**Dysgonomonas gen. nov. to accommodate Dysgonomonas gadei sp. nov., an organism isolated from a human gall bladder, and Dysgonomonas capnocytophagoides (formerly CDC group DF-3)**

Tor Hofstad,¹ Ingar Olsen,² Emenike R. Eribe,² Enevold Falsen,³ Matthew D. Collins⁴ and Paul A. Lawson⁴

Results of a polyphasic taxonomic study on an unknown Gram-negative, facultatively anaerobic, coccobacillus-shaped organism isolated from an infected human gall bladder are presented. Phenotypic and molecular taxonomic studies revealed the organism to be close to, but distinct from, organisms designated CDC (Centers for Disease Control and Prevention) group DF-3. The unknown bacterium was readily distinguished from reference strains of *Bacteroides*, *Prevotella*, *Porphyromonas* and related taxa by 16S rRNA gene sequencing, biochemical tests, analysis of cellular long-chain fatty acids and electrophoretic analysis of whole-cell proteins. Based on the results of the present study, it is proposed that the unknown bacterium be classified in a new genus, *Dysgonomonas*, as *Dysgonomonas gadei* sp. nov. (type strain CCUG 42882T = CIP 106420T). In addition, a new species, *Dysgonomonas capnocytophagoides* sp. nov., is proposed to accommodate strains previously belonging to CDC group DF-3. The type species of the genus *Dysgonomonas* is *Dysgonomonas gadei*.

**Keywords:** taxonomy, phylogeny, *Dysgonomonas*, CDC group DF-3, 16S rRNA

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**INTRODUCTION**

CDC (Centers for Disease Control and Prevention) group DF-3 (dysgonic fermenter 3) is a group of hitherto unclassified, fastidious, facultatively anaerobic, Gram-negative coccobacilli (Wallace et al., 1989). CDC group DF-3 strains grow slowly on blood agar medium, but not on MacConkey agar, ferment several carbohydrates, hydrolyse aesculin, do not reduce nitrate, and are catalase- and oxidase-negative. These organisms have a distinct cellular fatty acid profile characterized by large amounts of straight-chain saturated, anteiso- and iso-methyl branched, and 3-hydroxy long-chain fatty acids (Wallace et al., 1989). Comparative 16S rRNA sequence analysis has indicated that CDC group DF-3 is phylogenetically related to, but nevertheless distinct from *Bacteroides*, *Porphyromonas*, *Prevotella* and related species (Paster et al., 1994; Vandamme et al., 1996). CDC DF-3 isolates are resistant to several antimicrobial agents, including penicillins, cephalosporins, aminoglycosides and ciprofloxacin. Most isolates are susceptible to clindamycin, tetracycline, chloramphenicol, imipenem and trimethoprim/sulfamethoxazole (Gill et al., 1991; Blum et al., 1992). CDC group DF-3 organisms are relatively rare isolates that have been recovered from stool samples, mainly in immunocompromised patients and patients with severe underlying diseases (Blum et al., 1992; Heiner et al., 1992), but also from clinical materials such as blood, wounds and abscesses (Aronson & Zbick, 1988; Bangsborg et al., 1990). The pathogenic potential of the organisms remains unknown. The isolation of organisms with biochemical properties similar, but not identical, to those of CDC group DF-3 (designated CDC group DF-3-like strains).

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**Abbreviation:** CDC, Centers for Disease Control and Prevention.

The GenBank accession number for the 16S rRNA gene sequence of *Dysgonomonas gadei* strain CCUG 42882T is Y18530.
organisms) has also been reported (Daneshvar et al., 1991).

In this study, the cultural and biochemical properties, cellular fatty acid composition and SDS-PAGE protein profile of an isolate, which resembles CDC group DF-3 organisms, recovered from an infected gall bladder are reported. In addition, results of 16S rRNA gene sequencing indicate that the organism represents a new species that clusters together with CDC group DF-3 organisms. It is therefore proposed that a new genus, *Dysgonomonas*, be created to accommodate the new organism isolated from an infected gall bladder classified as *Dysgonomonas gadei* sp. nov. (type strain CCUG 42882T = CIP 106420T) and organisms previously designated CDC group DF-3 be classified as *Dysgonomonas capnocytophagoides* sp. nov. The type species of the genus *Dysgonomonas* is *Dysgonomonas gadei*.

