Alistipes indistinctus sp. nov. and *Odoribacter laneus* sp. nov., common members of the human intestinal microbiota isolated from faeces

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Two anaerobic, non-spore-forming, non-motile, Gram-negative-staining bacteria, strains YIT 12060^T and YIT 12061^T, were isolated from human faeces. Cells of strain YIT 12060^T were coccoid to rod-shaped with round ends, positive for catalase, negative for indole and oxidase production, produced succinic and acetic acids as end products of glucose metabolism in peptone/yeast extract/glucose medium and had a DNA G + C content of 55.2 mol%. The main respiratory quinones were MK-10 (40 %) and MK-11 (57 %). Fatty acid analysis demonstrated the presence of a high concentration of iso-C_{15:0} (56 %). Following 16S rRNA gene sequence analysis, this strain was found to be most closely related to species of the genus *Alistipes*, with 90.9–92.6 % gene sequence similarities to type strains of this species. Phylogenetic analysis and biochemical data supported the affiliation of strain YIT 12060^T to the genus *Alistipes* of the family 'Rikenellaceae'. Strain YIT 12060^T therefore represents a novel species of the genus *Alistipes* for which the name *Alistipes indistinctus* sp. nov. is proposed; the type strain is YIT 12060^T (=DSM 22520^T=JCM 16068^T). Cells of the other isolate, strain YIT 12061^T, were pleomorphic rods that were asaccharolytic, catalase- and oxidase-negative, positive for gelatin hydrolysis and indole production, produced small amounts of succinic, acetic and iso-valeric acids as end products of metabolism in peptone/yeast extract medium and had a DNA G + C content of approximately 42.4 mol%. On the basis of 16S rRNA gene sequence similarity values, this strain was shown to belong to the family 'Porphyromonadaceae' and related to the type strains of *Odoribacter splanchnicus* (89.6 %) and *Odoribacter denticanis* (86.2 %); similarity values with strains of recognized species within the family 'Porphyromonadaceae' were less than 84 %. Biochemical data supported the affiliation of strain YIT 12061^T to the genus *Odoribacter*. Strain YIT 12061^T therefore represents a novel species for which the name *Odoribacter laneus* sp. nov. is proposed; the type strain is YIT 12061^T (=DSM 22474^T=JCM 16069^T).

Members of the families *Bacteroidaceae*, 'Porphyromonadaceae', 'Prevotellaceae' and 'Rikenellaceae' within the order 'Bacteroidales' in the phylum 'Bacteroidetes' have been found to be major constituents of the human gastrointestinal (GI) microbiota (see review by Rajilić-Stojanović *et al.*, 2007). The taxonomy of these families has undergone considerable changes because of the advent of 16S rRNA gene sequence analysis, which has vastly improved the ability of scientists to genetically place a

bacterium into an appropriate genus. The type species of the genus *Alistipes* within the family 'Rikenellaceae', *Alistipes putredinis*, was previously known as *Bacteroides putredinis* (Weinberg *et al.*, 1937) and was reclassified as *A. putredinis* (Rautio *et al.*, 2003). The recent description of the genus *Alistipes* included three other species, *Alistipes finegoldii*, *Alistipes onderdonkii* and *Alistipes shahii*. These species have been isolated from appendix tissue, abdominal abscess, urine and/or intra-abdominal fluid (Song *et al.*, 2006). All of these species have also been isolated from the faeces of healthy subjects (Song *et al.*, 2006) indicating that these are normal members of the human intestinal microbiota. Meanwhile, the type species of the genus *Odoribacter* within the family 'Porphyromonadaceae', *Odoribacter splanchnicus* (Hardham *et al.*, 2008), previously known as *Bacteroides splanchnicus*, was first isolated from

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Abbreviations: ECL, equivalent chain-length; FAMES, fatty acid methyl esters; GI, gastrointestinal.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains YIT 12060^T and YIT 12061^T are AB490804 and AB490805, respectively.

human faeces and surgically removed appendices (Werner & Reichertz, 1971) and identified later as *B. splanchnicus* (Werner *et al.*, 1975). At the time of writing, the genus *Odoribacter* comprised only two recognized species, namely *O. splanchnicus* and *Odoribacter denticanis* (List of Prokaryotic Names with Standing in Nomenclature; <http://www.bacterio.cict.fr/>). *O. denticanis* was isolated from crevicular spaces of dogs with periodontitis (Hardham *et al.*, 2008).

