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 12060T and YIT 12061T, were isolated from human faeces. Cells of strain YIT 12060T 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-C15:0 (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 12060T to the genus Alistipes of the family ‘Rikenellaceae’. Strain YIT 12060T therefore represents a novel species of the genus Alistipes for which the name Alistipes indistinctus sp. nov. is proposed; the type strain is YIT 12060T (=DSM 22520T=JCM 16068T). Cells of the other isolate, strain YIT 12061T, 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 denticans (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 12061T to the genus Odoribacter. Strain YIT 12061T therefore represents a novel species for which the name Odoribacter laneus sp. nov. is proposed; the type strain is YIT 12061T (=DSM 22474T=JCM 16069T).

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...
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, 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 12060T was isolated from a modified GAM agar plate supplemented with norfloxacin (40 µg ml⁻¹; Sigma) and inoculated with a 10⁻⁴ serially diluted faecal sample from subject H. Strain YIT 12061T 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 Komaga & 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 TREEVIEWS 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 PHYLP program package (Felsenstein, 1993) were used to confirm the phylogenetic placement of the aligned sequences.

Cells of YIT 12060T 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 12060T 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
quinone system of strain YIT 12060\textsuperscript{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\textsubscript{15}:0 (56.0\%) and C\textsubscript{18}:1\textit{v}\textsubscript{7}c (18.9\%). Other fatty acids detected were C\textsubscript{15}:0 (5.8\%), C\textsubscript{16}:0 (4.0\%), iso-C\textsubscript{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\textsuperscript{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 \textit{A. putredinis}; 91.9\% to \textit{A. finegoldii}; 91.6\% to \textit{A. onderdonkii}; and 90.9\% to \textit{A. shahii}). Phylogenetic analysis of these and other related sequences was performed and confirmed that strain YIT 12060\textsuperscript{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 (\textit{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\textsuperscript{T}, indicate that this bacterium is a common member of the human intestinal microbiota. The DNA G+C content of strain YIT 12060\textsuperscript{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 \textit{Alistipes}.

Cells of YIT 12061\textsuperscript{T} stained Gram-negative and were obligately anaerobic, non-motile, pleomorphic rods (0.4–1.9 x 1.4–19.1 mm) (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 \textit{b}-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-,
Table 1. Major characteristics of strain YIT 12060T and other members of the genus Alistipes

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<tbody>
<tr>
<td>Isolation source</td>
<td>Human faeces</td>
<td>Human faeces</td>
<td>Appendix tissue</td>
<td>Abdominal abscess</td>
<td>Appendix tissue</td>
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<tr>
<td>Morphology</td>
<td>Coccolid to rods</td>
<td>Slender rods</td>
<td>Straight rods</td>
<td>Slender rods</td>
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<td>Products from PYG</td>
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<td>Sap†</td>
<td>Sap†</td>
<td>Sap</td>
<td>Sap</td>
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<td>Aesculin hydrolysis</td>
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<td>−</td>
<td>+</td>
<td>+</td>
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<td>Indole production</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Catalase</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Resistance to 20 % bile</td>
<td>−</td>
<td>−†</td>
<td>+†</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>55.2</td>
<td>35</td>
<td>57</td>
<td>58</td>
<td>56</td>
</tr>
<tr>
<td>Major cellular fatty acid</td>
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<td>NA</td>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
</tr>
<tr>
<td>Major quinones</td>
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<td>NA</td>
<td>NA</td>
<td>NA</td>
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<tr>
<td>Enzyme activity‡</td>
<td></td>
<td></td>
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<tr>
<td>N-Acetyl-β-glucosaminidase</td>
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<td>NA</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Chymotrypsin</td>
<td>−</td>
<td>−†</td>
<td>+†</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>α-Galactosidase</td>
<td>NA</td>
<td>NA</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>+</td>
<td>+†</td>
<td>−†</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>β-Glucosidase</td>
<td>+</td>
<td>−†</td>
<td>−†</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>α-Fucosidase</td>
<td>+</td>
<td>−†</td>
<td>−†</td>
<td>−</td>
<td>−</td>
</tr>
</tbody>
</table>

*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 12061T were iso-C<sub>15:0</sub> (52.5 %), C<sub>16:1</sub>ω9c (10.8 %) and anteiso-C<sub>15:0</sub> (8.8 %); other fatty acids detected (>1 %) were C<sub>16:0</sub> (3.4 %), C<sub>14:0</sub> (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<sub>17:0</sub>ω3t and C<sub>18:1</sub>ω7t, C<sub>18:2</sub>ω9,12c were also detected. Major characteristics and similarity values between the 16S rRNA genes of strain YIT 12061T and other members of the genus Odoribacter are shown in Table 2.

