Falsiporphyromonas endometrii gen. nov., sp. nov., isolated from the post-partum bovine uterus, and emended description of the genus Porphyromonas

Shah and Collins 1988

K. Wagener, 1,2 M. Drillich, 2 S. Baumgardt, 3 P. Kämpfer, 4 H.-J. Busse 3 and M. Ehling-Schulz 1

1 Abteilung für Funktionelle Mikrobiologie, IBMH, Department für Pathobiologie, Veterinärmedizinische Universität, A-1210 Wien, Austria
2 Abteilung für Bestandsbetreuung bei Wiederkäuern, Klinik für Wiederkäuern, Veterinärmedizinische Universität, A-1210 Wien, Austria
3 Abteilung für Klinische Mikrobiologie und Infektionsmedizin, IBMH, Department für Pathobiologie, Veterinärmedizinische Universität, A-1210 Wien, Austria
4 Institut für Angewandte Mikrobiologie, Justus-Liebig Universität Giessen, D-35392 Giessen, Germany

Two black-pigmented, anaerobic bacterial strains, designated LMM 40 T and LMM 41, were isolated from the bovine post-partum endometrium of two Holstein cows. The 16S rRNA gene sequences of the two strains were identical and showed the highest similarity to the 16S rRNA gene sequence of the type strain of Porphyromonas crevioricanis (90.2 %) but only 85.1 % 16S rRNA gene sequence similarity to the type strain of the type species of the genus Porphyromonas, Porphyromonas asaccharolytica. The major fatty acid profiles of the two strains were similar to those of species of the genus Porphyromonas, containing iso-C15 : 0 as the major component and moderate amounts of anteiso-C15 : 0, iso-C13 : 0, C15 : 0 and C16 : 0. Hydroxylated fatty acids, such as iso-C14 : 0 3-OH, iso-C16 : 0 3-OH and iso-C17 : 0 3-OH, were also detected. The quinone profiles were dominated by the menaquinones MK-8 and MK-9, while spermidine was the major polyamine. The polar lipid profiles contained major amounts of phosphatidylethanolamine, an unidentified phospholipid, an unidentified aminophospholipid and two unidentified lipids and minor amounts of phosphatidyglycerol, an unidentified aminolipid, a second unidentified aminophospholipid and an unidentified glycolipid. The cell-wall peptidoglycan contained meso-diaminopimelic acid. The genomic DNA G+C contents of LMM 40 T and LMM 41 were 40.7 and 41.3 mol%, respectively. Based on a polyphasic approach, including phylogenetic analysis, physiological and biochemical tests as well as metabolic fingerprinting, it is proposed that the two strains are members of a novel genus and species, for which the name Falsiporphyromonas endometrii is proposed. The type strain of Falsiporphyromonas endometrii is LMM 40 T (= DSM 27210 T = CCUG 64267 T). An emended description of the genus Porphyromonas is also presented.

The genus Porphyromonas represents a deeply branching clade within the phylum Bacteroidetes. The interspecies 16S rRNA gene sequence variability within the genus is generally high. For instance, the type strains of Porphyromonas asaccharolytica and P. catoniae show a 16S rRNA gene sequence divergence of 15.6 %. Chemotaxonomically, the genus Porphyromonas is known for quinone profiles dominated by menaquinone MK-9 or MK-10 and fatty acid profiles predominated by iso-methyl-branched acids, with the major compound iso-C15 : 0, and lower levels of straight-chain saturated acids. Shah & Collins (1988) proposed lysine

Abbreviations: Dpm, diaminopimelic acid; FT-IR, Fourier-transform infrared.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains LMM 40 T and LMM 41 are respectively HF969314 and HF969313. The accession numbers for the rpoB and hsp60 sequences of strains LMM 40 T and LMM 41 are HF969317 and HF969316 (rpoB) and HG423150 and HG423151 (hsp60), respectively. The accession number for the rpoB sequence of P. crevioricanis CCUG 47794 T, also determined in this study, is HF969315.