To better understand the physiological characteristics and function of the majority of human GI microbiota, we have performed several intensive cultivation trials aimed at isolating so-called 'unculturable' or 'as-yet-uncultured' bacteria from the human GI tract (Sakon *et al.*, 2008; Morotomi *et al.*, 2008, 2009; Nagai *et al.*, 2009). In this article, the isolation of novel species of the genera *Alistipes* and *Odoribacter* from human faeces is reported. Although a novel taxonomic unit (species) based on a single faecal isolate from a Japanese healthy adult is proposed, each isolate displayed >99 % 16S rRNA gene sequence similarity to some of the human intestinal uncultured clones reported by several groups in the USA, as described below, indicating that these bacteria are common members of the human GI microbiota.

Faecal samples were collected from two healthy Japanese males (subjects H and O, 57 and 40 years old, respectively) and immediately transferred anaerobically. Initial processing and subsequent weighing and dilution of the specimens were carried out under strictly anaerobic conditions as described by Holdeman *et al.* (1977). The samples were weighed and diluted with pre-reduced 0.1 M PBS (0.145 M NaCl, 0.15 M sodium phosphate; pH 7) and spread onto modified Gifu anaerobic medium (GAM; Nissui Pharmaceutical) agar supplemented with ox gall, NaCl or antibiotics (described below) to isolate subdominant groups of intestinal microbiota. Plates were incubated at 37 °C for 3 days in an anaerobic glove box (Coy Laboratory Products) that contained 88 % nitrogen, 7 % hydrogen and 5 % carbon dioxide. The composition of modified GAM agar was described in our previous report (Sakon *et al.*, 2008). Strain YIT 12060^T was isolated from a modified GAM agar plate supplemented with norfloxacin (40 µg ml⁻¹; Sigma) and inoculated with a 10⁻⁶ serially diluted faecal sample from subject H. Strain YIT 12061^T was isolated from a modified GAM agar plate supplemented with oxacillin (4 µg ml⁻¹; Sigma) and inoculated with a 10⁻⁵ serially diluted faecal sample from subject O. Single colonies were picked and streaked out until single cultures were obtained on modified GAM agar.

The end products of bacterial metabolism in pre-reduced peptone-yeast extract (PY) medium (Holdeman *et al.*, 1977) and PY medium supplemented with glucose (PYG medium) were analysed by HPLC as described previously (Chonan *et al.*, 1995). Cellular morphology was examined by phase-contrast light microscopy of 5-day-old modified GAM agar cultures. Biochemical characteristics were

determined in duplicate by using the API Rapid ID 32A, API ZYM and API 20A systems (bioMérieux) according to the manufacturer's instructions. Production of indole (Rapid ID 32A and API 20A) and liquefaction of gelatin (API 20A) were determined by the API systems and also according to the conventional methods described by Holdeman *et al.* (1977). Haemolysis was tested on Columbia agar plates supplemented with 5 % sheep blood (BBL Microbiology Systems, Becton Dickinson). Sensitivity to bile was determined by comparing growth of the strain on modified GAM agar with and without 2 % Bacto-Oxgall (Difco) after 5 days incubation.

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

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). Closely related sequences were retrieved from GenBank/EMBL/DDBJ using the FASTA program (Pearson & Lipman, 1985). Sequences were aligned and used to produce an unrooted phylogenetic tree by the neighbour-joining method (Saitou & Nei, 1987) using CLUSTAL_X (version 1.83) (Thompson *et al.*, 1997). The stability of the groupings was estimated by bootstrap analysis (1000 replications) in CLUSTAL_X. Trees were visualized by using the TREEVIEW program (version 1.6.6) (Page, 1996). The minimal evolution method (1000 bootstrap replicates) in MEGA4 (Tamura *et al.*, 2007) and the maximum-likelihood method from the PHYLIP program package (Felsenstein, 1993) were used to confirm the phylogenetic placement of the aligned sequences.

