A novel anaerobic, Gram-positive, sporulating and strictly chemoorganoheterotrophic bacterium, designated strain DV1184\(^T\), was isolated from a deep-sea hydrothermal vent sample from the Mid-Atlantic Ridge. The cells were short, straight rods (4 \(\mu\)m long and 0.8 \(\mu\)m wide) and were motile with peritrichous flagella. They grew between 35 and 55 °C (optimum, 45 °C), between pH 5-0 and 8-0 (optimum, 6-0) and at 20–60 g sea salts l\(^{-1}\) (optimum sea salts concentration, 30 g l\(^{-1}\)). Strain DV1184\(^T\) was able to ferment yeast extract, tryptone, peptone, glucose, sucrose, maltose and pyruvate. The main fermentation products from glucose were (in decreasing order) formate, acetate and ethanol. The genomic DNA G+C content was 29 mol\%. Phylogenetic analysis of the 16S rRNA gene located the strain within cluster XI of the lineage that encompasses the genus Clostridium and related genera in the bacterial domain. On the basis of 16S rDNA sequence comparison and physiological and biochemical characteristics, it is proposed that the isolate should be described as a novel species, Tepidibacter formicigenes sp. nov. The type strain is DV1184\(^T\) (=CIP 107893\(^T\) = DSM 15518\(^T\)).

Among extreme environments, deep-sea hydrothermal vents contain large reservoirs of a wide variety of thermo-philic and hyperthermophilic micro-organisms that belong to the Bacteria and Archaea. Micro-organisms from these environments use different metabolic ways to grow; they may be chemolithoautotrophs, chemooorganoheterotrophs or mixotrophs (Jeanthon, 2000). Several studies have demonstrated the presence of thermophilic bacterial aerobes (Marteinson et al., 1995, 1996) and anaerobes (Antoine et al., 1997; Takai & Horikoshi, 2000).

The order Clostridiales represents one of the largest bacterial groups, comprising a wide range of Gram-negative or -positive, psychrophilic to thermophilic, spore-forming or non-spore-forming, chemolithoautotrophic or chemooorganoheterotrophic strains that colonize various habitats. The presence of members of the order Clostridiales in hydrothermal vent environments was revealed by 16S rDNA sequence analysis (Alain et al., 2002a; Wery et al., 2002). Anaerobic, heterotrophic thermophiles of the order Clostridiales have already been isolated from hydrothermal vents (Wery et al., 2001b; Alain et al., 2002b; Slobodkin et al., 2003). According to phylogenetic analysis based on 16S rDNA sequences, 19 clusters were proposed within the genus Clostridium (Collins et al., 1994). Members of cluster XI exhibit a wide diversity of physiological and metabolic characteristics; alkaliiphiles (Li et al., 1993, 1994), halophiles (Fendrich et al., 1990) and thermophiles (Alain et al., 2002b) have already been described.

In this paper, we describe a moderately thermophilic, spore-forming bacterium that was collected from deep-sea vents located on the Mid-Atlantic Ridge and has phenotypic and phylogenetic characteristics that allow its assignment to a novel species within cluster XI of the order Clostridiales. Samples were collected by the man-operated submersible DSV Nautil in 1994, during the DIVA2 cruise of deep-sea vent fields of the Mid-Atlantic Ridge: Lucky Strike (37°17’ N 32°16’ W; –1600 to –1700 m) and Menez-Gwen (37°51’ N 31°31’ W; –800 to –1000 m). Titanium tubes that were half-filled with PEXS medium, solidified with Gelrite (Scott Laboratories) as a gelling agent, were placed near the plume of hydrothermal vents to allow circulation of hydrothermal fluid over the surface of the medium. PEXS medium was composed as follows: 0.5 g peptone l\(^{-1}\), 0.25 g yeast extract l\(^{-1}\), 15 g NaCl l\(^{-1}\), 5.0 g xylan l\(^{-1}\) and 15 g Gelrite l\(^{-1}\). PEXS medium was prepared with a salinity lower than that of sea water, as it was considered that this could be a characteristic of undiluted vent fluid. Each tube was collected by the DSV Nautil and placed in an insulated box filled with sterile sea water. The box was opened in an onboard laboratory under sterile conditions. Bottled tubes were shaken in an anaerobic chamber after addition of sterile sea water and...
The new isolate was grown on glucose/yeast extract/peptone/sea salts (GYPS) medium that contained [(l)]−1: 30 g sea salts (Sigma), 1 g bacto-peptone (Difco), 0·5 g yeast extract (Difco), 6·05 g PIPES buffer (Sigma), 5 g D-(+)-glucose (Sigma) and 0·1% (v/v) resazurin solution. The pH was adjusted to 6·0 before autoclaving for 20 min at 121°C. The medium was reduced by addition of 0·5 g sodium sulfide before inoculation. Cultures were incubated at 45°C under anaerobic conditions at atmospheric pressure. Methods for the determination of growth parameters and enumeration of cells were reported previously (Wery et al., 2001b). Growth was observed at 35–55°C and the optimum temperature was around 45°C. No growth was observed at 30 or 60°C. The strain required NaCl for growth and grew at sea salt concentrations from 20 to 60 g l−1 (corresponding to 15–46 g NaCl l−1). No growth was observed in the absence of sea salts or at a concentration of 80 g sea salts l−1. The optimum sea salt concentration was approximately 30 g l−1 (corresponding to 23 g NaCl l−1). Growth occurred at pH 5·0–8·0; the optimum pH was around 6·0. In optimal conditions, the maximum cell concentration obtained was 109 cells ml−1 and the shortest generation time observed was 16 min.

