Isolation from oil reservoirs of novel thermophilic anaerobes phylogenetically related to *Thermoanaerobacter subterraneus*: reassignment of *T. subterraneus*, *Thermoanaerobacter yonseiensis*, *Thermoanaerobacter tengcongensis* and *Carboxydibrachium pacificum* to *Caldanaerobacter subterraneus* gen. nov., sp. nov., comb. nov. as four novel subspecies

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Novel thermophilic, anaerobic, Gram-positive, rod-shaped bacteria, strains SL9 and OCA1, were isolated from oilfields in France and Australia, respectively. Both strains, together with *Thermoanaerobacter yonseiensis* KB-1 T (= DSM 13777 T), *Thermoanaerobacter tengcongensis* MB4 T (= DSM 15242 T) and *Carboxydibrachium pacificum* JM T (= DSM 12653 T), possessed genomic (DNA–DNA hybridization studies) and phylogenetic similarities with *Thermoanaerobacter subterraneus* SEBR 7858 T (= DSM 13054 T), which was isolated recently from an oilfield reservoir in south-west France. Marked phenotypic differences exist between the three oilfield isolates (*T. subterraneus*, strain OCA1 and strain SL9): they include temperature range for growth and substrates used. Differences were also observed in the DNA G+C contents of all organisms. Similarly to *T. subterraneus*, strains SL9 and OCA1, and also *T. yonseiensis*, *T. tengcongensis* and *Carboxydibrachium pacificum*, produced acetate and L-alanine as major end products of glucose metabolism \[0.8–1.0 \text{ mol L-alanine produced (mol glucose consumed)}^-1\] and reduced thiosulfate, but not sulfate, to sulfide. Because of these significant metabolic and phylogenetic differences between the oilfield isolates (*T. subterraneus*, strain OCA1 and strain SL9), *T. yonseiensis*, *T. tengcongensis* and *Carboxydibrachium pacificum* and other *Thermoanaerobacter* species, it is proposed to reassign them as a novel genus and species, *Caldanaerobacter subterraneus* gen. nov., sp. nov., comb. nov. with the creation of four novel subspecies, *Caldanaerobacter subterraneus* subsp. *subterraneus* subsp. nov., *Caldanaerobacter subterraneus* subsp. *yonseiensis* subsp. nov., *Caldanaerobacter subterraneus* subsp. *tengcongensis* subsp. nov., and *Caldanaerobacter subterraneus* subsp. *pacificus* subsp. nov., comb. nov.

INTRODUCTION

Petroleum reservoirs constitute a group of unique terrestrial sites, as they present an unusual combination of extreme environmental conditions, including temperature, pressure and salinity. It is also known that petroleum composition varies widely between reservoirs, which may
have an impact on the microbial biodiversity of such environments. Attention has recently been paid to the microbial ecology of petroleum reservoirs, where anaerobes have always been considered to be the dominant micro-organisms. They include fermentative and sulfate-reducing bacteria and methanogenic Archaea (Magot et al., 2000). Among the fermentative anaerobes, thermophiles have been studied the most, probably because most oil reservoirs occur at a depth where in situ temperatures exceed 100 °C (Stetter et al., 1993). Many of them belong to the Bacteria (Jeanthon et al., 1995; Ravot et al., 1995a; Grassia et al., 1996; Fardeau et al., 1997; Rees et al., 1997). They include members of the family ‘Thermoanaerobiaceae’ (genera Thermoanaerobacter and Thermoanaerobacterium) that were isolated from low-saline reservoirs (Grassia et al., 1996). Most oilfield isolates of the genus Thermoanaerobacter have not been characterized formally, except for two isolates from French hot continental oil reservoirs belonging to the family ‘Thermotogales’ (Cayol et al., 1995). Members of the order Thermo- togales have also been isolated from oil reservoirs (Stetter et al., 1993). Within this order, novel species of the genera Thermotoga (Jeanthon et al., 1995; Ravot et al., 1995a; Fardeau et al., 1997), Petrotoga and Geotoga (Davey et al., 1993; Lien et al., 1998) have been characterized. Most of these oilfield thermoanaerobes, which belong to the family ‘Thermoanaerobiaceae’ (Fardeau et al., 1993, 1996) or to the order Thermotogales (Ravot et al., 1995b; Lien et al., 1998), reduced thiosulfate mostly to hydrogen sulfide. All produced acetate as a major end product of sugar metabolism. t-Alanine production from sugar metabolism. Similarly to Carboxydribacrium pacificum (Sokolova et al., 2001), Thermoanaerobacter yonseiensis (Kim et al., 2001) and Thermoanaerobacter tengcongensis (Xue et al., 2001), they share genotypic and phylogenetic similarities with T. substraneeus (Fardeau et al., 2000), which was isolated recently from an oil reservoir in the Paris Basin, France. These six thermoanaerobes are proposed as members of a novel genus of the family ‘Thermoanaerobiaceae’, Caldanaerobacter gen. nov., comb. nov.

