Dethiosulfovibrio peptidovorans gen. nov., sp. nov., a New Anaerobic, Slightly Halophilic, Thiosulfate-Reducing Bacterium from Corroding Offshore Oil Wells

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A strictly anaerobic thiosulfate-reducing bacterium was isolated from a corroding offshore oil well in Congo and was designated strain SEBR 4207T. Pure culture of the strain induced a very active pitting corrosion of mild steel, with penetration rates of up to 4 mm per year. This constitutes the first experimental evidence of the involvement of thiosulfate reduction in microbial corrosion of steel. Strain SEBR 4207T cells were vibrios (3 to 5 by 1 μm), stained gram negative, and possessed lateral flagella. Spores were not detected. Optimum growth occurred in the presence of 3% NaCl at pH 7.0 and 42°C. Strain SEBR 4207T utilized peptides and amino acids, but not sugars or fatty acids. It fermented serine, histidine, and Casamino Acids, whereas arginine, glutamate, leucine, isoleucine, alanine, valine, methionine, and asparagine were only used in the presence of thiosulfate. Peptides were fermented to acetate, isobutyrate, isovalerate, 2-methylbutyrate, H2S, and CO2. The addition of either thiosulfate or sulfur but not sulfate increased peptide utilization, growth rate, and biomass; during growth, H2S was produced and a concomitant decrease in H2 was observed. The addition of either thiosulfate or sulfur also reversed H2 inhibition. 16S rRNA sequence analysis indicates that strain SEBR 4207T is distantly related to members of the genus Thermoanaerobacter (83% similarity). Because the phenotypic and phylogenetic characteristics cannot be assigned to any described genus, strain SEBR 4207T is designated as a new species of a new genus, Dethiosulfovibrio peptidovorans gen. nov., sp. nov. Strain SEBR 4207T has been deposited in the Deutsche Sammlung von Mikroorganismen und zellkulturen GmbH (= DSM 11002).

In 1989, Elf Congo experienced corrosion of the first 5 km of a 23-km main subsea pipeline that transported sour oil (i.e., H2S-containing petroleum) produced from the Emeraude oil field. The corroded segment was replaced, but it corroded again a year later. The whole line was then replaced and operated under a specifically designed biocide treatment regimen. The preliminary examination of the corroded iron during our microbiological investigations, the production fluids and wellhead fluids of sour oil, and the composition of the reservoir water. It contained (per liter) 13 mg of SrCl2, 3.907 g of MgCl2 · 6H2O, 0.148 g of Na2SO4, 2.021 g of CaCl2 · 2H2O, 31.541 g of NaCl, 1.336 g of KCl, 0.054 g of NH4Cl, 0.309 g of NaHCO3, and 0.001 g of FeCl3 · 4H2O. Half-strength tryptone-yeast extract-glucose (TYG) medium (HSTYG) was used to grow fermentative anaerobes (5). SRB detection kits (Labège) were used for enumerating sulfate-reducing bacteria (27). Methano- genic bacteria were grown with either sodium acetate (10 mM), methanol (40%), or H2CO3 (2 bars [2 × 105 Pa]) as the substrate. Enrichment, isolation, and growth conditions. Strain SEBR 4207T was purified by streaking the inoculum from the last positive dilution of HSTYG tube on HSTYG agar plates (2.5% Noble agar; Difco Laboratories, Detroit, Mich.) in an anaerobic chamber (La Calhène, Vélizy, France) followed by incubation at 30°C under anaerobic conditions. For subsequent studies, a different medium (DP) was used. Medium DP contained (per liter) 1 g of NH4Cl, 0.3 g of K2HPO4, 0.3 g of KH2PO4, 3.0 g of MgCl2 · 6H2O, 0.1 g of CaCl2 · 2H2O, 30 g of NaCl, 10 g of

