Thermodesulfovibrio aggregans sp. nov. and Thermodesulfovibrio thiophilus sp. nov., anaerobic, thermophilic, sulfate-reducing bacteria isolated from thermophilic methanogenic sludge, and emended description of the genus Thermodesulfovibrio

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Four obligately anaerobic, thermophilic, sulfate-reducing bacterial strains, designated TGE-P1T, TDVT, TGL-LS1 and TSL-P1, were isolated from thermophilic (operated at 55–60 °C) methanogenic sludges from waste and wastewater treatment. The optimum temperature for growth of all the strains was in the range 55–60 °C. The four strains grew by reduction of sulfate with a limited range of electron donors, such as hydrogen, formate, pyruvate and lactate. In co-culture with the hydrogenotrophic methanogen Methanothermobacter thermautotrophicus ΔH, strains TGE-P1T, TGL-LS1 and TSL-P1 were able to utilize lactate syntrophically for growth. The DNA G+C contents of all the strains were in the range 34–35 mol%. The major cellular fatty acids of the strains were iso-C17 : 0, iso-C16 : 0, C16 : 0 and anteiso-C15 : 0. Phylogenetic analyses based on 16S rRNA gene sequences revealed that the strains belong to the Thermodesulfovibrio clade of the phylum 'Nitrospirae'. On the basis of their physiological, chemotaxonomic and genetic properties, strains TGL-LS1 (=JCM 13214) and TSL-P1 (=JCM 13215) were classified as strains of Thermodesulfovibrio islandicus. Two novel species of the genus Thermodesulfovibrio are proposed to accommodate the other two isolates: Thermodesulfovibrio aggregans sp. nov. (type strain TGE-P1T =JCM 13213T =DSM 17283T) and Thermodesulfovibrio thiophilus sp. nov. (type strain TDVT =JCM 13216T =DSM 17215T). To examine the ecological aspects of Thermodesulfovibrio-type cells in the sludge from which the strains were originally isolated, an oligonucleotide probe targeting 16S rRNA of all Thermodesulfovibrio species was designed and

Abbreviations: CLSM, confocal laser scanning microscope; FISH, fluorescence in situ hybridization; NTA, nitritotriacetate; UASB, upflow anaerobic sludge blanket.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains TGE-P1T, TDVT, TGL-LS1 and TSL-P1 and Thermodesulfovibrio yellowstonii DSM 11347T are AB021302, AB231857, AB021303, AB021304 and AB231858, respectively.

Photomicrographs of the strains isolated in this study, graphs showing lactate degradation by strain TGE-P1T in the presence and absence of Methanothermobacter thermautotrophicus, in situ hybridization of sections from thermophilic granules viewed by CLSM and probe/target sequences of TDV1015 are available as supplementary material with the online version of this paper.
The genus *Thermodesulfovibrio* was described as a group of obligately anaerobic, curved rod-shaped, thermophilic bacteria that reduce sulfate and other sulfur compounds (Garrity & Holt, 2001; Henry et al., 1994). The genus belongs to a deeply branched lineage of descent in the domain *Bacteria*, forming the bacterial phylum *Nitrospirae* (Garrity & Holt, 2001). To date, there are two species of the genus with validly published names: *Thermodesulfovibrio yellowstonii* and *Thermodesulfovibrio islandicus* (Henry et al., 1994; Sonne-Hansen & Ahring, 1999). In addition, *Thermodesulfovibrio hydrogenophilus* has been proposed very recently as a novel species of the genus (Haouari et al., 2008), but the name has not yet been validly published. All three species were isolated from environments associated with freshwater hydrothermal sites; it was suggested that they perform oxidation of hydrogen and other organic matter through the reduction of sulfate in their original ecosystems (Henry et al., 1994).