**METHODS**

Source of the organism. Strain CCUG 42882T was originally isolated from a 68-year-old male with known non-insulin-dependent diabetes mellitus and essential hypertension. The patient was admitted to hospital because of fractures of the left tibia and the left third, fourth and fifth metatarsal bones following a car accident. Treatment was conservative. Nine days later, the patient was suddenly ill with fever, chills and vascular collapse. *Escherichia coli* was recovered in blood cultures. Ultrasound scanning of the abdomen, performed a few days later, showed gallstones and a distended gall bladder. Aerobic and anaerobic cultivation of pus (which contained no trace of bile) aspirated from the gall bladder yielded growth of *E. coli*, a *Klebsiella* species and enterococci. In addition, a slow-growing, Gram-negative coccobacillus was recovered by anaerobic cultivation on kanamycin-laked blood agar. The patient was treated with cefuroxime and metronidazole for 2 weeks and recovered.

Cultural and biochemical characterization. The unknown Gram-negative coccobacillus from the infected gall bladder was cultured aerobically at 35 °C in a thermostat supplemented with 7.5% CO₂ on Fastidious Anaerobic Agar (FAA; Lab M) and Columbia agar base (Difco), both of which were supplemented with 5% human blood. Growth requirements for X and V factors were examined using discs impregnated with X factor, V factor or both, and nutrient agar as basal medium. Bile sensitivity was determined by the Oxgall test using Diatabs diagnostic tablets (Rosco) as described by Weinberg et al. (1983). The strain was biochemically characterized by using a combination of conventional tests and the API ID32A, API ID32E and API ZYM systems according to the manufacturer’s instructions (API bioMérieux).

Susceptibility to antimicrobial agents. MICs of a range of antibacterial agents, including penicillins, cephalosporins, glycopeptide antibiotics, aminoglycosides, fluoroquinolones, macrolides, quinolones, chloramphenicol, doxycycline, metronidazole, sulfadiazine and trimethoprim/sulfamethoxazole, were examined using the E-test (AB Biodisk). The tests were performed as recommended by the manufacturers and read after incubation aerobically for 2 d. MIC of metronidazole was determined after 2 d anaerobic incubation (Mart Anoxomat system; Mart Microbiology Automation). FAA, supplemented with 5% human blood, was used as growth medium instead of PDM Antibiotic Sensitivity medium because of poor growth on the latter, even when supplemented with 5% horse blood.

**SDS-PAGE of whole-cell proteins.** To assess the overall phenotypic resemblance of the new isolate and reference species, a comparative analysis of whole-cell protein profiles by SDS-PAGE was performed. PAGE analysis of whole-cell proteins was performed as described by Pot et al. (1994) and Vandamme et al. (1998). For densitometric analysis, normalization and interpretation of protein patterns the GCW 3.0 software package (Applied Maths) was used. The similarity between all pairs of traces was expressed by the Pearson product–moment correlation coefficient, converted for convenience to a percentage similarity.

**Long-chain cellular fatty acid analysis.** Cells were cultured on chocolate agar using Columbia agar base and incubated for 48 h at 37 °C and centrifuged. Saponification, methanolysis, extraction and identification of the fatty acid methyl esters were made using the Microbial Identification system (Microbial ID) as described previously (Moore et al., 1994; Delbel et al., 1997).