Cells of YIT 12060^T were Gram-negative, obligately anaerobic, non-motile and coccoid to rod-shaped with round ends (0.5–0.7 × 1.0–3.8 µm) (Fig. 1a). They were non-haemolytic on sheep-blood agar. Colonies after 4 days anaerobic incubation on modified GAM agar were 0.1–0.5 mm in diameter, slightly opaque, circular and grey. The major end products of glucose fermentation in PYG broth were succinic (20.5 mM) and acetic (15.2 mM) acids. Strain YIT 12060^T was saccharolytic in API test systems and positive for catalase, but negative for indole production, nitrate reduction, oxidase, urease, and hydrolysis of aesculin and gelatin. Indole production was not detected in PY culture. Cells were not resistant to 20 % bile. The

Fig. 1. Phase-contrast micrographs showing the morphology of cells of strains YIT 12060^T (a) and YIT 12061^T (b). Bars, 10 µm.

quinone system of strain YIT 12060^T consisted of MK-10 (40 %) and MK-11 (57 %). The major components (>10 % of total fatty acids) of the cellular fatty acids were iso-C_{15:0} (56.0 %) and C_{18:1ω9c} (18.9 %). Other fatty acids detected were C_{15:0} (5.8 %), C_{16:0} (4.0 %), iso-C_{16:0} (1.2 %) and an unknown fatty acid [equivalent chain-length (ECL) of 17.879; 6.4 %]. Other biochemical characteristics obtained by using the API systems (API Rapid ID 32A, API ZYM and API 20A) are given in the species description.

Regions of the 16S rRNA gene of YIT 12060^T of approximately 1500 bp were sequenced and database searches revealed highest sequence similarities to the type strains of members of the genus *Alistipes* (92.6 % to *A. putredinis*; 91.9 % to *A. finegoldii*; 91.6 % to *A. onderdonkii*; and 90.9 % to *A. shahii*). Phylogenetic analysis of these and other related sequences was performed and confirmed that strain YIT 12060^T was phylogenetically most closely associated with species of the genus *Alistipes* (Fig. 2). These results are congruent with those obtained using the maximum-parsimony and maximum-likelihood methods

(data not shown). In contrast, the most similar 16S rRNA gene sequences (99.9–97.1 %) were derived from one unnamed faecal isolate (*Bacteroides* bacterium Eg28, unpublished data by M.-S. Kim, GenBank accession no. FJ611795) and from some of the uncultured human faecal or colonic bacteria reported by Eckburg *et al.* (2005) (accession no. AY916354) and Li *et al.* (2008) (accession nos EF400613 and EF404328). These clones, with highly similar 16S rRNA gene sequences to that of strain YIT 12060^T, indicate that this bacterium is a common member of the human intestinal microbiota. The DNA G+C content of strain YIT 12060^T was 55.2 mol%; those of the known species of the genus *Alistipes* range from 55.0 to 58.0 mol% (Rautio *et al.*, 2003; Song *et al.*, 2006). Table 1 shows the primary characteristics of this isolate that can be used to differentiate it from members of the genus *Alistipes*.

Cells of YIT 12061^T stained Gram-negative and were obligately anaerobic, non-motile, pleomorphic rods (0.4–1.9 × 1.4–19.1 µm) (Fig. 1b). Colonies after 4 days anaerobic incubation on GAM agar were 0.1–0.5 mm in diameter, circular, grey-beige and slightly opaque. The organism produced large zones of β-haemolysis after 7–10 days on Columbia blood agar. Growth of the strain in PY or PYG broth was weak and small amounts of succinic, acetic and iso-valeric acids were detected as end products of metabolism. Cells were asaccharolytic in API 20A test systems. They hydrolysed gelatin and were positive for indole production. Indole production was detected in PY medium culture; however, results differed depending on the micro-test kit used (positive in the API Rapid ID 32A and negative in the API 20A) under the conditions recommended by the supplier. Cells were catalase-,

Fig. 2. Phylogenetic tree showing the positions of strains YIT 12060^T, YIT 12061^T and other species belonging to the order 'Bacteroidales' based on 16S rRNA gene sequence similarity data. The tree was rooted with *Escherichia coli* and constructed by using the neighbour-joining method; bootstrap values from 1000 replications are given at the nodes. GenBank accession numbers are shown in parentheses. Bar, 0.1 substitutions per nucleotide position.

