000), which belong to the family *Alcaligenaceae*, class *Betaproteobacteria*. This observation can be attributed, at least to some extent, to the lack of appropriate cultivation techniques.

To understand better the physiological characteristics and function of the majority of the human gastrointestinal microbiota, we have performed several intensive cultivation trials aimed at isolating so-called ‘unculturable’ or ‘as-yet-uncultured’ bacteria from the human gastrointestinal tract (Sakon *et al.*, 2008; Morotomi *et al.*, 2008).

Here we report the isolation of a novel member of the family *Alcaligenaceae* isolated from human faeces. Although we propose novel taxonomic units (genus and species) based on a single isolate, this isolate displayed more than 98 % 16S rRNA gene sequence similarity to some of the human intestinal uncultured clones reported by several groups in the USA and other countries, as described below, indicating that these bacteria are common members of the human intestinal microbiota.

A faecal sample was collected from a healthy Japanese male (29 years old) and immediately transferred anaerobically. The sample was weighed and diluted with pre-reduced

Abbreviations: FAME, fatty acid methyl ester; ML, maximum likelihood; MP, maximum parsimony.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIT 11859^T is AB370250.

Maximum-likelihood and maximum-parsimony phylogenetic trees based on 16S rRNA gene sequences and a table giving the cellular fatty acid compositions of strain YIT 11859^T and the type strains of related type species in the family *Alcaligenaceae* are available as supplementary material with the online version of this paper.

0.1 M PBS (pH 7) in an anaerobic glove box (Coy Laboratory Products), which contained 88 % nitrogen, 7 % hydrogen and 5 % carbon dioxide. Each dilution was then spread on anaerobe basal agar (Oxoid). The medium was adjusted to pH 5.0, 6.0, 7.0, 8.0 or 9.0 with HCl or NaOH before use. Plates were incubated at 37 °C for 3 days in the same anaerobic cabinet. Strain YIT 11859^T was isolated from a pH 6.0 plate inoculated with a 10⁻⁶ serially diluted faecal sample. Single colonies were picked and streaked out until single cultures were obtained on the same plate (anaerobe basal agar, pH 6.0). The end products of bacterial metabolism of glucose, lactate or succinate in pre-reduced peptone-yeast extract (PY) medium (Holdeman *et al.*, 1977) supplemented with glucose, lactate or succinate, respectively, were analysed by HPLC according to a previously described procedure (Chonan *et al.*, 1995). Cellular morphology was recorded after Gram-staining of 3-day-old plates or 1-day broth cultures. Cell dimensions were determined by phase-contrast microscopy (Olympus system microscope BX-50) by using an ocular micrometer ($\times 10$) and objective lens ($\times 100/1.25$ numerical aperture). Biochemical characteristics were determined by using the API Rapid ID 32A, API ZYM and API 20A systems (bioMérieux) according to the manufacturer's instructions. Sensitivity to bile was determined by comparing growth of the strain on modified Gifu anaerobic medium (GAM) agar (Nissui Pharmaceutical) with and without 2 % Bacto oxgall (Difco) after 5 days of incubation. The composition of the modified GAM agar was as given previously (Sakon *et al.*, 2008).

Isoprenoid quinones were extracted as described by Komagata & Suzuki (1987) and were analysed by using an HPLC-atmospheric pressure chemical ionization-MS/MS system (API3200; Applied Biosystems) with an L-column ODS (2.1 $\times$ 150 mm; Chemicals Evaluation and Research Institute) according to a modification of the method of Katsuta *et al.* (2005). Fatty acid methyl esters (FAMES) were obtained from lyophilized cells grown on modified GAM agar by saponification, methylation and extraction with minor modifications (Kuykendall *et al.*, 1988) of the method of Miller (1982). FAMES were identified with a Shimadzu model GC-14A gas chromatograph and a Shimadzu model C-R5A chromatograph-data processor. FAME peaks were identified by using retention time comparisons against standard compounds (bacterial acid methyl ester mix; Supelco).

The DNA G+C content was determined by hydrolysing the DNA enzymically and quantifying the nucleosides by HPLC according to the method of Ezaki *et al.* (1990).

16S rRNA gene sequences of reference species were retrieved from the DNA DataBank of Japan (DDBJ) by using the program FASTA (Pearson & Lipman, 1985). The sequences were aligned and used to produce an unrooted phylogenetic tree according to the neighbour-joining method (Saitou & Nei, 1987) by using CLUSTAL X (version 1.83) (Thompson *et al.*, 1997). Stability of the groupings was estimated by

bootstrap analysis (1000 replications) in CLUSTAL X. All phylogenetic trees were visualized by using the program TreeView version 1.6.6 (Page, 1996). Maximum-parsimony (MP) and maximum-likelihood (ML) methods were used to confirm the phylogenetic placement of the aligned sequences. MP analysis was performed by using the software package MEGA4 (Tamura *et al.*, 2007). The ML tree was constructed via the program PHYML (Guindon & Gascuel, 2003) by using Kimura's two-parameter nucleotide substitution model (Kimura, 1980). The input file was prepared via the program SEQBOOT within the PHYLIP package (Felsenstein, 2004). 16S rRNA gene sequence similarity values between strain YIT 11859^T and all other described species within the family *Alcaligenaceae* were calculated by using EzTaxon (Chun *et al.*, 2007).