**Determination of 16S rRNA gene sequences and phylogenetic analysis.** Phylogenetic determination was performed by comparative 16S rRNA gene sequence analyses. A large fragment of the 16S rRNA gene (corresponding to positions 30–1521 of the *E. coli* 16S rRNA gene) was amplified by PCR using conserved primers close to the 3′ and 5′ ends of the gene. The PCR products were directly sequenced using a *Taq* dye-deoxy terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 373A; Applied Biosystems). The closest known relatives of the new isolate were determined by performing a database search using the program FASTA of the Genetics Computer Group package (Pearson & Lipman, 1985). These sequences and those of other known related strains were retrieved from the EMBL or Ribosomal Database Project databases and those of other known related strains were retrieved from the EMBL or Ribosomal Database Project databases and aligned with the newly determined sequences using the program FILEUP (Devereux et al., 1984). The resulting multiple sequence alignment was corrected manually and approximately 100 bases at the 5′ end of the rRNA were omitted from further analyses because of alignment ambiguities. Pairwise evolutionary distances were then computed from a continuous stretch of 1320 bases using the correction of Jukes & Cantor (1969). A phylogenetic tree was constructed according to the neighbour-joining method with the program NEIGHBOR (Felsenstein, 1989). The stability of the groupings was estimated by bootstrap analysis (500 replications) using the programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE (Felsenstein, 1989).

**RESULTS**

Cultural and biochemical properties

The isolate originating from the infected gall bladder consisted of non-motile, Gram-negative coccobacilli that grew relatively slowly on blood agar. The organism grew with or without the addition of 7.5% CO₂, in addition to growing anaerobically. After 48 h incubation aerobically at 35 °C in a CO₂-enriched atmosphere (7.5%), the colonies were 1–2 mm in
lactose, was produced from fermented with production of acid but no gas. Acid
the organism was resistant to ox bile. Glucose was observed around the Oxgall tablets demonstrating that
and urea were not. Growth and precipitation were
produce indole. Aesculin was hydrolysed, but gelatin
did not produce hydrogen sulphide or acetoin, but did
strictly anaerobic conditions. It was catalase-positive
haem. The organism grew under microaerophilic and
XV discs, suggesting a growth factor dependency for
The coccobacillus grew on nutrient agar around X and
°
43
°C, but not at
C. Growth was not observed on MacConkey agar.

Fig. 1. Similarity dendrogram based on whole-cell protein patterns of Dysgonomonas gen. nov., sp. nov. and related
species. Levels of correlation are expressed as percentages of similarity for convenience.


diameter, non-adherent, entire, grey-white, smooth
and non-haemolytic, and had a slightly aromatic odour. Following incubation for a few more days, the
colonies were somewhat coalesced, butyrous and x-
haemolytic. Growth was obtained at 25 °C, but not at
43 °C. Growth was not observed on MacConkey agar.
The coccobacillus grew on nutrient agar around X and

SDS-PAGE of whole-cell proteins
A numerical analysis of the whole-cell protein patterns
of the unknown bacterium and two CDC group DF-3
strains (CCUG 17996, CCUG 42515) together with
reference strains of Bacteroides, Capnocytophaga and
Prevotella is shown in Fig. 1. The unknown gall
bladder isolate was shown to be separate from the two
DF-3 strains and all reference strains used. The nearest
correlation was with Dysgonomonas gadel