Materials and Methods
Sample collection and sample source. Strain SEBR 4207T was isolated from the Emeraude oil field, which is an offshore oil-producing well (BB325, Congo). Water samples were aseptically collected as described previously (2). The in situ temperature of the oil field was 38°C, and the total salinity was 52 g/liter. Bacterial counts. Acidine orange direct counting was used to determine the total number of bacterial cells in the sample (21). Cultivable bacteria were enumerated by the three-tube most-probable-number (MPN) procedure. A saline solution was used for the preparation of all culture media in order to mimic the composition of the reservoir water. It contained (per liter) 13 mg of SrCl2, 3.907 g of MgCl2 · 6H2O, 0.148 g of Na2SO4, 2.021 g of CaCl2 · 2H2O, 31.541 g of NaCl, 1.336 g of KCl, 0.054 g of NH4Cl, 0.309 g of NaHCO3, and 0.001 g of FeCl3 · 4H2O. Half-strength tryptone-yeast extract-glucose (TYG) medium (HSTYG) was used to grow fermentative anaerobes (5). SRB detection kits (Labège) were used for enumerating sulfate-reducing bacteria (27). Methanogenic bacteria were grown with either sodium acetate (10 mM), methanol (40%), or H2CO3 (2 bars [2 × 105 Pa]) as the substrate. Enrichment, isolation, and growth conditions. Strain SEBR 4207T was purified by streaking the inoculum from the last positive dilution of HSTYG tube on HSTYG agar plates (2.5% Noble agar; Difco Laboratories, Detroit, Mich.) in an anaerobic chamber (La Calhène, Vélizy, France) followed by incubation at 30°C under anaerobic conditions. For subsequent studies, a different medium (DP) was used. Medium DP contained (per liter) 1 g of NH4Cl, 0.3 g of K2HPO4, 0.3 g of KH2PO4, 3.0 g of MgCl2 · 6H2O, 0.1 g of CaCl2 · 2H2O, 30 g of NaCl, 10 g of

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INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, July 1997, p. 818–824
0020-7713/97/$04.00 + 0

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Light and electron microscopy. Light microscopy was performed as previously described (9). Exponentially grown cells were negatively stained with 1% sodium phosphotungstic acid (pH 7.2). For preparation of thin sections, exponentially grown cells were centrifuged and fixed for 1 h in 3% (wt/vol) glutaraldehyde prepared in HCl-cacodylate buffer (pH 6.0) containing 0.7 M sucrose and fixed again overnight in 1% (wt/vol) osmium tetroxide prepared in 0.75 M sucrose. The cells were then washed and embedded in 3% agarose and stained with 4% uranyl acetate. The agar was cut into small cubes, dehydrated in acetone, and embedded in Araldite. Thin sections were stained with 5% uranyl acetate for 20 min and with 2% lead citrate for 10 min. Electron microphotographs were taken with a Hitachi H600 electron microscope at an accelerating voltage of 75 kV.

Cytochrome analysis. Cell extracts were examined for the presence of cytochrome and dsoxoflavin as already reported (33).

Analytical techniques. Unless otherwise indicated, experiments were conducted in triplicate. Growth was measured at 580 nm by inserting tubes directly into a Shimadzu (Kyoto, Japan) UV-160A spectrophotometer. Sulfide was determined photometrically as colloidal CuS according to the method of Cord-Ruwisch (12). H₂ and fermentation products (alcohols and fatty acids) were measured as described previously (17).

Determination of G+C content. DNA was extracted and purified by chromatography on hydroxyapatite. The guanine-plus-cytosine (G+C) content was determined by high-performance liquid chromatography by the method of Mesbah et al. (31). Nonmethylated lambda DNA (Sigma) was used as a standard (8).