**METHODS**

**Sample and strain source.** Oil-water mixture samples were collected in sterile 250 ml glass bottles from production well-heads in France and Australia through a tapping that was fitted on the production line. Samples were stored at 4 °C before being used as inocula. Carboxydribacrium pacificum JM 1 (DSM 12653), T. yonseiensis KB-1 (DSM 13777), T. brockii DSM 1457 and Thermoanaerobacter ethanolicus DSM 2246 were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Braunschweig, Germany. T. tengcongensis MB 4 (DSM 15242) was provided by the authors.

**Media and cultivation conditions.** The technique of Hungate (1969) was used throughout this study. Enrichments with oilfield samples were performed in medium that contained (l distilled water): 1 g NH₄Cl, 3-45 g PIPES, 0-3 g KH₂PO₄, 0-2 g MgCl₂·6H₂O, 0-1 g CaCl₂·2H₂O, 15 g NaCl, 0-1 g KCl, 0-5 g sodium acetate, 1 g glucose, 5 g yeast extract (Difco), 5 g bio-tryptica (bioMérieux) and 0-001 g resazurin. T. substraneeus, T. tengcongensis and T. yonseiensis were cultivated in medium that contained (l distilled water): 1 g NH₄Cl, 0-3 g KH₂PO₄, 0-3 g KH₂PO₄, 0-1 g CaCl₂·2H₂O, 0-1 g KCl, 0-5 g MgCl₂·6H₂O, 1 g yeast extract, 2 g NaCl, 3-6 g glucose, 0-5 g cysteine/HCl and 10 ml trace elements solution (Balch et al., 1979). Carboxydribacrium pacificum was cultivated in the latter medium, modified by replacing NaCl by 30 g sea salts and reducing the yeast extract concentration to 0-5 g l⁻¹. Depending on the medium used, the pH was adjusted to 7-0 with either HCl (5 M) or KOH (10 M). After autoclaving, thiosulfate (10 mM) was added. Aliquots of the medium (9 ml) were then dispensed into Hungate tubes. Prior to inoculation, Nₐ,S,H₂O was injected from sterile stock solutions, to obtain a final concentration of 0-1 % (w/v).

**Isolation.** Isolation medium (9 ml) was inoculated with 1 ml oil-water mixture, pressurized with N₂ (100 kPa) and incubated without shaking at the reservoir temperature (65 °C). Positive enrichments were subcultured and purified by streaking onto plates that contained the same medium, solidified with 0-7 % (w/v) Phytagel (Sigma). Plates were incubated in anaerobic jars pressurized with N₂ (100 kPa) at 65 °C for 3 days. Cultures of T. substraneeus were also incubated at 65 °C, whereas those of T. tengcongensis, T. yonseiensis and Carboxydribacrium pacificum were incubated at 70 °C.

**Characterization.** Temperature, pH and NaCl ranges for growth were determined by using the following medium, which contained (1 distilled water): 1 g NH₄Cl, 0-3 g KH₂PO₄, 0-3 g KH₂PO₄, 0-5 g MgCl₂·6H₂O, 0-1 g CaCl₂·2H₂O, 1 g NaCl, 0-1 g KCl, 0-5 g cysteine/HCl, 2 g yeast extract, 0-001 g resazurin and 10 ml trace elements solution (Balch et al., 1979). In Hungate tubes, medium was adjusted to different pH values by injecting NaHCO₃ or Na₂CO₃ from 10 % (w/v) sterile anaerobic stock solutions. For studies of NaCl requirements, NaCl was weighed directly in tubes and measuring OD₅80. Sulfide was determined photometrically as colloidal CuS, by using the method of Cord-Ruwisch (1985). H₂, CO₂, sugars, alcohols and volatile and non-volatile fatty acids were measured as described previously (Fardeau et al., 1996). t-Alanine was measured by HPLC (Moore et al., 1958). Light microscopy was performed as described previously (Fardeau et al., 1997).
**Determination of DNA G+C content.** DNA G+C content was determined at DSMZ. DNA was isolated and purified by chromatography on hydroxyapatite and its G+C content was determined by using HPLC, as described by Mesbah et al. (1989). Non-methylated DNA (Sigma) was used as the standard.