Susceptibility to antimicrobial agents
The unknown clinical isolate was sensitive to metronidazole (MIC 1.5 µg ml⁻¹), clindamycin (MIC
0.25 µg ml⁻¹), doxycycline (MIC 0.19 µg ml⁻¹), imipenem (MIC 0.5 µg ml⁻¹), meropenem (MIC 0.064 µg ml⁻¹) and trimethoprim/sulphamethoxazole
(MIC 0.125 µg ml⁻¹). The organism was resistant to
cefotaxin (MIC 24 µg ml⁻¹) and the other cephalo-
sporins tested [cefotaxime, cefpirome, ceftazidime, ceftriaxone, cefuroxime and cefalothin (MIC
256 µg ml⁻¹)]. In addition, the isolate was resistant to the aminoglycosides [gentamicin (MIC 256 µg ml⁻¹), netilmicin (MIC 256 µg ml⁻¹) and sulphadiazine (MIC
256 µg ml⁻¹)], fluoroquinolones [ciprofloxacin (MIC
32 µg ml⁻¹) and oxafloxacin (MIC 8 µg ml⁻¹)] and the
glycopeptide antibiotics [vancomycin (MIC 48 µg ml\(^{-1}\)) and teicoplanin (MIC 256 µg ml\(^{-1}\))]. The MICs of other antibiotics tested were: ampicillin, 6 µg ml\(^{-1}\); amoxicillin, 6 µg ml\(^{-1}\); amoxicillin/clavulanic acid, 1 µg ml\(^{-1}\); benzylpenicillin, > 32 µg ml\(^{-1}\); erythromycin, 16 µg ml\(^{-1}\); azithromycin, 16 µg ml\(^{-1}\); clarithromycin, 16 µg ml\(^{-1}\); and chloramphenicol, 4 µg ml\(^{-1}\).

**Phylogenetic analysis**

To investigate the genealogical affinity between the unknown bacterium and its relationship with other Gram-negative taxa, comparative 16S rRNA gene sequence analysis was performed. The almost complete gene sequence (> 1400 nt) of the unknown isolate was determined. Sequence searches of GenBank and RDP databases revealed that the unknown isolate was phylogenetically most closely associated with members of the genera *Bacteroides*, *Prevotella* and *Porphyromonas*, which belong to the *Bacteroides* subgroup of the flavobacterium–bacteroides subphylum. A tree constructed by the neighbour-joining method depicting the phylogenetic affinity of the unknown cocobacillus is shown in Fig. 2. The unknown bacterium was phylogenetically placed on the periphery of members of the genus *Porphyromonas* clustering with CDC group DF-3 strain CCUG 17996.

**Table 1.** Composition (%) of cellular fatty acids in strain CCUG 42882\(^{T}\) and CDC group DF-3 strains CCUG 17996\(^{T}\) and 42515

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Strain</th>
<th>DF-3 CCUG 17996(^{T})</th>
<th>DF-3 CCUG 42515</th>
<th>CCUG 42882(^{T})</th>
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<tr>
<td>iso-C(_{12:0})</td>
<td>ND</td>
<td>0.3</td>
<td>1.9</td>
<td></td>
</tr>
<tr>
<td>C(_{13:0})</td>
<td>ND</td>
<td>0.9</td>
<td>ND</td>
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<td>0.5</td>
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<tr>
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<td>3.5</td>
<td></td>
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<tr>
<td>C(_{14:0})</td>
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<td>1.9</td>
<td>1.6</td>
<td></td>
</tr>
<tr>
<td>iso-C(_{14:0})</td>
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<td>12.3</td>
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<td></td>
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<tr>
<td>C(_{15:0})</td>
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<td>14.2</td>
<td>2.9</td>
<td></td>
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<tr>
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<td>19.4</td>
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<tr>
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<td>ND</td>
<td>1.3</td>
<td></td>
</tr>
<tr>
<td>iso-3OH C(_{16:0})</td>
<td>12.3</td>
<td>9.3</td>
<td>10.5</td>
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<tr>
<td>3OH C(_{16:0})</td>
<td>4.6</td>
<td>5.3</td>
<td>7.9</td>
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<tr>
<td>C(_{16:0})</td>
<td>4.7</td>
<td>3.9</td>
<td>1.2</td>
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<tr>
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<td>3.5</td>
<td>ND</td>
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<tr>
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<td>1.6</td>
<td>0.5</td>
<td></td>
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<tr>
<td>anteiso-C(_{17:1})</td>
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<td></td>
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<tr>
<td>2OH C(_{17:0})</td>
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<td>1.8</td>
<td></td>
</tr>
<tr>
<td>C(_{18:0})</td>
<td>ND</td>
<td>1.4</td>
<td>1.1</td>
<td></td>
</tr>
</tbody>
</table>

ND, Not detected.