16S rRNA sequence studies. Amplification of the 16S rRNA from semipurified DNA followed by purification of the amplified product was described previously (26, 38). The sequence was determined with an automated DNA sequencer by using a Prism dideoxy terminator cycling sequencing kit and the protocols recommended by the manufacturer (Applied Biosystems Inc.). The 12 primers used for sequencing have been described previously (38). The 16S ribosomal RNA sequence was manually aligned with reference sequences of various members of the domain Bacteria by using the alignment editor see2. Reference sequences were obtained from the Ribosomal Database Project (25, 30). A phylogenetic analysis was performed with various programs implemented as part of the PHYLIP package (19) as described below. The pairwise evolutionary distances based on 1,245 unambiguous bases were determined by the method of Jukes and Cantor (25), and dendrograms were constructed from evolutionary distances by the neighbor-joining method. A transversion analysis was performed with the program DNAFLAPS. Tree topology determined with 100 data sets was examined by running a script file consisting of the following programs: SEQBOOT, DNADIST, FITCH, and CONSENSE. Programs available in the Molecular Evolutionary Genetic Analysis (MEGA) package, version 1 (24), were also used in the analysis. All of the programs except MEGA were run on a Sun Sparc workstation. MEGA was run on a Compaq Contura 410CX IBM-compatible notebook computer.

Nucleotide sequence accession number. The nucleotide sequence of the 16S rRNA of strain SEBR 4207T has been deposited in the GenBank database under accession no. U52817.

RESULTS

Bacterial counts in BB325 wellhead sample. At the time of our investigation, the new oil pipeline was treated by frequent biocide injections at elevated concentration. Since this treatment drastically reduced the bacterial numbers within the line, we collected water samples upstream of the corroded pipe and from the non-biocide-treated producing wellheads whose tubings were actively corroded. The bacterial community (Table 1) was exclusively composed of strict anaerobes. The MPN counts showed that most bacterial cells enumerated under the epifluorescence microscope were cultivable. Fermentative bacteria outnumbered

<table>
<thead>
<tr>
<th>TABLE 1. Bacterial counts in well BB325 water sample</th>
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<tbody>
<tr>
<td><strong>Sampling group</strong></td>
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<tr>
<td>Epifluorescence microscopy</td>
</tr>
<tr>
<td>Aerobes or facultative anaerobes</td>
</tr>
<tr>
<td>Sulfate-reducing bacteria (SRB test kits)</td>
</tr>
<tr>
<td>Methanogens</td>
</tr>
<tr>
<td>Fermentative anaerobes</td>
</tr>
</tbody>
</table>

* ND, not detected.

a Methanogens comprise hydrogenotrophs (0.5 × 10³/ml) and methylotrophs (0.5 × 10³/ml).
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Titre original : Dethiosulfovibrio peptidovorans gen. nov., sp. nov., a new anaerobic, slightly halophilic, thiosulfate-reducing bacterium from corroding offshore oil wells.


Titre en Français : Dethiosulfovibrio peptidovorans gen. nov., sp. nov., une nouvelle bactérie anaérobie, modérée halophile, thiosulfato-réductrice isolée d'un puits pétrolier offshore corrodé.

Mots-clés matières : Dethiosulfovibrio peptidovorans - Halophilie - (10 au plus) Anaérobie - Taxonomie - Réduction du thiosulfate - Pétrole - Corrosion

Résumé en Français : (150 mots maximum)

Plan de classement : Monde végétal et Animal - Fermentations
both sulfate-reducing and methanogenic bacteria. Seven different fermentative strains were purified, and six of them were shown to reduce sodium thiosulfate to hydrogen sulfide (28), including the recently described novel species Halooaerobibium congolense (37). Two SRB strains (42) and two methanogens, including the new species Methanoplanus petrolearius (34), were also isolated. None of these isolates displayed characteristics common to the described species (34, 37, 42).

**Enrichment and isolation.** Strain SEBR 4207T was purified from the last positive MPN HSTYG tube by three consecutive streakings on HSTYG agar plates, followed by incubation at 30°C in an anaerobic chamber. After 7 days of incubation, colonies 2 mm in diameter developed. The colonies were white and round with smooth edges. A single colony (designated as strain SEBR 4207T) was picked and transferred into HSTYG liquid medium.