In addition to oxidation with sulfate reduction, one of the other ecologically important physiological capabilities of some sulfate-reducing organisms is syntrophic degradation of organic compounds in the absence of sulfate (Bryant et al., 1977). Without oxidized forms of sulfur compounds, some known sulfate-reducers can synthetically degrade organic substances, such as lactate, ethanol and propionate, in close association with hydrogenotrophic methanogens via interspecies hydrogen (electron) transfer (Bryant et al., 1977; Klemps et al., 1985; Pluge et al., 2002). The capability for syntrophic growth of members of the genus *Thermodesulfovibrio* has not been examined previously; hence, it remains unconfirmed. However, during a molecular survey of methanogenic sludge of a thermophilic (operated at 55°C) upflow anaerobic sludge blanket (UASB) reactor fed with artificial organic wastewater, abundant 16S rRNA gene clones, accounting for 19% of the total prokaryotic clones examined, that were very closely related to members of the genus *Thermodesulfovibrio* were retrieved (Sekiguchi et al., 1998). Because sulfate concentrations in the wastewater were insufficient for this abundance on the basis of dissimilatory sulfate reduction, it was presumed that the detected phylotypes degraded the organic substances either fermentatively or syntrophically in association with methanogens. Therefore, cultivation of such potentially facultatively syntrophic organisms was attempted.

Four strains (TGE-P1T, TDVt, TGL-LS1 and TSL-P1) belonging to the genus *Thermodesulfovibrio*, some of which were capable of degrading lactate in co-culture with hydrogenotrophic methanogens without sulfate, were isolated. A brief communication on the isolation of strains TGE-P1T, TGL-LS1 and TSL-P1 has been published previously (Sekiguchi et al., 2002). In addition to these strains, strain TDVt was newly isolated as a non-syntrophic member of the genus in this study. In this paper, detailed morphological, physiological and chemotaxonomic characteristics of the strains are reported and two novel species are proposed. In addition, an oligonucleotide probe specific for the 16S rRNA of members of the genus *Thermodesulfovibrio* was designed and used in the detection of members of the genus by fluorescence in situ hybridization (FISH) to determine their spatial distribution and abundance within the original sludge sample.

Strains TGE-P1T and TGL-LS1 (=JCM 13214) were isolated from methanogenic sludge of a laboratory-scale, thermophilic (55°C) UASB reactor treating artificial wastewater containing sucrose, fatty acids and peptone (Sekiguchi et al., 1998). Strain TSL-P1 (=JCM 13215) was obtained from thermophilic (55°C) anaerobic wastewater treatment sludge fed with pulp industry wastewater. Strain TDVt was obtained from sludge of a full-scale anaerobic digester decomposing sewage sludge under thermophilic (53°C) conditions (Osaka, Japan). *Thermodesulfovibrio islandicus* DSM 11347T, *Thermodesulfovibrio islandicus* DSM 12570T, *Thermodesulfobacterium commune* DSM 2178T, *Thermodesulfobacterium thermophilum* DSM 1276T, *Clostridium acetobutylicum* DSM 792T, *Desulfotomaculum thermobenzoicum* subsp. *thermobenzoicum* DSM 6193T, *Desulfotomaculum thermocystenum* DSM 10259T, *Desulfovibrio vulgaris* DSM 644T, *Desulfbulbus propionicus* DSM 6523 (=strain MUD) and *Methanothermobacter thermautotrophicus* DSM 1053T (=AH1) were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ; Braunschweig, Germany). The basal medium used for enrichment, isolation and maintenance of strains TGE-P1T, TDVt, TGL-LS1 and TSL-P1 was prepared on the basis of that of Widdel & Pfennig (1981). The medium composition and cultivation have been described previously (Sekiguchi et al., 2000). Primary enrichments were carried out anaerobically at 55°C. A solid medium was prepared by adding purified agar (agar noble; Difco) to the medium as described above at a final concentration of 20 g l−1. Methanogenic and various anaerobic strains were cultured at either 37 or 55°C using the same medium except that their substrates were supplemented in vials in accordance with the instructions of the DSMZ.