**DNA–DNA hybridization studies.** DNA was isolated by chromatography on hydroxyapatite by the procedure of Cashion et al. (1977). DNA–DNA hybridization was performed at DSMZ as described by De Ley et al. (1970), with the modification described by Huss et al. (1983) and Escara & Hutton (1980), by using a Gilford System model 2600 spectrophotometer equipped with a Gilford model 2527-R thermoprocessor and plotter. Renaturation rates were computed with the program TRANSFER.BAS (Jahnke, 1992).

**16S rRNA gene sequence analysis.** The 16S rRNA gene was amplified as described previously (Miranda-Tello et al., 2003). PCR products were cloned by using a pGEM-T Easy cloning kit (Promega), according to the manufacturer’s protocols. Clone libraries were screened by direct PCR amplification from a colony by using the vector-specific primers SP6 (5′-ATTAGTGACATATAGAA-3′) and T7 (5′-TAATACGACTCACTATAGG-3′) and the following reaction conditions: 2 min at 96°C; 40 cycles of 30 s at 94°C, 1 min at 55°C and 3 min at 72°C; and a final extension of 10 min at 72°C. Plasmids that contained an insert of the right length were isolated by using the Wizard Plus SV Minipreps DNA purification system (Promega), according to the manufacturer’s protocol. Purified plasmids were sent for sequencing to Genome Express (Grenoble, France). Sequence data were imported into the sequence editor BioEdit version 5.0.9 (Hall, 1999), base-calling was examined and a contiguous consensus sequence was obtained for each isolate. The full sequence was aligned by using the Ribosomal Database Project (RDP)’s Sequence Aligner program (Maidak et al., 2001). The consensus sequence was then adjusted manually to conform to the 16S rRNA secondary structure model (Winker & Woese, 1991). A non-redundant BLASTN search (Altschul et al., 1997) of the full sequence through GenBank (Benson et al., 1999) identified its closest relatives. Sequences used in phylogenetic analysis were obtained from the RDP (Maidak et al., 2001) and GenBank (Benson et al., 1999). Positions of sequence and alignment ambiguity were omitted and pairwise evolutionary distances, based on 1152 unambiguous nucleotides, were calculated by using the method of Jukes & Cantor (1969). Dendrograms were constructed by using the neighbour-joining method (Saitou & Nei, 1987). Confidence in the tree topology was determined by using 100 bootstrap trees (Felsenstein, 1993). GenBank accession numbers of rDNA sequences from reference organisms are included in Fig. 1.

**RESULTS AND DISCUSSION**

Although microaerophilic micro-organisms have been reported to inhabit oil reservoirs (Voordouw et al., 1996), their activities have never been interpreted as significant, as the oil-bearing subsurface is essentially anaerobic. Anaerobes have therefore been considered to be dominant in this ecosystem (Magot et al., 2000). The importance of micro-organisms that are closely related, morphologically and physiologically, to members of the order Thermotogales, namely the genera Thermotoga, Geotoga and Petroto, has been established from various hot oil reservoirs throughout the world (Davey et al., 1993; Stetter et al., 1993; Jeanthon et al., 1995; Ravot et al., 1995a; Grassia et al., 1996; Fardeau et al., 1997; L’Haridon et al., 1995; Grassia et al., 1996; Magot et al., 2000). Members of the family ‘Thermoanaerobiaceae’, which includes the genera Thermoanaerobacter and Thermoanaerobacterium, were also isolated frequently, in particular from low-saline reservoirs (Cayol et al., 1995; L’Haridon et al., 1995; Grassia et al., 1996; Magot et al., 2000). Species of the genus Thermoanaerobacter reduced thiosulfate to sulfide, whereas those of the genus Thermoanaerobacterium reduced thiosulfate to elemental sulfur.