**Corroding activity of strain SEBR 4207T.** Figure 2 shows the pit penetration rates (in millimeters per year) versus time after the preconditioning for one experimental cell kept sterile and three independent experimental cells inoculated with strain SEBR 4207T. Under sterile conditions, the penetration rate decreased to a fraction of millimeters per year within a few hours of coupling, after the preconditioning current was stopped. In the presence of strain SEBR 4207T, a stable galvanic current of 130 to 350 µA/cm² was measured. When expressed as a penetration rate, this corresponded to 325 to 865 mg of iron per dm² per day, or 1.5 to 4.0 mm/y (Fig. 2).

These differences were suspected to result from differences in biofilm formation. These values are far above the accepted industrial limit of 0.1 mm/y for mild steel corrosion.

**Morphology.** Strain SEBR 4207T was a vibrio measuring 3 to 5 µm by 1 µm (Fig. 3). Electron microscopy of negatively stained cells indicated the presence of from one up to five lateral flagella (Fig. 4). Electron microscopy of thin sections of cells of strain SEBR 4207T exhibited a multilayered cell wall ultrastructure with an outer membrane typical of gram-negative bacteria (Fig. 5).

**Growth characteristics.** Strain SEBR 4207T grew from 20 to 45°C, with an optimum temperature for growth at 42°C. No growth was observed at 50°C (Fig. 6a). It required NaCl for growth, with an optimum of 3% NaCl. No growth occurred at 11% NaCl (Fig. 6b). The optimum pH for growth was 7.0, with no growth at pH 5.5 and 8.8.

**Substrate utilization and physiological characteristics.** Strain SEBR 4207T utilized peptides in the form of bio-Trypticase and Bacto Peptone and amino acids in the form of Casamino Acids as its sole carbon and energy sources. Proteins such as gelatin or casein, carbohydrates (arabinose, fructose, galactose, glucose, lactose, maltose, mannose, rhamnose, ribose, sucrose, sorbose, trehalose, and xylose), and fatty acids (acetate, butyrate, propionate, citrate, and lactate) were not utilized. End products formed from peptide utilization included acetate, isobutyrate, isovalerate, 2-methylbutyrate, CO₂, and H₂. Serine and histidine were fermented, whereas arginine, glutamate, leucine, isoleucine, alanine, valine, methionine, and asparagine were only oxidized in the presence of thiosulfate as an electron acceptor. Lysine, proline, threonine, and glycine were not used in either the presence or the absence of thiosulfate. Serine was fermented to acetate. In the presence of thiosulfate, alanine was oxidized to acetate, leucine to 2-methylbutyrate, valine to isobutyrate, asparagine to acetate, and methionine to propionate. Although yeast extract was not required for utilization of peptides and Casamino Acids, its presence improved growth. In contrast, yeast extract was required for the use of any single amino acid as an energy source. Strain SEBR 4207T used elemental sulfur and thiosulfate, but not sulfate, as electron acceptors with peptides. Strain SEBR 4207T did not perform thiosulfate or elemental sulfur disproportionation in the presence of acetate or yeast extract as a carbon source. Moreover, growth did not occur on H₂ plus thiosulfate and acetate as the carbon source. The presence of either elemental sulfur or thiosulfate increased the biomass and the growth rate (Fig. 7). In addition, H₂S was produced with a commensurate decrease in H₂ when thiosulfate or sulfur was present. H₂ inhibited the growth of strain SEBR 4207T, but this inhibition could be partially reversed by the addition of thiosulfate and sulfur. Overall, the presence of thiosulfate had a much greater effect on growth than sulfur did. Strain SEBR 4207T was unable to use carbohydrates and volatile fatty acids as carbon and energy sources with yeast extract and/or thiosulfate. The cells did not contain cytochrome or desulfoviridin.