**Comment**

The percentage fatty acid compositions of strain CCUG 42882\(^{T}\) and two reference CDC group DF-3 strains (CCUG 17996 and CCUG 42515) are given in Table 1. The fatty acids of the unknown isolate CCUG 42882\(^{T}\) were found to be iso-C\(_{14:0}\), anteiso-C\(_{15:0}\), C\(_{16:0}\) and iso-3OH C\(_{16:0}\). This fatty acid pattern was similar to those of the two reference CDC group DF-3 strains examined.

**Cellular fatty acid composition**

The percentage fatty acid compositions of strain CCUG 42882\(^{T}\) and CDC group DF-3 strains (CCUG 17996 and CCUG 42515) are given in Table 1. The fatty acids of the unknown isolate CCUG 42882\(^{T}\) were found to be iso-C\(_{14:0}\), anteiso-C\(_{15:0}\), C\(_{16:0}\) and iso-3OH C\(_{16:0}\). This fatty acid pattern was similar to those of the two reference CDC group DF-3 strains examined.

**Phylogenetic analysis**

To investigate the genealogical affinity between the unknown bacterium and its relationship with other Gram-negative taxa, comparative 16S rRNA gene sequence analysis was performed. The almost complete gene sequence (> 1400 nt) of the unknown isolate was determined. Sequence searches of GenBank and RDP databases revealed that the unknown isolate was phylogenetically most closely associated with members of the genera *Bacteroides*, *Prevotella* and *Porphyromonas*, which belong to the *Bacteroides* subgroup of the flavobacterium–bacteroides subphylum. A tree constructed by the neighbour-joining method depicting the phylogenetic affinity of the unknown cocobacillus is shown in Fig. 2. The unknown bacterium was phylogenetically placed on the periphery of members of the genus *Porphyromonas* clustering with CDC group DF-3 strain CCUG 17996.
Fig. 2. Unrooted tree showing the phylogenetic relationships of *Dysgonomonas* species and some related Gram-negative bacteria. The tree constructed using the neighbour-joining method was based on a comparison of approx. 1327 nt. Bootstrap values, expressed as a percentage of 500 replications, are given at branching points. Scale bar, 1% sequence divergence.

A second strain belonging to CDC group DF-3 (CCUG 42515) was found to be identical to CCUG 17996 (100% sequence similarity in 1420 bases compared). The sequence divergence between strain CCUG 42882$^T$ and CDC group DF-3 strains was 7%.

**DISCUSSION**

It is evident from the findings of this investigation that the bacterium originating from a human gall bladder infection represents a hitherto unrecognized species within the *Bacteroides* subgroup of the flavobacterium–bacteroides subphylum. Phylogenetically, the coccobacillus-shaped bacterium clustered together with strain CDC group DF-3 (93% sequence similarity) and bootstrap resampling showed this relationship to be statistically significant (100% recovery in 500 resamplings). Other taxa displayed significantly lower levels of sequence similarity including *Bacteroides* (85–87%), *Porphyromonas* (84–88%) and *Prevotella* (79–85%) and the misclassified strict anaerobes *Bacteroides distasonis* (86% sequence similarity), *Bacteroides forsythus* (89% sequence similarity), *Bacteroides merdae* (89% sequence similarity) and *Bacteroides splanchnicus* (83% sequence similarity) (Fig. 2). Based on tree topology considerations and sequence divergence values, it is clear that the unknown bacterium cannot be assigned to any of the currently described genera. The association between the unknown bacterium and the CDC group DF-3 strains is, however, very significant and the depth of the cluster formed by the two taxa is indicative of a single genus. Chemotaxonomic findings (analysis of whole-cell proteins and long-chain fatty acids) and its facultative nature also demonstrate the separateness of the unknown clinical isolate from currently named members of the *Bacteroides* subgroup and strongly support its affinity with the CDC group DF-3 strains, which also exhibit a facultative mode of respiration.