Table 1. Major characteristics of strain YIT 12060^T and other members of the genus *Alistipes*

Strains: 1, YIT 12060^T; 2, *A. putredinis* ATCC 29800^T; 3, *A. finegoldii* CCUG 46020^T; 4, *A. onderdonkii* WAL 8169^T; 5, *A. shahii* WAL 8301^T. Data for strain YIT 12060^T are from this study. Data for *A. onderdonkii* and *A. shahii* are from Song *et al.* (2006). Data for *A. putredinis* and *A. finegoldii* are from Rautio *et al.* (2003) unless otherwise indicated. +, Positive; –, negative; w, weakly positive; v, variable; NA, no data available.

Characteristic	1	2	3	4	5
Isolation source	Human faeces	Human faeces	Appendix tissue	Abdominal abscess	Appendix tissue
Morphology	Coccoid to rods	Slender rods	Straight rods	Slender rods	Slender rods
Products from PYG*	SA	Sap†	Sap†	Sap	Sap
Aesculin hydrolysis	+	NA	–	v	+
Indole production	–	+	+	+	+
Catalase	+	+	–	–	–
Resistance to 20 % bile	–	–†	+†	+	+
DNA G + C content (mol%)	55.2	55	57	58	56
Major cellular fatty acid	iso-C _{15:0}	NA	iso-C _{15:0}	iso-C _{15:0}	iso-C _{15:0}
Major quinones	MK-10, MK-11	NA	NA	NA	NA
Enzyme activity‡					
N-Acetyl-β-glucosaminidase	+	NA	+	+	+
Chymotrypsin	–	–†	+†	v	w
α-Galactosidase	+	NA	+	+	+
β-Galactosidase	+	NA	+	+	+
β-Glucosidase	+	–†	–†	–	+
α-Fucosidase	+	–†	+†	–	+

*A, Acetic acid; P, propionic acid; S, succinic acid; lower-case letters indicate minor amounts.

†Data from Song *et al.* (2006).

‡Based on reactions obtained using the API ZYM system.

oxidase-, and urease-negative and negative for aesculin hydrolysis and nitrate reduction. Other biochemical characteristics obtained by using the API Rapid ID 32A and API ZYM test systems are given in the species description for *Odoribacter laneus* sp. nov. The major cellular fatty acids of strain YIT 12061^T were iso-C_{15:0} (52.5 %), C_{18:1ω9c} (10.8 %) and anteiso-C_{15:0} (8.8 %); other fatty acids detected (>1 %) were C_{16:0} (3.4 %), C_{14:0} (1.1 %) and unknown fatty acids (ECL 17.3, 8.5 %; ECL 17.9, 7.1 %; ECL 15.0, 2.6 %; ECL 19.4, 2.4 %; ECL 19.7, 1.9 %). Trace amounts of iso-C_{17:0}, C_{18:1ω9t} and C_{18:2ω9,12c} were also detected. Major characteristics and similarity values between the 16S rRNA genes of strain YIT 12061^T and other members of the genus *Odoribacter* are shown in Table 2.

An almost-complete 16S rRNA gene sequence of strain YIT 12061^T was determined (1478 bp) and database searches revealed the highest sequence similarity to that of the type strain of *Odoribacter splanchnicus* (89.6 %; Table 2). Phylogenetic analysis of these and other related sequences was performed and the data confirmed that strain YIT 12061^T was phylogenetically most closely associated with *O. splanchnicus* and *O. denticanis* (Fig. 2). These results were congruent with those obtained using the maximum-parsimony and maximum-likelihood methods (data not shown). Currently, only two species of the genus *Odoribacter* are known: *O. splanchnicus*, formerly classified as *Bacteroides splanchnicus* and originally isolated from

human faeces and surgically removed appendices (Werner & Reichertz, 1971); and *O. denticanis*, isolated from the crevicular spaces of dogs with periodontitis (Hardham *et al.*, 2008). Although there is no direct evidence that members of the species represented by strain YIT 12061^T (*O. laneus* sp. 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 12061^T have been deposited with the DDBJ/GenBank. At the time of writing, 24 clones had been deposited by three different study groups: Ley *et al.* (2006) (GenBank accession nos. DQ793556 and DQ793745), Eckburg *et al.* (2005) (AY975536 and 20 other clones) and Mai *et al.* (2006) (DQ905265). The DNA G + C content of strain YIT 12061^T was 42.4 mol%.