To determine the optimum pH for growth of the four isolates, the pH of the medium containing 20 mM lactate and 20 mM sulfate was adjusted to between pH 5.0 and 9.0 by adding HCl or NaOH under a 100% N2 atmosphere. To evaluate the optimum temperature for growth, the isolates were cultivated anaerobically in lactate plus sulfate medium (pH35°C 7.0) at 20, 25, 37, 45, 50, 55, 60, 70 and 80°C. For all cultivations, duplicate cultures (1% inoculum) were incubated and optical density (OD400) was measured.
Growth and substrate utilization were examined in accordance with a previous report (Sekiguchi et al., 2000). All cultures were incubated anaerobically at 55 °C, pH25 7.0 for over 4 weeks. Growth and substrate utilization of the strains were determined using potential carbon and energy sources by monitoring OD400 increase and acetate production. In syntrophic growth/substrate utilization tests, cells of Methanotrophs were added to the medium (2 % inoculum); growth and substrate utilization were examined by measuring OD400 and methane production.

Cell morphology was examined under a phase-contrast microscope (Olympus AX80T). Scanning electron microscopy was performed using a Hitachi S4500 as described previously (Sekiguchi et al., 2000; Uemura & Harada, 1993). Gram-staining was performed by Hucker’s method (Doetsch, 1981). Phase-contrast micrographs were obtained using wet mounts on agar-coated slides (Pfennig & Wagener, 1986) for exponential phase cultures. Short-chain fatty acids, methanol, hydrogen and carbon dioxide were identified by GC (Sekiguchi et al., 2000). Other compounds, such as lactate, were determined by HPLC as described previously (Imachi et al., 2000). For fatty acid methyl ester analysis, fatty acids of cells were converted to methyl esters using HCl/methanol and were determined by GC-MS (Hitachi M7200A FC/3DQMS system) (Hanada et al., 2002). For the analysis, cells were harvested from cultures grown on lactate plus sulfate medium at 55 °C.

DNA was extracted and purified in accordance with the method described previously (Kamagata & Miyaki, 1991). DNA G+C content was determined by HPLC (Shimadzu LC-6A) with a UV detector (Shintani et al., 2000). Genetic relatedness was investigated by slot-blot DNA–DNA hybridization with a DIG DNA Labelling and Detection kit (Roche). Target DNA (10–100 ng) denatured with 0.8 M NaOH was slotted onto a nylon membrane (Hybond-N; Amersham Pharmacia Biotech) and the labelled DNA was reassociated in DIG Easy Hyb (Roche). After incubation overnight at 40 °C, membranes were washed with SSC (0.15 M NaCl plus 0.015 M sodium citrate) containing 0.1 % SDS. Hybridization signals were generated by NBT/BCIP solution included in the DIG detection kit (Roche) and measured by scanning colour intensities. Tests were performed at least in triplicate for each assay and self-hybridization of the probe with homologous target DNA was set to 100 %.

The genomic DNAs of the strains were recovered according to the method of Hiraishi (1992). 16S rRNA genes were amplified by PCR using Taq polymerase (Perkin Elmer) as described previously (Sekiguchi et al., 2000). The PCR primers used in the amplification were the bacterial domain-universal primer 8F (5′-AGAGTTTGATCCTGGCTCAG-3′; positions 8–27 in Escherichia coli) and the prokaryote-universal primer 1490R (5′-GGTTACCTTGTTACGACTT-3′; E. coli positions 1491–1509) (Weisburg et al., 1991). The PCR product was directly sequenced on a Beckman CEQ8000 DNA sequencer using a CEQ DTC quick start kit (Beckman Coulter). Sequence data were aligned in an ARB dataset using the ARB program package (Ludwig et al., 2004) and the aligned data were corrected manually by using the editing tool in the package. Phylogenetic trees were constructed on the basis of 16S rRNA gene sequences by the neighbour-joining method (Saitou & Nei, 1987) with the ARB program package. To estimate the confidence of tree topologies, bootstrap resampling analysis (Felsenstein, 1985) for 1000 replicates was performed for the neighbour-joining and maximum-likelihood methods using the PAUP* 4.0 and TREEFINDER program packages, respectively.