Two supplementary figures are available with the online version of this paper.
to be the diagnostic peptidoglycan diamino acid for the genus *Porphyromonas*. However, Schleifer & Kandler (1972) reported previously that typical Gram-negative-staining bacteria, nowadays assigned either to the phyla *Proteobacteria* or *Bacteroidetes*, contain exclusively meso-diaminopimelic acid (mDpm) as the peptidoglycan diamino acid; therefore, the description of lysine as the diagnostic peptidoglycan diamino acid for *Porphyromonas* was quite unusual. Since no further species of the genus *Porphyromonas* have been analysed for their diagnostic diamino acids, the observations of Shah & Collins (1988) have never been confirmed with results from related species, although a number of novel species of the genus *Porphyromonas* have been isolated from various clinical samples of human and animal origin during the last two decades (Shah et al., 2009).

Occasionally, members of the genus *Porphyromonas* have been recovered from cows with necrotic vulvovaginitis, bovine interdigital necrobacillosis and retained fetal membranes (Driilich et al., 2001; Sweeney et al., 2009; Blum et al., 2012). Previous studies, using culture-independent pyrosequencing methods, indicated that the bovine uterus is a habitat of species of the genus *Porphyromonas* and other related anaerobes (Machado et al., 2012). During a comprehensive study of the uterine bacterial flora by means of Fourier-transform infrared (FT-IR) spectroscopy, strains LMM 40T and LMM 41 attracted our attention. The strains were isolated from the endometrium of two Holstein cows 9 days after calving, using a previously described technique (Kasimanickam et al., 2004). Primary cultivation was performed anaerobically on Columbia sheep blood agar (Oxoid). After isolation, bacteria were subjected to FT-IR spectroscopy followed by chemometric analysis as described previously (Fricker et al., 2011). Spectra were recorded using an HTS-XT microplate adaptor coupled to a Tensor 27 FT-IR spectrometer (Bruker Optics) in the transmission mode, covering the spectral range 3000–700 cm⁻¹. Data analysis of IR spectra was carried out using the OPUS software (version 5.5; Bruker Optics). For hierarchical cluster analysis, second derivatives of the original spectra were calculated and spectral windows from 3030 to 2830, 1350 to 1200 and 900 to 700 cm⁻¹ were used with weight factor 1, repro-level 30. Strains LMM 40T and LMM 41 were clearly differentiated from other intrauterine anaerobes (not shown), and no similar spectra were found in our database.

Partial 16S rRNA genes of strains LMM 40T and LMM 41 were amplified using universal sequencing primers described by Stackebrandt & Liesack (1992). Purified PCR products were sequenced on an ABI PRISM 3730xl automated DNA sequencer (Applied Biosystems) by Eurofins MWG Operon (Ebersberg, Germany). The FinchTV software version 1.4 (Geospiza) was used for sequence editing. Sequence similarity searches using the EzTaxon server (http://eztaxon-e.ezbiocloud.net; Kim et al., 2012) showed that the 16S rRNA gene sequences of strains LMM 40T and LMM 41 were identical and that the closest relatives were the type strains of *Porphyromonas crevioricanis* and *P. gulae*, respectively showing 90.2 and 88.8% similarity. The similarity to the type strain of the type species of the genus, *P. asaccharolytica* CCUG 7834T, was only 85.1%. The sequence divergence of 15% from the type species of the genus *Porphyromonas* demonstrates unambiguously that the two isolates are representatives of a novel species and are potentially members of a hitherto-unknown genus. The CLC Main Workbench 6.7 software (CLC bio) and the MEGA software package (Tamura et al., 2011) were used for phylogenetic analyses. Using the maximum-likelihood algorithm, strains LMM 40T and LMM 41 formed a distinct branch, with the type strain of *P. crevioricanis* being their closest neighbour (Fig. 1). In addition to the 16S rRNA gene, two other genes were analysed that have been shown previously to be suitable genetic markers for classification of Gram-negative anaerobic rods (Ko et al., 2007; Sakamoto & Ohkuma, 2010). Partial *rpoB* genes of the two isolates and *P. crevioricanis* CCUG 47794T were amplified using primers and conditions described previously (Ko et al., 2007). The two isolates showed 100% identity in analyses of the nucleotide sequences (335 bp length), suggesting that the isolates are members of a single species. A comparison of *rpoB* sequences revealed that *P. crevioricanis* CCUG 47794T is the closest relative of LMM 40T (76% nucleotide and 98% amino acid sequence similarity, respectively), whereas *P. asaccharolytica* is only distantly related (73 and 87% similarity, respectively, to the type strain). Partial *hsp60* genes of LMM 40T and LMM 41 were amplified using the newly designed primers HSPP50F (5'-GTGGTATNGAYAARGCWGT-3') and HSPP60R (5'-ACN-GCACANAYCTTNAG-3'). Similarly to the *rpoB* gene, the *hsp60* gene sequences of LMM 40T and LMM 41 showed 100% nucleotide identity in the analysed sequence (400 bp), and *P. crevioricanis* JCM 15906T clustered closest to LMM 40T. However, sequence analysis revealed only weak relatedness of the two novel strains to the type strains of *P. crevioricanis* and *P. asaccharolytica* (77 and 71% similarity in the nucleotide sequence and 84 and 72% in the amino acid sequence, respectively). As shown in Fig. 2, strains LMM 40T and LMM 41 form a distinct branch within the members of the genus *Porphyromonas*.