Until a more complete inventory of the organisms present within this supercluster of bacteria is established, it is not possible to draw conclusions on the significance of the association of facultative organisms with strict anaerobes. The recovery of the newly
described organism from the diseased gall bladder may be indicative that it was present as an opportunistic pathogen. Moore et al. (1994) found that anteiso-C_{15:0}, iso-C_{15:0}, iso-3OH C_{17:0} and C_{16:0} are the major cellular fatty acids in *Bacteroides* and *Prevotella*. These findings were consistent with earlier studies (Miyagawa et al., 1979; Shah & Collins 1980; Mayberry et al., 1982). There is a general consensus that iso-C_{15:0} is the major fatty acid in *Porphyromonas* strains, accounting for 33–58% of the fatty acids present (Moore et al., 1994). Therefore, the fatty acid profile of strain CCUG 42882T is incompatible with the genus *Porphyromonas*. The fatty acids of the aforementioned strain, however, closely resemble those reported for CDC group DF-3 strains (Daneshvar et al., 1991; Wallace et al., 1989; Table 1). Therefore, based on both phenotypic and phylogenetic findings of this and previous studies, it is proposed that the unknown Gram-negative cocco-bacillus and organisms previously designated CDC group DF-3 merit classification in a new genus, *Dysgonomonas* gen. nov., as *Dysgonomonas gadei* sp. nov. and *Dysgonomonas capnocytophagoides* sp. nov., respectively.

**Description of *Dysgonomonas* gen. nov.**

*Dysgonomonas* (Dys.go.no.mo.nas. N.L. n. Dysgonic a type of fermenter; Gr. fem. n. monas a monad, unit; N.L. fem. n. *Dysgonomonas* a monad from a Dysgonic fermenter).

Cells consist of non-motile, Gram-negative cocco-bacilli to short rods. Growth is not observed on MacConkey agar. Requires X growth factor. Facultatively anaerobic. May be catalase-positive or -negative. Oxidase-negative. Glucose is fermented producing acid but no gas. Alkaline phosphatase is produced but not arginine dihydrolase. Does not reduce nitrate. Hydrogen sulphide and acetoin are not produced. Aesculin may or may not be hydrolysed but gelatin and urea are not. Indole may or may not be produced. The long-chain cellular fatty acids are of the straight-chain saturated, anteiso- and iso-methyl branched and 3-hydroxy types. The G+C content of DNA is 38 mol% (Vandamme et al., 1996). Isolated from human clinical specimens and stool samples. Habitat is not known. The type species is *Dysgonomonas gadei*.

**Description of *Dysgonomonas gadei* sp. nov.**

*Dysgonomonas gadei* (ga’di.ei. N.L. gen. masc. n. gadei of Gade Institute, Bergen, Norway where the organism was first isolated).

Cells consist of non-motile, Gram-negative cocco-bacilli that grow relatively slowly on blood agar. After 48 h incubation aerobically at 35 °C in a CO_{2}-enriched atmosphere, the colonies are 1–2 mm in diameter, non-adherent, entire, grey-white, smooth and non-haemolytic, and have a slightly aromatic odour. Following incubation for a few more days, the colonies become somewhat coalesced, butyrous and α-haemolytic. Growth is obtained at 25 °C but not at 43 °C. Grows under microaerophilic and strictly anaerobic conditions. The organism does not grow on MacConkey agar but grows on nutrient agar around X and XV discs, suggesting a growth factor dependency for haem. The organism is catalase-positive and oxidase-negative. It does not reduce nitrate or produce hydrogen sulphide or acetoin. Aesculin is hydrolysed but gelatin and urea are not. Indole is produced. Resistant to ox bile. Glucose is fermented with production of acid but no gas. Acid is produced from L-arabinose, celllobiose, fructose, lactose, D-mannose, melezitose, melibiose, raffinose, L-rhamnose, D-ribose (weak reaction), salicin, starch, sucrose, trehalose and xylose. Adonitol, dulcitol, erythritol, glycogen, inositol, D-mannitol and D-sorbitol are not acidified. Positive reactions for N-acetyl-β-glucosaminidase, acid phosphatase, alanine arylamidase, alkaline phosphatase, α-arabinosidase, ester lipase C8 (weak reaction), α-galactosidase, β-galactosidase (weak reaction), α-glucosidase, β-glucosidase, glutamyl glutamic acid arylamidase, α-mannosidase (weak reaction), α-fucosidase, chymotrypsin, alginic acid arylamidase, leucyl glycine arylamidase, phosphoamidase and trypsin. Arginine dihydrolase, arginine arylamidase, cystine arylamidase, esterase C4, β-galactosidase 6-phosphate, glutamic acid decarboxylase, glycine arylamidase, histidine arylamidase, lipase C14, leucine arylamidase, phenylalanine arylamidase, proline arylamidase, pyroglutamic acid arylamidase, serine arylamidase, tyrosine arylamidase, urease and valine arylamidase are not detected. The type strain of *Dysgonomonas gadei* is CCUG 42882^T (= CIP 106420^T). The type strain was recovered from a human infected gall bladder. Habitat is not known.