It was reported recently that, similarly to some members of the order Thermotogales (Ravot et al., 1996), a novel species of *Thermoanaerobacter* *T. subterraneus* (Fardeau et al., 2000), also produced L-alanine as a major end product of glucose fermentation. Enrichment cultures that were performed at 65°C for 3 days with oil–water mixture samples that originated from oil reservoirs in France and Australia led to the isolation of strains SL9 and OCA1, respectively. Both strains were related phylogenetically to *T. subterraneus* (Table 1). Strains SL9 and OCA1 were rod-shaped bacteria, 0.5–2.5–8.0 μm, that mostly occurred singly or in pairs. They did not grow in oxidized medium. They grew at temperatures that ranged from 45 to 80°C (no growth was obtained at 85°C for strain SL9 or at 80°C for strain OCA1). At pH 7·0, growth was optimum around 75°C for strain SL9 and around 70°C for strain OCA1 (data not shown). Growth occurred at initial pH values between 5.7 and 9.2 at 70°C; the optimum was at pH 7·0 (data not shown). The isolates grew in the presence of MES and the activity of the isolates was measured as growth on media containing MES as sole carbon source.
of NaCl concentrations that ranged from 0 to 2%. Growth was optimum in the absence of NaCl at pH 7·0 (data not shown). Yeast extract was required for growth on carbohydrates and could not be replaced by vitamins. Strains SL9 and OCA1 grew on the following substrates (at a concentration of 20 mM unless indicated otherwise) in the presence of thiosulfate as the electron acceptor: D-fructose, D-galactose, D-glucose, DL-maltose, D-mannose, D-ribose, starch and glycerol. In contrast to strain OCA1, strain SL9 used cellobiose, lactose, D-xylose and pyruvate and did not use CO. Mannitol, melibiose and xylan were not used by either strain. In the presence of thiosulfate, the glucose metabolic profile of both strains changed dramatically, with an increase in acetate production and disappearance of L-alanine production. Use of valine, isoleucine and leucine was highly enhanced by the presence of thiosulfate. Valine, isoleucine and leucine were oxidized to isobutyrate, 2-methylbutyrate and isovalerate, respectively. Acetate, L-alanine, H₂ and CO₂ were the major end products of glucose fermentation (in the absence of thiosulfate). Similarly to T. subterraneus, strains SL9 and OCA1 produced around 1 mol L-alanine (mol glucose consumed)⁻¹. Small amounts of lactate were produced, but no ethanol was produced from glucose fermentation by either strain. Serine was fermented to acetate. These bacteria reduce thiosulfate to sulfide and have a DNA G+C content of 38·4 (strain SL9) and 39·4 (strain OCA1) mol%.

As well as phylogenetic and phenotypic similarities, strains SL9 and OCA1 share genotypic similarities with T. subterraneus (DNA–DNA hybridization values between T. subterraneus and strains SL9 and OCA1 were 92·4 and 78·5 %, respectively), suggesting that they all belong to the same species. Surprisingly, the closest phylogenetic relatives of T. subterraneus, including Carboxydibrachium pacificum (96·8% sequence similarity), T. tengcongensis (97·7% and T. yonseiensis (98%), also presented significant DNA–DNA homology (values ≥ 70%) with this species (DNA–DNA hybridization values between T. subterraneus and the three species T. tengcongensis, T. yonseiensis and Carboxydibrachium pacificum were 67·9, 70·5 and 91·0%, respectively; DNA–DNA hybridization values between T. tengcongensis and the two species T. yonseiensis and Carboxydibrachium pacificum were 78·3 and 74·4%, respectively; DNA–DNA hybridization between T. yonseiensis and Carboxydibrachium pacificum was 90·4%), so that they should also be considered as members of T. subterraneus (Wayne et al., 1987). Despite phylogenetic and genomic similarities, significant phenotypic differences were found between all these micro-organisms (Table 1), including their DNA G+C contents and their ability to oxidize CO. In particular, T. subterraneus, strain OCA1 and strain SL9 have been isolated from oil reservoirs several hundred kilometres apart, thus suggesting that the phenotypical characteristics that distinguish strains SL9 and OCA1 from T. subterraneus