In summary, the results of housekeeping gene sequence analysis corroborate the results from 16S rRNA gene sequence analyses, providing clear evidence that LMM 40T and LMM 41 are only distantly related to hitherto-known species of the genus *Porphyromonas* (Figs 2 and S1, available in IJSEM Online).ERIC PCR, carried out as described previously (Loncaric et al., 2011), also clearly distinguished the two isolates from the type strains of *P. crevioricanis* and *P. asaccharolytica* (77 and 71% similarity in the nucleotide sequence and 84 and 72% in the amino acid sequence, respectively).
fingerprints, suggesting that the two isolates included in this study represent distinct strains. The DNA G+C contents of LMM 40\textsuperscript{T} and LMM 41, analysed by the Identification Service of the German Collection of Microorganisms (DSMZ), were 40.7 and 41.3 mol\%, respectively.

Throughout this study, bacteria were grown in tryptic soy broth (Oxoid) enriched with haemin (1 μg ml\textsuperscript{-1}; BD) and vitamin K\textsubscript{1} (0.1 μg ml\textsuperscript{-1}; BD), on Brucella blood agar supplemented with vitamin K\textsubscript{1} and haemin (BD) or on Columbia agar with 5% sheep blood (Oxoid) at 37°C under anaerobic conditions using GENbag or GENbox (bioMérieux). P. crevioricanis CCUG 47794\textsuperscript{T} and P. asaccharolytica CCUG 7834\textsuperscript{T} were used for comparative analyses. On Columbia sheep blood agar, strains LMM 40\textsuperscript{T} and LMM 41 showed active growth at 23–41°C, with optimal growth at 37°C. Black pigmentation of the bacteria was noted on Columbia sheep blood agar after 12 days and on Brucella blood agar after 6 days of incubation at 37°C. Gram-staining was performed as described in the manufacturer’s instructions (Merck) for the Gram-colour stain set; cells of both strains stained Gram-negative. Cell morphology was studied using an Olympus light microscope at a magnification of ×1000. Cells grew as short rods (0.4–0.5 × 1.3–2.3 μm) after 2–4 days of incubation; occasionally, filamentous cells (0.4–0.5 × 4.4–12.1 μm) were observed after prolonged incubation. Biochemical characterization was carried out using API 20A, API ZYM and Rapid ID 32A strips (bioMérieux). API strips were inoculated and cultivated for 2 days at 37°C. The results for strains LMM 40\textsuperscript{T} and LMM 41 are provided in the description of the species.