Cells of strain YIT 11859^T were Gram-negative, obligately anaerobic, non-motile coccobacilli (0.4–1.1 $\times$ 0.9–2.6 μ m), occurring singly and in pairs. Colonies after 3 days anaerobic incubation on anaerobe basal agar were translucent, entire, circular, convex and pinpoint. Growth of strain YIT 11859^T in PY broth produced no visible turbidity; a trace amount of propionate was detected as an end product of metabolism. Addition of glucose, succinate or lactate did not enhance growth or the production of short-chain fatty acids. The strain was asaccharolytic in API test systems. In the API Rapid ID 32A and API ZYM test systems, strain YIT 11859^T was largely unreactive. It was positive for esterase (C4), arginine arylamidase and leucine arylamidase and weakly positive for acid phosphatase, alanine arylamidase, alkaline phosphatase, esterase lipase (C8), glycine arylamidase and naphthol-AS-BI-phosphohydrolase. All other test results were negative.

The quinone system of strain YIT 11859^T consisted of menaquinone (MK-6) and methylated menaquinone (MMK-6).

The only fatty acid comprising more than 10 % of the total for strain YIT 11859^T was C_{18:1 ω 9c} (74.96 %). Other fatty acids detected were C_{14:0} (6.34 %), C_{16:0} (6.31 %), C_{18:1 ω 9t} (2.74 %), C_{18:0} (1.99 %) and unknown fatty acids (equivalent chain-lengths of 15.306 and 17.478) (7.67 %). The detailed cellular fatty acid profiles of strain YIT 11859^T and related type species in the family *Alcaligenaceae* are presented in Supplementary Table S1 (available in IJSEM Online). The cellular fatty acid profile of strain YIT 11859^T was clearly different from those of related type species in the family *Alcaligenaceae*.

An approximately 1500-bp region of the 16S rRNA gene of strain YIT 11859^T was sequenced. Database searches of recognized taxa revealed that strain YIT 11859^T was related most closely to the type strains of *Sutterella* species (*Sutterella parvirubra*, 90.8 % 16S rRNA gene sequence similarity; *Sutterella wadsworthensis*, 89.3 %; *Sutterella stercoricanis*, 88.0 %). Levels of 16S rRNA gene sequence similarity between strain YIT 11859^T and the type strains of all other recognized species within the family *Alcaligenaceae* were less than 90 %, namely species of

Achromobacter (89.1–88.2%), *Advenella* (88.8–84.9%), *Alcaligenes* (88.4–86.7%), *Azohydromonas* (88.2–87.7%), *Bordetella* (89.0–88.5%), *Brackiella* (87.6%), *Castellaniella* (88.5–88.2%), *Derxia* (89.0%), *Kerstesia* (88.6%), *Oligella* (87.4–86.7%), *Pelistega* (87.6%), *Pigmentiphaga* (88.8–88.7%), *Pusillimonas* (88.3%), *Taylorella* (88.5–87.4%) and *Tetrathiobacter* (88.4–87.7%).

Phylogenetic analysis of these and other related sequences of recognized taxa was performed and confirmed that strain YIT 11859^T was phylogenetically related most closely to *Sutterella* species, but formed a separate cluster in the neighbour-joining tree (Fig. 1). Other taxa (e.g. *Alcaligenes*, *Achromobacter* or *Bordetella* species) were more distantly related. These results were consistent with those obtained by using the MP and ML methods (Supplementary Figs S1 and S2). Strain YIT 11859^T did, however, show higher levels of 16S rRNA gene sequence similarity (99.7–98.2%) to uncultured human faecal or colonic bacteria (Eckburg *et al.*, 2005; Hold *et al.*, 2002; Mai *et al.*, 2006; Ley *et al.*, 2006) (Fig. 1 and Supplementary Figs S1 and S2).

Table 1 shows the main characteristics of strain YIT 11859^T that can be used to differentiate it from members of the genus *Sutterella*. The G + C content of the DNA of strain YIT 11859^T was 49.8 mol%, whereas that of recognized *Sutterella* species ranges from 60 to 64.5 mol% (Sakon *et al.*, 2008; Greetham *et al.*, 2004).

Although there is no direct evidence that members of the genus represented by strain YIT 11859^T (*Parasutterella* gen. nov.) have been isolated from human faeces as common members of the human indigenous microbiota, evidence in favour of this comes from the fact that many uncultured human intestinal bacterial clones with highly similar 16S rRNA gene sequences to that of strain YIT 11859^T have been deposited with the DDBJ (Fig. 1).

It is evident from the results presented that strain YIT 11859^T recovered from human faeces represents a novel species of a new genus within the family *Alcaligenaceae*, for which the name *Parasutterella excrementihominis* gen. nov., sp. nov. is proposed.

Description of *Parasutterella* gen. nov.