**Description of *Dysgonomonas capnocytophagoides* sp. nov.**

*Dysgonomonas capnocytophagoides* (cap.no.cy.to.pha.go’i.des. Gr. n. kapnos smoke; Gr. n. kyotos hollow vessel; Gr. v. phagein to eat; Gr. adj. suffix -oides alike; N.L. adj. *capnocytophagoides* capnocytophagoid-like, referring to some properties shared between these organisms).

The description is based on results obtained in this study and those obtained by Wallace et al. (1989). Cells consist of non-motile, Gram-negative cocco-bacilli to short rods. After 48 h incubation aerobically at 35 °C in a CO_{2}-enriched atmosphere (7.5%), the colonies are 1–2 mm in diameter, non-adherent, entire, grey-white, smooth and non-haemolytic and have a slight aromatic odour. The organism does not grow on MacConkey agar. Facultatively anaerobic. The organism is catalase- and oxidase-negative. It does not produce hydrogen sulphide or acetoin. Aesculin may or may not be hydrolysed but gelatin and urea are not. Indole may or may not be produced. Resistant to ox bile. Nitrate is not reduced. Major products of glucose
fermentation are propionic, lactic and succinic acids. Glucose is fermented with production of acid but no gas. Acid is produced from L-arabinose, lactose, maltose, d-mannose, melibiose, raffinose, sucrose and D-xylose. Adonitol, D-arabitol, L-arabitol, dulcitol, inositol, D-mannitol, D-sorbitol and trehalose are not acidified. Positive reactions are obtained for acid phosphatase, alanine arylamidase, alkaline phosphatase, \( \alpha \)-arabinosidase, \( \alpha \)-galactosidase, \( \beta \)-galactosidase, \( \beta \)-galactosidase 6-phosphate, \( \alpha \)-glucosidase, \( \beta \)-glucosidase, glutamyl glutamic acid arylamidase, leucyl glycine arylamidase and phosphoamidase. Arginine arylamidase, arginine dihydrolase, \( N \)-acetyl-\( \beta \)-glucosaminidase, \( \alpha \)-fucosidase, \( \beta \)-glucuronidase, glutamic acid decarboxylase, glycine arylamidase, histidine arylamidase, lysine decarboxylase, leucine arylamidase, \( \alpha \)-mannosidase, ornithine decarboxylase, chymotrypsin, cystine arylamidase, ester lipase C8, lipase C14, phenylalanine arylamidase, proline arylamidase, pyrogallamide arylamidase, serine arylamidase, tyrosine arylamidase, trypsin and valine arylamidase are not detected. Esterase C4 production is variable. Isolated from human clinical specimens. Habitat is not known. The type strain is CCUG 17996\(^T\) (= LMG 11519\(^T\)). The G+C content of DNA of the type strain is 38 mol%.

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We are grateful to Hans Trüper for help in the derivation of the genus name and species epithets.

REFERENCES