**G+C content.** The G+C content of isolate SEBR 4207T was 56 mol%.

**16S rRNA sequence analysis.** Using 12 primers, we determined 1,505 nucleotide bases from positions 8 to 1542 (Escherichia coli numbering of Winker and Woese [44] of the 16S rRNA gene of strain SEBR 4207T). A phylogenetic analysis performed with representatives of the domain Bacteria revealed that strain SEBR 4207T was a member of the subdivision containing gram-positive bacteria with DNA G+C content less than 55 mol% and clustered with members of the clostridial group. A recent phylogenetic analysis of the 16S
rRNAs of the members of the clostridial group revealed that there are at least 19 defined clusters and several lines of descent. This led to the creation of five new genera and 11 new species combinations to accommodate phylogenetically distinct organisms (11). Phylogenetic analysis revealed that strain SEBR 4207T was peripherally related to cluster V, consisting of the family *Thermoanaerobacteraceae*, with a similarity value of 83%. A bootstrap value of 53 was obtained from a 100 data sets, indicating a poor relationship between strain SEBR 4207T and cluster V. Several data sets, which included different representatives from the various clusters of the subdivision containing gram-positive bacteria with DNA G+C content less than 55 mol%, consistently placed strain SEBR 4207T as a member of a novel line of descent at the periphery of cluster V and the genus *Dictyoglomus* (39). Transversion analysis did not affect the position of strain SEBR 4207T in the phylogenetic tree. The evolutionary distances separating strain SEBR 4207T and its relative and the dendrogram derived from these distances are depicted in Table 2 and Fig. 8, respectively. The G+C content of the 16S rRNA gene was 56 mol%.

**DISCUSSION**

The bacterial flora of oil field production water transported in an actively corroded undersea oil pipeline was shown to be composed of only strict anaerobes, which appear to commonly dominate such ecosystems (2, 20). Most of the bacteria that compose this consortium were cultivated (Table 1), although it is generally considered that very few bacteria from the natural environment are cultivable under laboratory conditions. Similar observations were recently reported from another oil field facility (32). Fermentative, thiosulfate-reducing anaerobic bacteria exhibited significant populations in the oil field studied (Table 1), a situation which seems to be common in oil field reservoirs (14, 20, 36).

Thiosulfate is produced from chemical oxidation of sulfide (10, 15, 22). It is common in aquatic environments and has also recently been detected in oil fields. It has been hypothesized from models (13, 16) and field observations (14, 28) that its presence in oil fields may increase the risk of biocorrosion of oil pipelines. We have therefore initiated studies of the isola-
tion of anaerobic thiosulfate-reducing bacteria from oil field environments undergoing active corrosion. Strain SEBR 4207T was isolated from an African oil field in Congo and was observed to use thiosulfate, but not sulfate, as an electron acceptor. One important characteristic of this strain, when tested in appropriate in vitro experiments, was that it induced corrosion rates into mild steel at least 1 order of magnitude higher than that recorded for sulfate-reducing bacteria in similar experiments (8). This paper thus shows for the first time that thiosulfate-, non-sulfate-reducing bacteria, as previously suspected, do have a significant corrosive activity.

Strain SEBR 4207T also used elemental sulfur as an electron acceptor. The reduction of elemental sulfur to sulfide is not an obligate physiological trait for strain SEBR 4207T and therefore it is different from the mesophilic sulfur-respiring bacterium, viz. Desulfuromonas acetoxidans, Desulfurella acetivorans, and Desulfuvibrio sp. (35), or the thermophilic members of domains Archaea and Bacteria (3, 40, 41). The metabolism of this isolate is unique among the mesophilic sulfur reducers because it resembles to some degree that of the hyperthermophilic members of the domain Archaea when proteinaceous compounds are used in the presence of elemental sulfur as an electron acceptor (4). Strain SEBR 4207T possesses unique phenotypic characteristics, because it utilizes only a limited range of substrates, which include amino acids and peptides, but not proteins such as gelatin and casein, carbohydrates, or volatile fatty acids.