Respiratory quinones and polar lipids were extracted and analysed using the methods described by Altenburger \textit{et al.} (1996) and Tindall (1990a, b). HPLC analyses of quinones and polyamines were carried out using the HPLC instrumentation reported by Stolz \textit{et al.} (2007). The quinone systems of strains LMM 40\textsuperscript{T} and LMM 41 showed a high degree of similarity; the predominant quinones of strain LMM 40\textsuperscript{T} were menaquinones MK-8 (56.7%) and MK-9 (31.4%) and those of strain LMM 41 were MK-8 (51.1%) and MK-9 (36.8%). Furthermore, minor amounts of MK-7 (7.3 and 5.3%, respectively) and MK-10 (4.3 and 5.8%, respectively) and traces of MK-6 (<1.0%) were detected. A clearly different quinone system was detected in P. crevioricanis CCUG 47794\textsuperscript{T}, consisting mainly of MK-9 (34.5%) and MK-10 (53.4%), with minor amounts of MK-8 (9.0%), MK-11 (2.5%) and MK-7 (0.6%). This quinone system perfectly matches that reported previously for the type strain and a second strain of \textit{P. crevioricanis}; Sakamoto & Ohkuma (2013) reported a quinone system predominated by MK-9 (30.7–33.9%), MK-10 (49.6–59.6%) and MK-8 (6.7–13.4%). These results also indicate that there is a rather low variability...
in the quinone system depending on growth conditions. Analysis of the quinone system of *P. asaccharolytica* CCUG 7834^T, carried out in this study, confirmed the results reported previously by Shah & Collins (1980). The quinone system of *P. asaccharolytica* CCUG 7834^T was composed of MK-10 (66.2%), MK-11 (22.2%), MK-9 (11.3%) and traces of MK-8 (1.0%). The polar lipid profiles of strains LMM 40^T (Fig. 4a) and LMM 41 (results not shown) were dominated by phosphatidylethanolamine, an unidentified phospholipid (PL1), an unidentified aminophospholipid (APL1) and two unidentified lipids (L1, L2) that were not stainable with molybdenum blue, ninhydrin or α-naphthol. Minor amounts of phosphatidylglycerol, an unidentified aminolipid (AL1), a second unidentified aminophospholipid (APL3) and an unidentified glycolipid (GL1) were also detected. *P. crevioricanis* CCUG 47794^T showed a similar polar lipid profile, but differed in the absence of AL1 and L2, the presence of relatively large amounts of a second unknown phospholipid (PL2) and an unidentified aminophospholipid (APL2) and minor amounts of another unknown aminophospholipid (APL4) and a second unknown aminolipid (AL2) (Fig. 4b). The polar lipid profile of *P. asaccharolytica* CCUG 7834^T (Fig. 4c) showed striking differences. The presence of phosphatidylethanolamine and phosphatidylglycerol observed in the species of the genus *Porphyromonas* included in this study is in accordance with previous reports (Korachi *et al.*, 2001;...
Tavana et al., 2000). However, in general, information on the complexity and divergence of the polar lipid profile within the genus is rather limited.

Polyamines were harvested in the stationary growth phase, extracted and analysed as reported by Busse & Auling (1988) and Busse et al. (1997). Spermidine was identified as the major polyamine in LMM 40T and LMM 41 [8.8 and 10.0 μmol (g dry weight)⁻¹, respectively] for P. crevioricanis CCUG 47794T and P. asaccharolytica CCUG 7834T [22.3 and 6.2 μmol (g dry weight)⁻¹, respectively]. Trace amounts [≤0.1 μmol (g dry weight)⁻¹] of putrescine, cadaverine, homospermidine and spermine were also detected in all strains. This polyamine pattern, with spermidine as the predominant compound, is in good agreement with reports on polyamine patterns in P. asaccharolytica, P. endodontalis, P. gingivalis, P. levii, P. macacae (Hosoya & Hamana, 2004) and P. canoris (Hamana et al., 2008).

Fatty acids were extracted from freeze-dried biomass harvested at the stationary growth phase. Fatty acid analysis, which was carried out according to Kämpfer & Kroppenstedt (1996), revealed that the major fatty acid of strains LMM 40T and LMM 41 was iso-C₁₅:0 (Table 1). Moderate amounts of iso-C₁₃:₀, C₁₄:₀, anteiso-C₁₅:₀, C₁₆:₀ and iso-C₁₇:₀ 3-OH were also detected. Additionally, minor amounts of iso-C₁₁:₀, C₁₂:₀, anteiso-C₁₃:₁ at 12–13, iso-C₁₅:₀ 3-OH, iso-C₁₇:₀, iso-C₁₆:₀ 3-OH and C₁₆:₀ 3-OH were detected. The fatty acid profiles of P. crevioricanis CCUG 47794T and P. asaccharolytica CCUG 7834T showed quantitative differences in the presence of the major fatty acids and are distinguished from those of strains LMM 40T and LMM 41 by the absence of iso-C₁₁:₀, C₁₂:₀ and anteiso-C₁₃:₁ at 12–13. The lack of C₁₀:₀ and the presence of iso-C₁₆:₀ 3-OH distinguished P. asaccharolytica CCUG 7834T from P. crevioricanis CCUG 47794T. As observed for P. asaccharolytica CCUG 7834T, strains LMM 40T and LMM 41 lack C₁₀:₀, which further discriminates them from P. crevioricanis CCUG 47794T.