Table 1. Discriminating characteristics of subspecies of Caldanaerobacter subterraneus gen. nov., sp. nov., comb. nov.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>subterraneus*</th>
<th>tengcongensis†</th>
<th>yonseiensis‡</th>
<th>pacificus§</th>
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<tr>
<td>Type strain</td>
<td>DSM 13054T</td>
<td>JCM 11007T</td>
<td>DSM 13777T</td>
<td>DSM 12653T</td>
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<tr>
<td>Source</td>
<td>Oil well</td>
<td>Hot spring</td>
<td>Geothermal water</td>
<td>Hydrothermal vent, oil well</td>
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<td>Temperature for growth (°C):</td>
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<tr>
<td>Range</td>
<td>40–75</td>
<td>50–80</td>
<td>50–85</td>
<td>50–80</td>
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<td>Optimum</td>
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<td>70</td>
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<tr>
<td>pH for growth:</td>
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<td></td>
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<tr>
<td>Range</td>
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<td>5·5–9·0</td>
<td>4·5–9·0</td>
<td>5·8–7·6</td>
</tr>
<tr>
<td>Optimum</td>
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<td>7·0–7·5</td>
<td>6·5</td>
<td>6·8–7·2</td>
</tr>
<tr>
<td>NaCl concentration for growth (%):</td>
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<td></td>
<td></td>
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<tr>
<td>Range</td>
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<td>0–2·5</td>
<td>0–4</td>
<td>ND</td>
</tr>
<tr>
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<td>0–2·5</td>
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<tr>
<td>DNA G+C content (mol%)</td>
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<td>33</td>
<td>37</td>
<td>33</td>
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<tr>
<td>Use of CO</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>Diagnostic fermentation products from glucose:</td>
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<tr>
<td>Ethanol</td>
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<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Lactate</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
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</table>

*Data from Fardeau et al. (2000).
†Data from Xue et al. (2001).
‡Data from Kim et al. (2001).
§Data from Sokolova et al. (2001).
might have resulted from in situ physicochemical conditions of the oil wells from which they originated. These findings raise questions on the possible indigenous nature of such micro-organisms in the subsurface environment and in oilfield reservoirs, as hypothesized previously by L’Haridon et al. (1995) and Ollivier et al. (1998).

To elucidate the taxonomic status of *T. subterraneus*, strains SL9 and OCA1, *Carboxydibrachium pacificum*, *T. yonseiensis* and *T. tengcongensis*, we conducted further experiments to determine whether 1-l-alanine is a major end product of glucose fermentation by the type species of the genus *Thermoanaerobacter*, *T. ethanolicus*, and *T. brockii*, the closest phylogenetic relative of the above bacteria (mean sequence similarity of 93%). Both microorganisms are known to be acetate/ethanol/lactate producers (Zeikus et al., 1979; Wiegel & Ljungdahl, 1981), but have not been reported to produce 1-l-alanine from glucose metabolism. We demonstrated that besides ethanol, *T. ethanolicus* and *T. brockii* also produced 1-l-alanine during glucose catabolism [values of <0.2 mol l-alanine produced (mol glucose consumed)\(^{-1}\)], but only as a minor end product, compared to *T. subterraneus* and its phylogenetic relatives (strains SL9 and OCA1, *Carboxydibrachium pacificum*, *T. yonseiensis* and *T. tengcongensis*). Therefore, the metabolic products of sugar fermentation by *T. subterraneus*, strains SL9 and OCA1, *Carboxydibrachium pacificum*, *T. yonseiensis* and *T. tengcongensis*, which produce significant quantities of alanine [approx. 1 mol l-alanine produced (mol glucose consumed)\(^{-1}\)], clearly differ from those of *T. ethanolicus* and *T. brockii*. In addition, all these bacteria constitute a distinct phylogenetic lineage in the family ‘*Thermoanaerobiaceae*’ (Fig. 1). Most of them (*T. tengcongensis*, *T. yonseiensis*, *Carboxydibrachium pacificum* and strain SL9) grow at 80 °C and are extreme thermophiles, rather than thermophiles. To our knowledge, among the 18 species and subspecies of the genus *Thermoanaerobacter*, only *T. tengcongensis* *T. yonseiensis* (both to be reclassified – this report) and *T. brockii* grow at 80 °C (Zeikus et al., 1979; Schmid et al., 1986; Cayol et al., 1995). Due to high DNA homologies (values close to or higher than 70%) and high 16S rRNA gene sequence similarities, *T. subterraneus*, *T. tengcongensis*, *T. yonseiensis*, *Carboxydibrachium pacificum*, strain OCA1 and strain SL9 should belong to the same species (Wayne et al., 1987). According to Rule 24a (note 3) of the Bacteriological Code (Lapage et al., 1992), *Carboxydibrachium pacificum* (Sokolova et al., 2001), *T. yonseiensis* (Kim et al., 2001) and *T. tengcongensis* (Xue et al., 2001) should be considered as later heterotypic synonyms of *T. subterraneus* (Fardeau et al., 2000), which has the benefit of anteriority over all these microorganisms. This automatically invalidates the name of the genus *Carboxydibrachium*. Due to significant phylogenetic and metabolic differences between *T. subterraneus* and *Thermoanaerobacter* species, we propose to reassign *T. subterraneus*, strain SL9, strain OCA1, *Carboxydibrachium pacificum*, *T. yonseiensis* and *T. tengcongensis* to a novel genus and species of the family ‘*Thermoanaerobiaceae*’, as *Caldanaerobacter subterraneus* gen. nov., sp. nov., comb. nov. In addition, marked phenotypic differences between these micro-organisms (Table 1) allow clear identification of three novel subspecies of this genus: *Caldanaerobacter subterraneus* subsp. pacificus subsp. nov., *Caldanaerobacter subterraneus* subsp. yonseiensis subsp. nov. and *Caldanaerobacter subterraneus* subsp. tengcongensis subsp. nov. This automatically places the type strain of *T. subterraneus* (DSM 13054\(^T\)) as the type strain of *Caldanaerobacter subterraneus* subsp. subterraneus subsp. nov. According to Fig. 1, strains SL9 and OCA1 are related phylogenetically to *Caldanaerobacter subterraneus* subsp. subterraneus and *Caldanaerobacter subterraneus* subsp. pacificus, respectively.