The isolation of strain SEBR 4207T extends the known diversity of microorganisms involved in amino acid and peptide degradation and emphasizes the importance of thiosulfate or sulfur reducers in the oxidation of peptides and amino acids. Thiolsulfate dramatically improves the utilization of amino acids and peptides by members of the genus Thermoaerobacter (18) in a manner similar to that of strain SEBR 4207T. Interestingly, Thermoaerobacter species are the nearest phylogenetic relatives of strain SEBR 4207T, although the distance separating them is very large (83% similarity). In addition, strain SEBR 4207T is a mesophile, utilizes a very limited range of substrates, and has G+C content of 56 mol%, traits which clearly differentiate strain SEBR 4207T from members of all known bacteria, including members of the genus Thermoaerobacter.

Strain SEBR 4207T stains gram-negative and has a gram-negative cell wall ultrastructure, but is phylogenetically related to members of the subdivision containing gram-positive subdivision bacteria with DNA G+C content of less than 55%. This discrepancy between phenotype and genotype is not new in this subdivision. For example, the closest relatives of strain SEBR 4207T are the members of the genus Thermoaerobacter. All members of this genus are gram-positive, except Thermoaerobacter ethanolicus, which possesses a gram-negative cell wall (43). Members of Dictyoglycosum, which are also distant phylogenetic relatives of strain SEBR 4207T and Thermoaerobacter species, possess gram-negative cell walls (39). Interestingly, the common phenotypic element binding strain SEBR 4207T with Thermoaerobacter and Dictyoglycosum is their obligate anaerobic nature.

Strain SEBR 4207T is an anaerobic, slightly halophilic vibrio but does not utilize sulfate as an electron acceptor, and despite its morphology and ability to utilize thiosulfate, it cannot be described as a member of the sulfate-reducing bacteria. Strain SEBR 4207T is also phylogenetically distinct from all sulfate-reducing bacteria and members of the family Thermoaerobacteriaceae. Because strain SEBR 4207T cannot be assigned to any known bacterial genera, we propose that it be designated a member of a new genus, Dethiosulfovibrio peptidovorans, gen. nov., sp. nov.

Description of Dethiosulfovibrio gen. nov. Dethiosulfovibrio (De.thi.o.sul.fo.vi.br'i.o. L. pref. de, from; Gr. n. thios, sulfur; L. n. sulfur, sulfur; thiosulf, thiosulfate; L. v. vibrio, to vibrate;
TABLE 2. Evolutionary distance matrix determined from a comparison of the 16S rRNA sequence of strain SEBR 4207T and related genera by the method of Jukes and Cantor (23)*