In this report, the isolation of two novel species from human faeces is described. Their phenotypic criteria corresponded to earlier studies of members of the genera *Alistipes* and *Odoribacter*, respectively. Based on its phylogenetic distinctiveness, it is considered that strain YIT 12060^T represents a novel species in the genus *Alistipes* for which the name *Alistipes indistinctus* sp. nov. is proposed. Likewise, on the basis of the presented findings, it is proposed that strain YIT 12061^T be assigned to the genus *Odoribacter* as a representative of a novel species, *Odoribacter laneus* sp. nov.

Table 2. Major characteristics and similarity values for the 16S rRNA genes of strain YIT 12061^T and other members of the genus *Odoribacter*

Strains: 1, YIT 12061^T; 2, *O. splanchnicus*; 3, *O. denticanis* B106^T. Data for strain YIT 12061^T are from this study. Data for *O. splanchnicus* (the type and 11 other strains) and *O. denticanis* B106^T are from Holdeman *et al.* (1984) and Hardham *et al.* (2008), respectively, except where otherwise indicated. +, Positive; –, negative; NA, no data available; tr, trace.

Characteristic	1	2	3
Isolation source	Human faeces	Human faeces, vagina and occasionally from abdominal infection	Crevicular spaces of canine periodontitis patients
Morphology	Pleomorphic rod-shaped	Rods	Fusiform-shaped
Cell dimensions (µm)	0.4–1.9 × 1.4–19.1	0.7 × 1.0–5.0	5.9*
DNA G + C content (mol%)	42.4	NA	NA
Major products from PY or PYG†	sa(ibiv)	SAPbivib(l)	NA
Sugar utilization	Asaccharolytic	Saccharolytic	Asaccharolytic
Catalase	–	+‡	+
Hydrolysis of gelatin	+	tr	NA
Resistance to 20 % bile	–	+	NA
Major cellular fatty acids	iso-C _{15:0} , C _{18:1} ω9c, anteiso-C _{15:0}	NA	NA
Similarity values (%) with 16S rRNA gene sequences from:			
1. <i>O. laneus</i> YIT 12061 ^T	100	89.6	86.2
2. <i>O. splanchnicus</i> NCTC 10825 ^T		100	85.4
3. <i>O. denticanis</i> B106 ^T			100

*Cells are fusiform with tapered ends and a mean cell length of 5.9 µm (Hardham *et al.*, 2008).

†Products from PY or PYG medium: upper-case letters, >1 meq acid per 100 ml broth; lower-case letters, <1 meq acid per 100 ml; A, acetic acid; B, butyric acid; L, lactic acid; P, propionic acid; S, succinic acid; iB, isobutyric acid; V, valeric acid; iV, isovaleric acid. Products in parentheses may or may not be detected.

‡Data from Holdeman *et al.* (1977), based on 9 strains.

Description of *Alistipes indistinctus* sp. nov.

Alistipes indistinctus (in.dis.tinc'tus. L. masc. adj. *indistinctus* not properly distinguished or indistinct, referring to the biochemical characteristics compared with those of phylogenetically related species).

Cells stain Gram-negative and are non-spore-forming, coccoid to rod-shaped with round ends and are strictly anaerobic. Cells are approximately 0.5–0.7 × 1.0–3.8 µm. After growth for 4 days with anaerobic incubation on modified GAM agar, colonies are 0.1–0.5 mm in diameter, slightly opaque, circular and grey. The major end products of glucose fermentation in PYG broth are succinic and acetic acids. Not resistant to 20 % bile. Aesculin and gelatin are not hydrolysed and nitrate is not reduced. Indole is not produced. Catalase is positive. Oxidase and urease are not produced. Positive for acid production from cellobiose, glucose, lactose, maltose, D-mannose, melezitose, raffinose, L-rhamnose, salicin, sucrose, trehalose and D-xylose. Acid production from L-arabinose, glycerol, D-mannitol and D-sorbitol is weakly positive. By using the commercially available API test systems (API Rapid ID 32A and API ZYM), positive for *N*-acetyl-β-glucosaminidase, alanine arylamidase, alkaline phosphatase,