Analysis of the diamino acids in the cell walls of LMM 40T, LMM 41, P. crevioricanis CCUG 47794T and P. asaccharolytica CCUG 7834T as described by Schleifer (1985) showed that the peptidoglycan contains mDPm. The detection of mDPm in P. asaccharolytica disagrees with previous results from Shah & Collins (1988), who reported the presence of lysine in the type species of the genus Porphyromonas and listed the presence of this diamino acid as a characteristic in the genus description. However, our observation of mDPm in P. asaccharolytica

### Table 1. Cellular fatty acid compositions of strains LMM 40T and LMM 41 and reference strains

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>C₁₀:₀</td>
<td></td>
<td></td>
<td></td>
<td>0.7</td>
</tr>
<tr>
<td>iso-C₁₁:₀</td>
<td>0.8</td>
<td>0.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C₁₂:₀</td>
<td>1.3</td>
<td>0.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C₁₃:₀</td>
<td>7.0</td>
<td>4.2</td>
<td>3.1</td>
<td>1.1</td>
</tr>
<tr>
<td>anteiso-C₁₃:₁ at 12–13</td>
<td>0.8</td>
<td>0.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C₁₄:₀</td>
<td>6.3</td>
<td>4.9</td>
<td>2.6</td>
<td>2.2</td>
</tr>
<tr>
<td>iso-C₁₅:₀</td>
<td>49.2</td>
<td>48.7</td>
<td>55.5</td>
<td>54.3</td>
</tr>
<tr>
<td>anteiso-C₁₅:₀</td>
<td>6.1</td>
<td>6.4</td>
<td>1.3</td>
<td>4.8</td>
</tr>
<tr>
<td>C₁₆:₀</td>
<td>5.2</td>
<td>6.4</td>
<td>5.1</td>
<td>3.4</td>
</tr>
<tr>
<td>iso-C₁₅:₀ 3-OH</td>
<td>1.1</td>
<td>0.9</td>
<td>4.6</td>
<td>0.9</td>
</tr>
<tr>
<td>iso-C₁₇:₀</td>
<td>2.0</td>
<td>2.5</td>
<td>5.3</td>
<td>6.6</td>
</tr>
<tr>
<td>iso-C₁₆:₀ 3-OH</td>
<td>2.0</td>
<td>2.2</td>
<td></td>
<td>1.0</td>
</tr>
<tr>
<td>C₁₆:₀ 3-OH</td>
<td>0.9</td>
<td>1.1</td>
<td>1.2</td>
<td>0.7</td>
</tr>
<tr>
<td>iso-C₁₇:₀ 3-OH</td>
<td>7.9</td>
<td>9.7</td>
<td>17.7</td>
<td>17.7</td>
</tr>
</tbody>
</table>

Data were obtained in this study and represent percentages of total fatty acids. –, Not detected.
CCUG 7834\textsuperscript{T} and \textit{P. crevioricanis} CCUG 47794\textsuperscript{T} supports the assumption of Schleifer & Kandler (1972) that all Gram-negative bacteria are characterized by peptidoglycan type A1\gamma; a three-digit code, indicating the presence of mLpm. The latter assumption is also supported by other analyses of diamino acids of the peptidoglycan of well-characterized type strains of species of the phylum \textit{Bacteroidetes}, which showed the presence of mLpm (Buczolits \textit{et al.}, 2002). mLpm is also listed as a characteristic in the description of the genus \textit{Prevotella}, which harbours several former species of the genus \textit{Bacteroides} (Hammann & Werner, 1981; Shah & Collins, 1990).