<table>
<thead>
<tr>
<th>Organism</th>
<th>Evolutionary distance of sequence from that of organism:</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Strain SEBR 4207</td>
<td>1 2 3 4 5 6 7 8 9 10 11 12 13 14 15</td>
</tr>
<tr>
<td>2 Thermoaerobacter thermoeotropiae</td>
<td>83.0</td>
</tr>
<tr>
<td>3 Thermoaerobacter acetoeothylicus</td>
<td>82.7 94.2</td>
</tr>
<tr>
<td>4 Thermoaerobacter ethanolicus</td>
<td>83.4 94.8 97.0</td>
</tr>
<tr>
<td>5 Thermoaerobacter kivai</td>
<td>83.8 94.2 96.1 97.1</td>
</tr>
<tr>
<td>6 Dietzyogloous thermophilum</td>
<td>80.3 85.5 85.1 85.8 85.1</td>
</tr>
<tr>
<td>7 Desulfotomaculum thermoacetatium</td>
<td>81.8 86.8 87.1 88.2 87.9 82.5</td>
</tr>
<tr>
<td>8 Desulfotomaculum thermosulfogranum</td>
<td>81.3 85.2 85.4 86.1 85.7 81.0 89.4</td>
</tr>
<tr>
<td>9 Desulfotomaculum australicum</td>
<td>81.3 85.3 86.4 87.6 87.6 82.9 94.6 89.3</td>
</tr>
<tr>
<td>10 Thermoaerobacterium thermosulfurigenes</td>
<td>80.2 85.3 87.1 87.6 87.4 81.5 86.0 84.3 85.4</td>
</tr>
<tr>
<td>11 Thermoaerobacterium thermodonaticum</td>
<td>79.8 86.0 87.4 87.3 81.8 86.3 84.5 85.4 89.8</td>
</tr>
<tr>
<td>12 Moorella thermaeotaica</td>
<td>81.6 87.9 88.2 89.1 88.3 89.4 88.6 89.8 86.9 87.1</td>
</tr>
<tr>
<td>13 Syntrophononas bohannai</td>
<td>80.1 84.9 85.3 85.0 85.4 81.6 85.6 84.1 85.7 84.2 84.5 86.9</td>
</tr>
<tr>
<td>14 Syntrophomonas wolfei</td>
<td>80.2 83.3 85.6 86.1 85.8 81.9 85.3 84.4 86.2 83.8 83.9 86.9 94.4</td>
</tr>
<tr>
<td>15 Selenomonas ruminantium</td>
<td>79.5 82.1 82.5 83.7 82.5 79.9 83.6 85.2 83.0 82.7 82.8 83.1 83.3 83.1</td>
</tr>
<tr>
<td>16 Megaplasma eldanii</td>
<td>80.2 81.0 81.7 82.9 82.7 79.4 81.9 83.0 81.0 82.7 83.3 81.0 81.3 87.9</td>
</tr>
</tbody>
</table>

* See Materials and Methods for details. The sequences used in the analysis were obtained from the Ribosomal Database Project, version 5 (25), and from EMBL/GenBank/DDBJ databases (accession no. Z26315). Only 1,253 unambiguous nucleotide positions were used in the analysis.

The organism ferments serine and histidine. D. peptidovorans uses alanine, arginine, asparagine, glutamate, methionine, and valine only in the presence of thiosulfate as an electron acceptor. The organism produces acetate, isobutyrate, isovalerate, 2-methylbutyrate, CO₂, and H₂ from peptides. Yeast extract is not required, but improves growth on Casamino Acids and peptides. Yeast extract is required for the use of a single amino acid. The organism uses elemental sulfur and thiosulfate, but not sulfate, as electron acceptors. Growth is inhibited by hydrogen. Cells do not contain cytochrome or desulfoviridin.

Description of Dethiosulfovibrio peptidovorans gen. nov., sp. nov. Dethiosulfovibrio peptidovorans (pep.ti.do.vo'rans. Gr. adj. pepto, to devour; M.L. part adj. peptido- vorans, to devour; M.L. masc. n. vibrio that devours, a generic name; M.L. masc. n. Dethiosulfovibrio, a vibrio that reduces thiosulfate). Cells are gram-negative vibrios, mesophilic, neutrophilic, and slightly halophilic strict anaerobes that use peptides and amino acids, but not sugars, as the sole carbon and energy sources. The organism uses elemental sulfur and thiosulfate, but not sulfate, as electron acceptors. Growth is inhibited by hydrogen. Cells do not contain cytochrome or desulfoviridin.

The DNA base composition (G+C content) is 56 mol%. D. peptidovorans lives in an oil-producing well in Africa. The type strain is SEBR 4207 (=DSM 11002).

ACKNOWLEDGMENTS

We thank C. E. Hatchikian for helpful discussions, O. Arnauld and C. Lanau for technical assistance, and P. A. Roger for critical comments on the manuscript.

This work was supported by grants from Elf Aquitaine (G.R. and X.C.) and in part from the Australian Research Council (B.K.C.P.).

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