**Description of *Caldanaerobacter gen. nov.*

*Caldanaerobacter* (cal.da.nae.ro.bac’ter. L. adj. caldus hot; Gr. pref. anot; Gr. n. aer air; N.L. masc. n. bacter equivalent of Gr. neut. n. bakterion rod, staff; N.L. masc. n. *Caldanaerobacter* rod that grows in the absence of air at high temperatures).

Cells are straight rods. Gram-reaction is positive or negative. Endospores may be observed. Growth is strictly anaerobic. Thermophilic, fermentative member of the domain *Bacteria*, family ‘*Thermoanaerobiaceae*’. Carbohydrates serve as fermentable substrates, with acetate and l-alanine as major end products. Approximately 1 mol l-alanine (mol glucose fermented)\(^{-1}\) is produced. DNA G+C content is 33–41 mol%. The type species is *Caldanaerobacter subterraneus*.

**Description of *Caldanaerobacter subterraneus* sp. nov., comb. nov.**

*Caldanaerobacter subterraneus* (sub.ter.ra’ne.us. L. pref. sub less than; L. n. terra earth; L. masc. adj. subterraneus underground, subterranean, describing its site of isolation).


Same description as that given for the genus. Acetate, l-alanine, lactate, H\(_2\) and CO\(_2\) are produced during glucose fermentation. Thiosulfate, but not sulfate, is produced during glucose fermentation. Thiosulfate, but not sulfate, is used as an electron acceptor.

The type strain is DSM 13054\(^T\) (=CNCM I-2383\(^T\)).

**Description of *Caldanaerobacter subterraneus* subsp. subterraneus subsp. nov.**

*Caldanaerobacter subterraneus* subsp. subterraneus (sub. ter. ra’ne.us. L. pref. sub less than; L. n. terra earth; L. masc. adj. subterraneus underground, subterranean, describing its site of isolation).

Rods (0.5–0.7 × 2–8 µm) that occur singly or in pairs and possess laterally inserted flagella. Spores are not observed under microscopic examination, but cultures exposed to...
120 °C for 45 min can be subcultured, indicating the presence of heat-resistant forms. Electron microscopic examination reveals a Gram-positive cell wall. Round colonies (3 mm in diameter) develop on Phytagel plates or in roll-tubes after 3 days incubation at 70 °C. Chemoorganotrophic and obligately anaerobic member of the domain Bacteria, family ‘Thermoaerobiaceae’. Thermophilic. Optimum temperature for growth is 65–75 °C at pH 7.5; temperature range for growth is 40–80 °C. Optimum pH is 7.0–7.5; growth occurs between pH 5.7 and 9.2. Halotolerant; grows in the presence of up to 3 % NaCl. Yeast extract or bio-trypticase is required for growth on carbohydrates. Growth on sugars is highly enhanced on sugars. Elemental sulfur, thiosulfate, but not sulfate, are used as electron acceptors. Reduced thiosulfate to sulfide. Oxidizes CO.

Description as that given by Sokolova et al. (2001). Approximately 1 mol L-alanine (mol glucose fermented)$^{-1}$ is produced. Reduces thiosulfate to sulfide. Oxidizes CO.

The type strain is JMT ($=$ DSM 12653$^T$), isolated from a submarine hot vent.

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