tase, glutamyl glutamic acid arylamidase, leucyl glycine arylamidase, α-fucosidase, α-galactosidase, β-galactosidase and β-glucosidase, and weakly positive for acid phosphatase, esterase lipase (C8), esterase (C4), naphthol-AS-BI-phosphohydrolase and α-arabinosidase. Depending on the micro-test kit used, variable results are obtained for α-glucosidase (positive in the API Rapid ID 32A and negative in the API ZYM) and β-glucuronidase (positive in the API ZYM and negative in the API Rapid ID 32A). Negative for arginine arylamidase, arginine dihydrolase, chymotrypsin, cystine arylamidase, 6-phosphate-β-galactosidase, glutamic acid decarboxylase, glycine arylamidase, histidine arylamidase, leucine arylamidase, lipase (C14), α-mannosidase, phenylalanine arylamidase, proline arylamidase, pyroglutamic acid arylamidase, serine arylamidase, trypsin, tyrosine arylamidase and valine arylamidase. The main respiratory quinones are MK-10 and MK-11. The fatty acid profile consists of iso-C_{15:0}, C_{18:1}ω9c, C_{15:0}, C_{16:0}, iso-C_{16:0}, anteiso-C_{15:0} and an unknown fatty acid (ECL 17.879).

The type strain, YIT 12060^T (=DSM 22520^T=JCM 16068^T), was isolated from human faeces. The DNA G + C content of the type strain is 55.2 mol%.

Description of *Odoribacter laneus* sp. nov.

Odoribacter laneus (la'ne.us. L. masc. adj. *laneus* woollen, soft as wool, referring to the growth appearance in liquid medium and to the cellular characteristics of the resulting fluffy precipitate after centrifugation).

Cells stain Gram-negative and are obligately anaerobic, non-motile, pleomorphic rods ($0.4\text{--}1.9 \times 1.4\text{--}19.1\ \mu\text{m}$) that hydrolyse gelatin and are positive for indole production. Catalase, urease and oxidase are not produced. Colonies after 4 days anaerobic incubation on GAM agar are 0.1–0.5 mm in diameter, circular, grey–beige and slightly opaque. After 7–10 days culture on sheep blood agar, colonies are surrounded by a clear haemolytic zone and demonstrate pigmentation after >2 weeks. Analysis of metabolic end products by HPLC from PY and PYG broth reveals small amounts of succinic, acetic and iso-valeric acids. Asaccharolytic. The major cellular fatty acids are iso- $\text{C}_{15:0}$, $\text{C}_{18:1\omega 9c}$ and anteiso- $\text{C}_{15:0}$. Using the commercially available API test systems (API ZYM and rapid ID 32A), positive for *N*-acetyl- β -glucosaminidase, acid phosphatase, alanine arylamidase, alkaline phosphatase, arginine arylamidase, chymotrypsin, esterase lipase (C8), esterase (C4), α -fucosidase, α -galactosidase, β -galactosidase, α -glucosidase, glutamic acid decarboxylase, glutamyl glutamic acid arylamidase, histidine arylamidase, leucine arylamidase, leucyl glycine arylamidase, phenylalanine arylamidase, pyroglutamic acid arylamidase and tyrosine arylamidase, but negative for α -arabinosidase, arginine dihydrolase, cystine arylamidase, 6-phospho- β -galactosidase, β -glucosidase, glycine arylamidase, lipase (C14), α -mannosidase, proline arylamidase, serine arylamidase, trypsin and valine arylamidase. Weak activity is detected for naphthol-AS-BI-phosphohydrolase and β -glucuronidase.

The type strain, YIT 12061^T (=DSM 22474^T=JCM 16069^T), was isolated from human faeces. The DNA G+C content of the type strain is 42.4 mol%.

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