An almost-complete 16S rRNA gene sequence of strain YIT 12061T was determined (1478 bp) and database searches revealed the highest sequence similarity to that of the type strain of Odoribacter splanchicus (89.6 %; Table 2). Phylogenetic analysis of these and other related sequences was performed and the data confirmed that strain YIT 12061T was phylogenetically most closely associated with O. splanchicus 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. splanchicus, formerly classified as Bacteroides splanchicus 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 12061T (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 12061T 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 12061T 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 12061T 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 12061T 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 12061T and other members of the genus Odoribacter

Strains: 1, YIT 12061T; 2, O. splanchnicus; 3, O. denticanis B106T. Data for strain YIT 12061T are from this study. Data for O. splanchnicus (the type and 11 other strains) and O. denticanis B106T are from Holdeman et al. (1984) and Hardham et al. (2008), respectively, except where otherwise indicated. +, Positive; −, negative; NA, no data available; tr, trace.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolation source</td>
<td>Human faeces</td>
<td>Human faeces, vagina and occasionally from abdominal infection</td>
<td>Crevicular spaces of canine periodontitis patients</td>
</tr>
<tr>
<td>Morphology</td>
<td>Pleomorphic rod-shaped</td>
<td>Rods</td>
<td>Fusiform-shaped</td>
</tr>
<tr>
<td>Cell dimensions (μm)</td>
<td>0.4–1.9 x 1.4–19.1</td>
<td>0.7 x 1.0–5.0</td>
<td>5.9*</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>42.4</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Major products from PY or PYG†</td>
<td>sa(rib)</td>
<td>SAPbivib(l)</td>
<td>NA</td>
</tr>
<tr>
<td>Sugar utilization</td>
<td>Asaccharolytic</td>
<td>Saccharolytic</td>
<td>Asaccharolytic</td>
</tr>
<tr>
<td>Catalase</td>
<td>+</td>
<td>+ §</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of gelatin</td>
<td>+</td>
<td>tr</td>
<td>NA</td>
</tr>
<tr>
<td>Resistance to 20% bile</td>
<td>–</td>
<td>+</td>
<td>NA</td>
</tr>
<tr>
<td>Major cellular fatty acids</td>
<td>iso-C15:0, C14:1t,9c, anteiso-C15:0</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

Similarity values (%) with 16S rRNA gene sequences from:
1. O. laneus YIT 12061T 100 89.6 86.2
2. O. splanchnicus NCTC 10825T 100 85.4 83.4
3. O. denticanis B106T 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. indis-\_tinctus 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, coccoïd to rod-shaped with round ends and are strictly anaerobic. Cells are approximately 0.5–0.7 x 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 D-xylose. Acid production from L-arabinose, from cellobiose, glucose, lactose, maltose, D-mannose, melezitose, raffinose, L-rhamnose, salicin, sucrose, trehalose and D-xylene. 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, glutamyl glutamic acid arylamidase, leucyl glycine arylamidase, z-fucosidase, z-galactosidase, β-galactosidase and β-glucosidase, and weakly positive for acid phosphatase, esterase lipase (C8), esterase (C4), naphthol-AS-BI-phosphohydrolase and z-arabinosidase. Depending on the micro-test kit used, variable results are obtained for z-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), z-mannosidase, phenylalanine arylamidase, proline arylamidase, pyroglycamic 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-C15:0, C14:1t,9c, C15:0, C16:0, iso-C16:0, anteiso-C15:0 and an unknown fatty acid (ECL 17.879).

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

F. Nagai and others

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International Journal of Systematic and Evolutionary Microbiology 60
**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 (0.4–1.9 × 1.4–19.1 μm) that hydrolyse gelatin and are positive for indole production. Catalase, urase 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-C₁₅:₀, C₁₈:₁ω9c and anteiso-C₁₅:₀. 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, β-glucosidase, glutamic acid decarboxylase, glutamyl glutamic acid phosphohydrolase and β-galactosidase. Weak activity is detected for naphthol-AS-BI-phosphate arylsulphatase, α-l-fucosidase, β-galactosidase, β-galactosidase, α-D-mannosidase, 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 12061ᵀ (=DSM 22474ᵀ=JCM 16069ᵀ), was isolated from human faeces. The DNA G+C content of the type strain is 42.4 mol%.

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**References**