Ability to use a single carbon source was investigated by adding one of the following compounds to GYPS medium (instead of glucose) to a final concentration of 0·5% (w/v): D-(+)-sucrose, D-(+)-glucose, D-(+)-cellobiose, D-(+)-xylose, D-(−)-fructose, starch, cellulose, dextran, xylan, ethanol, pyruvate, succinate, lactate, maltose, D-(+)-mannose, D-(+)-trehalose, lactose, D- arabino- side, D-(+)- galactose, D-(−)-ribose, L-(+)- rhamnose, D-mannitol, D-sorbitol, glycerol, peptone, tryptone, casein, albumin, gelatin, chitin, urea and olive oil. Strain DV1184T was able to grow mainly on complex proteinaceous substrates and carbohydrates. Very weak growth was observed on yeast extract as the sole energy and carbon source. In the presence of 0·05% (w/v) yeast extract, D-(+)-glucose, pyruvate, sucrose, fructose and maltose supported growth (maximum cell concentration, 8 × 107–1 × 108 cells ml−1) and poor growth was observed on ethanol, D-(+)-mannose (5 × 106–6 × 106 cells ml−1) and peptone (2 × 107–2·5 × 107 cells ml−1), with regard to growth on a control medium that was made without substrates (1 × 106–2 × 106 cells ml−1). As ethanol-dependent growth is unusual, analysis of products was performed. The results showed an increase in acetate production of 21% (2·25 mM), with regard to the control medium without ethanol (1·86 mM). None of the other organic acids,
alcohols or carbohydrates that were tested in combination with 0·05 % (w/v) yeast extract supported growth (maximum cell concentration, $1 \times 10^6 - 2 \times 10^6$ cells ml$^{-1}$). Production of H$_2$S was investigated by using lead acetate paper, as indicated by Alain et al. (2002b). No significant production was observed with regard to the control. No requirement for an external electron acceptor was observed, as elemental sulfur (10 g l$^{-1}$), polysulfides (Blumentals et al., 1990), sodium thiosulfate (20 mM), sodium sulfite (20 mM), sodium sulfate (20 mM), sodium nitrite (20 mM), sodium nitrate (20 mM) and FeCl$_3$ (10 mM) did not enhance growth.

Amino acids and organic acids as metabolic end products were analysed by means of HPLC, as described by Wery et al. (2001b). Products of glucose fermentation were acetate, ethanol and formate. After 24 h growth, final production per bacterial cell was 0·765 nmol ethanol, 0·794 nmol acetate and 1·29 nmol formate. Production (mol glucose used)$^{-1}$ was about 1·1 mol ethanol, 1·2 mol acetate and 1·9 mol formate. Production of formate was not reported for Clostridium paradoxum, Clostridium thermoalcaliphilum or Tepidibacter thalassicus, which were the most closely related micro-organisms. Such production has been reported for C. sporogenes, but the concentrations obtained were 20-fold lower (Alain et al., 2002b). No production of lactate or succinate was observed. Thus, a modified mixed acid fermentation type for this organism is a hypothesis to be tested in the future. In such a case, lack of lactate and succinate production could lead to unusual production of the other compounds in this pathway, particularly formate.

During growth on GYPS medium, concentrations of serine, arginine, threonine and proline decreased quickly to zero during the early-exponential phase. A decrease in concentrations of isoleucine, methionine and leucine occurred during growth. Concentrations of tyrosine, valine, phenylalanine, aspartate, histidine and glutamate were reduced only during the stationary phase. An increase in concentrations of alanine and glycine was observed during the stationary phase. Such results have not been reported before.