Currently, the genus \textit{Porphyromonas} comprises 15 species, including the type species \textit{P. asaccharolytica}. The majority of species share 16S rRNA gene sequence similarities with the type species in the range 84–88\%. Such a high degree of 16S rRNA gene sequence variability in other lines of descent would indicate members of different genera or even families. Within the 16S rRNA gene similarity range mentioned above, two species from other genera are also found, \textit{Tannerella forsythia} and \textit{Dysgonomonas gadei}. The type strains of the latter two species share 85.2 and 84.7\% 16S rRNA gene sequence similarity, respectively, with the type strain of \textit{P. asaccharolytica}. The phylogenetic distance of the majority of species of the genus \textit{Porphyromonas} from \textit{P. asaccharolytica}, as indicated by low 16S rRNA gene sequence similarity, is also reflected in the heterogeneity observed in the polar lipid profiles (Fig. 4) and quinone systems. Except for the data from our current study, few detailed polar lipid analyses have been carried out for other species of the genus \textit{Porphyromonas} and, when they have been attempted, the data are not directly comparable (Tavana \textit{et al.}, 2000). The heterogeneity of the genus regarding the quinone system, containing either MK-9 (\textit{P. gingivalis}) or MK-10 (\textit{P. asaccharolytica}), was already mentioned in the description of the genus \textit{Porphyromonas} by Shah & Collins (1988). Another species, \textit{P. levii} (formerly \textit{Bacteroides levii}), also contains predominantly MK-9 (Shah & Collins, 1980). An additional quinone system composed of menaquinones MK-10 and MK-9 is characteristic of \textit{P. crevioricanis} (Sakamoto & Ohkuma, 2013; this study). Phylogenetically, the two species that exhibit MK-9 as the predominant respiratory quinone are located on separate branches within the \textit{Porphyromonas} clade, clearly separated from the branch bearing \textit{P. asaccharolytica} (Fig. 1). \textit{P. crevioricanis}, with MK-10 and MK-9, forms another branch with strains LMM 40\textsuperscript{T} and LMM 41 and is also clearly separated from \textit{P. asaccharolytica}. In summary, these data (low 16S rRNA sequence similarities and heterogeneity in the polar lipid and quinone systems) indicate that the genus \textit{Porphyromonas} should be dissected into three genera or even more. However, such a reclassification should await the availability of data from further detailed analyses of quinones, polar lipids and housekeeping gene sequences of the majority of species of the genus \textit{Porphyromonas} and is beyond the scope of this study.

Identical 16S rRNA gene sequences, identical sequences of the genotypic markers \textit{rpoB} and \textit{hsp60} and the highly similar quinone systems and fatty acid and polar lipid profiles demonstrate that the two isolates can be considered to be strains of a novel, as-yet undescribed species within the family \textit{Porphyromonadaceae}. The 16S rRNA gene sequence similarity of less than 86\% to \textit{P. asaccharolytica}, the type species of the genus \textit{Porphyromonas}, is within the range of similarities found among other established species of the genus, and would allow classification of the two strains within a species of the genus \textit{Porphyromonas}. However, the two isolates clearly differ from \textit{P. crevioricanis} and \textit{P. asaccharolytica} with respect to conserved chemotaxonomic markers in the quinone system and polar lipid profiles as well as in their metabolic fingerprints determined by FT-IR. Hence, their classification within a novel species of the genus \textit{Porphyromonas} would create an even more heterogeneous genus, which is not desirable. The phylogenetic distance from the type species of the genus \textit{Porphyromonas}, \textit{P. asaccharolytica}, and the most closely related species, \textit{P. crevioricanis}, as well as the presence of distinguishing chemotaxonomic traits, suggest the placement of the two isolates in a novel genus and species, for which we propose the name \textit{Falsiporphyromonas endometrii} gen. nov., sp. nov.

The detection of the peptidoglycan diamino acid mLpm rather than lysine [as reported by Shah & Collins (1988)] in the type species of the genus \textit{Porphyromonas}, \textit{P. asaccharolytica}, and a second species, \textit{P. crevioricanis}, is in good agreement with data from related species and illustrates the conserved character of this trait. Hence, an emended description of the genus \textit{Porphyromonas} is needed.

**Emended description of the genus \textit{Porphyromonas}**

Shah and Collins 1988

The description is as given by Shah & Collins (1988) with the exception that the characteristic diamino acid of the peptidoglycan is meso-diaminopimelic acid, not lysine.

**Description of \textit{Falsiporphyromonas} gen. nov.**

\textit{Falsiporphyromonas} (Fal’si.por.phy.ro.mo’nas. L. adj. falsus false; N.L. fem. n. Porphyromonas a bacterial genus name; N.L. fem. n. \textit{Falsiporphyromonas} false \textit{Porphyromonas}).