Parasutterella (Pa.ra.sut.te.rel'la. Gr. prep. *para* besides, next to; N.L. fem. n. *Sutterella* name of a bacterial genus; N.L. fem. n. *Parasutterella* a genus similar to *Sutterella*).

Cells are Gram-negative, non-motile, strictly anaerobic, non-spore-forming cocci to coccobacilli. Oxidase-, urease- and catalase-negative. Asaccharolytic. Grow in the presence of bile. Aesculin and gelatin are not hydrolysed and nitrate is not reduced. Indole is not produced. The main respiratory quinones are MK-6 and MMK-6. The only major fatty acid (>10% of the total) is C_{18:1}ω₉c. The type species is *Parasutterella excrementihominis*.

Description of *Parasutterella excrementihominis* sp. nov.

Parasutterella excrementihominis (ex.cre.men.ti.ho'mi.nis. L. n. *excrementum* excrement; L. n. *homo* -inis human being, man; N.L. gen. n. *excrementihominis* of faeces of a human).

The description of the species is as given for the genus above. In addition, cells are approximately 0.4–1.1 × 0.9–2.6 µm in size. After 3 days anaerobic incubation on anaerobe basal agar (pH 6.0) colonies are translucent, entire, circular, convex and pinpoint. In the API test systems, positive for esterase (C4), arginine arylamidase and leucine arylamidase, weakly positive for acid phosphatase, alanine arylamidase, alkaline phosphatase, esterase

Fig. 1. Phylogenetic tree showing the positions of strain YIT 11859^T and the type strains of species of the family *Alcaligenaceae* based on 16S rRNA gene sequence similarity data. The tree was rooted with *Escherichia coli* ATCC 11775^T and was constructed by using the neighbour-joining method, with bootstrap values expressed as percentages of 1000 replications. GenBank/EMBL/DDBJ accession numbers are shown in parentheses. Bar, 0.1 substitutions per nucleotide position. MP and ML phylogenetic trees are available as Supplementary Figs S1 and S2.

Table 1. Differential characteristics between strain YIT 11859^T and members of the genus *Sutterella*

Strains: 1, YIT 11859^T; 2, *S. parvirubra* YIT 11816^T; 3, *S. wadsworthensis* WAL 9799^T; 4, *S. stercoricanis* CCUG 47620^T. Data for strain YIT 11859^T and cellular fatty acid data for *S. parvirubra* YIT 11816^T are from the present study. Other data for *S. parvirubra* YIT 11816^T, *S. wadsworthensis* WAL 9799^T and *S. stercoricanis* CCUG 47620^T are from Sakon *et al.* (2008), Wexler *et al.* (1996) and Greetham *et al.* (2004), respectively. No data are available for major quinones of *Sutterella* species. +, Positive; –, negative; w, weakly positive; NA, no data available.

Characteristic	1	2	3	4
Isolation source	Human faeces	Human faeces	Gastrointestinal tract infection	Dog faeces
Cell morphology	Coccobacilli	Coccobacilli	Straight rods	Short, straight rods
Cell size (µm)	0.4–1.1 × 0.9–2.6	0.4–1 × 0.4–2	0.5–1 × 1–3	0.8 × 1.5–2
DNA G + C content (mol%)	49.8	64.4	NA	60
Nitrate reduction	–	–	+	+
API ZYM results				
Acid phosphatase	w	–	NA	–
Esterase (C4)	+	–	–	–
Esterase lipase (C8)	w	w	–	–
Rapid ID 32A API results				
Alkaline phosphatase	w	–	NA	–
Arginine arylamidase	+	w	NA	–
Glycine arylamidase	w	–	NA	w
Leucine arylamidase	+	–	NA	–
Major cellular fatty acid(s)	C _{18:1} ω9c	C _{16:0} , C _{18:1} ω9c	C _{16:0} , C _{16:1} ω7c, SF10*	C _{16:0} , C _{16:1} ω7c, C _{18:1} ω9c

*Summed feature 10 (SF10) comprises one or more of C_{18:1}ω7c/ω9t/ω12t and an unknown peak at 17.834.

lipase (C8), glycine arylamidase and naphthol-AS-BI-phosphohydrolase, but negative for *N*-acetyl-β-glucosaminidase, α-arabinosidase, arginine dihydrolase, chymotrypsin, cystine arylamidase, α-fucosidase, α-galactosidase, β-galactosidase, 6-phospho-β-galactosidase, α-glucosidase, β-glucosidase, β-glucuronidase, glutamic acid decarboxylase, glutamyl glutamic acid arylamidase, histidine arylamidase, leucyl glycine arylamidase, lipase (C4), α-mannosidase, phenylalanine arylamidase, proline arylamidase, pyroglutamic acid arylamidase, serine arylamidase, trypsin, tyrosine arylamidase and valine arylamidase. The fatty acid profile of the type strain contains C_{14:0}, C_{16:0}, C_{18:1}ω9c, C_{18:1}ω9t, C_{18:0} and unknown fatty acids (equivalent chain-lengths of 15.306 and 17.478). The DNA G + C content of the type strain is 49.8 mol%.

The type strain, YIT 11859^T (=DSM 21040^T =JCM 15078^T), was isolated from human faeces.

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