Genomic DNA was extracted as described by Wery et al. (2001a), purified by CsCl gradient centrifugation (Wery et al., 2001b) and its G+C content was determined by thermal denaturation, according to the method of Marmur & Doty (1962) under the conditions reported by Raguènes et al. (1997). A calibration curve was obtained by using ultrapure DNA from Escherichia coli strain B (G+C content, 50 mol%), Clostridium perfringens (26·5 mol%) and calf thymus DNA (42 mol%) as standards (Sigma). The genomic DNA G+C content of strain DV1184$^T$ was 29 mol%. The 16S rRNA gene was amplified selectively from purified genomic DNA by using the bacterial forward primer SAdir (5'-AGAGTTTGTATGGCTCAGA-3'), which corresponds to positions 8–28 of the E. coli 16S rRNA gene, and the bacterial reverse primer S17rev (5'-GTTACCTTGACGACTT-3'), which corresponds to positions 1493–1509. The reaction was performed as described by Wery et al. (2001b). The PCR product was sequenced by using primers described by Raguènes et al. (1996). This work was done by Genome Express (France); 1380 nt of the 16S rDNA sequence was determined. This sequence was then compared with others that were available in GenBank by using BLAST (Altschul et al., 1997). A multiple sequence file was obtained by using the MEGALIGN program of the DNASTAR package (Promega). Alignments and similarity levels were obtained by the CLUSTAL W method with weighted residues (Thompson et al., 1994). Alignments were corrected manually by using the multiple sequence alignment editor SEAVIEW and a phylogenetic tree was produced by using PHYLO_WIN (Galtier et al., 1996) with the following algorithms: Jukes–Cantor distance matrix and successively the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony and maximum-likelihood (Felsenstein, 1981) methods. Bootstraps values were determined according to Felsenstein (1985). Strain DV1184$^T$ was affiliated phylogenetically to the low-G+C content, Gram-positive bacteria. The nearest relatives with validly published names were T. thalassicus, C. paradoxum and C. thermoalcaliphilum, with respective 16S rDNA sequence similarity values of 95, 93 and 93 %. According to these results, it was concluded that strain DV1184$^T$ belonged to cluster XI of the lineage that encompasses the genus Clostridium and related genera. Cluster XI is very large and, consequently, the final phylogenetic reconstruction (Fig. 2) was performed only with closely related species among this cluster (with Caloranaerobacter azoresis as an outgroup).

![Fig. 2. Phylogenetic position of strain DV1184$^T$ within cluster XI of the order Clostridiales. Caloranaerobacter azoresis and Clostridium acidurici were used as outgroups. GenBank accession numbers are noted in parentheses. The topology shown corresponds to an unrooted tree obtained by the neighbour-joining algorithm (Kimura correction) that was established by using PHYLO_WIN and refined manually by using SEAVIEW. Bootstrap values are displayed on their relative branches. Bar, 0·011 substitutions per nucleotide position.](http://ijs.sgmjournals.org)
Pairwise evolutionary distances were computed by use of Kimura’s two-parameter model (Kimura, 1980) and a dendrogram was constructed from these distances by use of the neighbour-joining method. The positioning of strain DV1184T was supported by the results of the three phylogenetic algorithms that were used.

Strain DV1184T, a strictly heterotrophic and spore-forming bacterium that is able to ferment complex proteinaceous substrates and carbohydrates, has the major characteristics of the order Clostridiales. The lineage that encompasses the genus Clostridium and related genera is metabolically heterogeneous, containing a large proportion of fermentative and spore-forming micro-organisms (Rainey et al., 1993; Hippe et al., 1999; Takai et al., 2001). Similarities between T. thalassicus and strain DV1184T include cell morphology, ability to form endospores and low genomic DNA G+C content. However, the position of the endospore was subterminal and not terminal, as has been shown for T. thalassicus. They also differ in geographical place of isolation, production of formic acid from glucose by strain DV1184T, efficient growth of strain DV1184T on glucose, maltose, pyruvate, sucrose and fructose and weak growth on ethanol.

Based on phenotypic and genotypic differences and a 16S rDNA dissimilarity value of 5% between strain DV1184T and the nearest described species, we propose that strain DV1184T should be assigned to a novel species of the recently described genus Tepidibacter in the order Clostridiales (Slobodkin et al., 2003). Due to its ability to produce formic acid, the name Tepidibacter formicigenes sp. nov. is proposed for this novel species.

Description of Tepidibacter formicigenes sp. nov.

Tepidibacter formicigenes (for.mi.ci.ge’nes. N.L. adj. formicicum from L. n. formico ant; Gr. v. gennao produce; N.L. adj. formicigenes producing formic acid).

Rod-shaped, motile by means of peritrichous flagella, Gram-positive and endospore-forming bacteria. Growth occurs between 35 and 55 °C (optimum, 45 °C), between pH 5.0 and 8.0 (optimum, 6.0) and at 20–60 g sea salts l⁻¹ (optimum sea salts concentration, 30 g l⁻¹). Anaerobic, heterotrophic, able to ferment mainly proteinaceous substrates and carbohydrates. Produces ethanol, acetate and especially formate. Genomic DNA G+C content is 29 mol%. The 16S rRNA gene locates the strain within cluster XI of the lineage that encompasses the genus Clostridium and related genera in the bacterial domain, in the genus Tepidibacter. 16S rDNA similarity to Tepidibacter thalassicus is 95%.

The type strain, DV1184T (= CIP 107893T = DSM 15518T), was isolated from a sample collected on the Menez-Gwen hydrothermal site on the Mid-Atlantic Ridge (37° 51’ N 31° 31’ W; −800 to −1000 m).

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