Cells are obligately anaerobic, Gram-negative, non-spor-forming rods (0.4–0.5 \times 1.3–2.3 \textmu m). Occasionally, filamentous cells (0.4–0.5 \times 4.4–12.1 \textmu m) are observed after longer incubation. The fatty acid profile is dominated by iso-branched acids and the major acid is iso-C\textsubscript{15:0} 3-OH fatty acids detected include iso-C\textsubscript{15:0} 3-OH, iso-C\textsubscript{16:0} 3-OH, iso-C\textsubscript{17:0} 3-OH and C\textsubscript{18:0} 3-OH. The polar lipid profile contains phosphatidylethanolamine, an unidentified phospholipid (PL1), an unidentified aminophospholipid (APL1), two unidentified lipids (L1, L2) and minor amounts of phosphatidyglycerol, an unidentified aminolipid (AL1), a second unidentified aminophospholipid (APL3) and an unidentified glycolipid (GL1). The quinone system contains...
predominantly menaquinones MK-8 and MK-9. Spermidine is the major compound in the polyamine pattern. meso-Diaminopimelic acid is the diamino acid of the cell-wall peptidoglycan. The DNA G+C content of the type strain of the type species is 40.7 mol%. The type species is Falsiporphyromonas endometrii.

Description of Falsiporphyromonas endometrii sp. nov.

Falsiporphyromonas endometrii (en.do.me’tri.i. N.L. gen. n. endometrii of the endometrium, referring to the isolation of the first strains).

Displays the following properties in addition to those described for the genus. Exhibits good growth in tryptic soy broth enriched with haemin (1 µg ml⁻¹) and vitamin K₁ (0.1 µg ml⁻¹), on Brucella blood agar supplemented with vitamin K₁ and haemin and on Columbia agar with 5% sheep blood. On Columbia sheep blood agar, shows active growth at 23–41 °C, with optimal growth at 37 °C. After incubation for 7 days on Columbia agar with 5% sheep blood, colonies are 1–2 mm in diameter, entire and convex. Black pigmentation is observed on Columbia sheep blood agar after 12 days at 37 °C and on Brucella blood agar after 6 days at 37 °C. Catalase- and oxidase-negative. In the API 20A system, positive for indole production and gelatin digestion and negative for ascusil hydrolisys and urease and catalase activities. None of the carbohydrates in the API 20A strip are fermented. Positive in the API ZYM system for alkaline and acid phosphatases and naphthol-AS-BI-phosphohydrolase and negative for esterase, esterase lipase, alkaline and acid phosphatases and naphthol-AS-BI-phosphohydrolase and negative for esterase, esterase lipase, alkaline and acid phosphatases and naphthol-AS-BI-phosphohydrolase. Positive in the Rapid ID 32A strip for indole production, alkaline phosphatase, leucine arylamidase, alanine arylamidase and glutamyl glutamic acid arylamidase and negative for urease, arginine dihydrolase, x-galactosidase, β-galactosidase, β-glucuronidase, x-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, x-mannosidase and x-fucosidase. Positive in the Rapid ID 32A strip for indole production, alkaline phosphatase, leucine arylamidase, alanine arylamidase and glutamyl glutamic acid arylamidase and negative for urease, arginine dihydrolase, x-galactosidase, β-galactosidase, β-galactosidase-6-phosphate, x-glucosidase, β-glucosidase, x-arabinosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, arginine arylamidase, proline arylamidase, leucyl glycine arylamidase, phenylalanine arylamidase, leucine arylamidase, pyrogalluc acid arylamidase, tyrosine arylamidase, glycine arylamidase, glutamic acid decarboxylase, x-fucosidase, histidine arylamidase, serine arylamidase, mannose fermentation, raffinose fermentation and reduction of nitrites.

The type strain LMM 40T (=DSM 27210T=CCUG 64267T) and a second strain LMM 41 were isolated from the endometrium of two Holstein cows in Klein Bennebek, Germany.

Acknowledgements

We are grateful to J. P. Euzéby for advice regarding nomenclature and etymology and thank I. Loncaric for his assistance with ERIC PCR.

References