Gently washed and homogenized sludge from the thermophilic UASB reactor used for the isolation of the Thermodesulfovibrio strains was fixed and sectioned as described previously (Sekiguchi et al., 1999; Yamada et al., 2005). The following 16S rRNA-targeted oligonucleotide probes were used in this study: probe ARC915 specific to archaea (Stahl et al., 1988) and probe TDV1015 (5′-CCCCCTAAAGTGCCTCCCCCTT-3′; E. coli positions 1015–1029) specific to virtually all members of the genus Thermodesulfovibrio (designated in this study). The probes were labelled with either Cy3 or Cy5 for in situ hybridization. In situ hybridization for thin sections of granules was performed as described previously (Sekiguchi et al., 1999). The hybridization stringency was adjusted by adding formamide to the hybridization buffer (35 % for ARC915, 15 % for TDV1015). The cells hybridized with the probes were observed under a confocal laser scanning microscope (CLSM; Olympus FLUOVIEW BX50).

With 20 mM pyruvate (without addition of sulfate), vibrio-shaped cells grew in cultures inoculated with the highly enriched ethanol culture. After three successive transfers into the pyruvate medium, roll-tube isolation was performed. White, very small, lens-shaped colonies, 0.1–0.2 mm in diameter were formed after 2 weeks of incubation. This step was repeated three times and the purified strain, designated TGE-P1T, was obtained.

Similarly, in the presence of 20 mM lactate and 20 mM sulfate, slightly short, vibrio-shaped cells grew in cultures.
inoculated with the highly enriched lactate culture. As observed with strain TGE-P1T, white, small, lens-shaped colonies, 0.1–0.2 mm in diameter were formed within 2 weeks of incubation in roll-tube isolation, after three successive transfers in the lactate/sulfate medium. The isolation step was repeated three times and the purified strain, designated TGL-LS1, was obtained.

Strains TDV\textsuperscript{T} and TSL-P1 were obtained from enrichment cultures syntrophically degrading lactate under thermophilic (55°C) conditions. These enrichment cultures were prepared from two types of thermophilic (53–55°C) anaerobic wastewater treatment sludge and seemed to contain several morphotypes, as observed in enrichment cultures of strains TGE-P1T and TGL-LS1. Strains TDV\textsuperscript{T} and TSL-P1 were isolated by roll-tube isolation from the enrichment cultures with pyruvate, similarly to strain TGE-P1T. White, small, lens-shaped colonies, 0.1–0.2 mm in diameter were formed within 2 weeks of incubation in roll-tube isolation.

Cells of isolates TGE-P1T, TDV\textsuperscript{T}, TGL-LS1 and TSL-P1 were curved rods, 1–7 μm long and 0.3–0.4 μm wide (see Supplementary Fig. S1 available in IJSEM Online; Table 1). The length of the cells differed slightly between the strains (Table 1). Spore formation was not observed and Gram staining was negative for all the isolates. Motility was not observed in any isolate. Strain TGE-P1T\textsuperscript{T} formed dense cell aggregates (flocs) in liquid medium, although the other strains showed dispersed cell growth in the same liquid medium.

Physiological properties of strain TGE-P1T\textsuperscript{T} are shown in Table 1. Strain TGE-P1T\textsuperscript{T} was an obligately anaerobic organism: no growth occurred in the presence of oxygen (20%, v/v, in the gas phase). Yeast extract was not required, but it stimulated growth. Growth and substrate

<table>
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Table 1. Characteristics of strains TGE-P1T\textsuperscript{T}, TDV\textsuperscript{T}, TGL-LS1 and TSL-P1 and related Thermodesulfovibrio species

Strains: 1, Thermodesulfovibrio aggregans sp. nov. TGE-P1T\textsuperscript{T}; 2, Thermodesulfovibrio thiophilus sp. nov. TDV\textsuperscript{T}; 3, Thermodesulfovibrio islandicus TGL-LS1; 4, Thermodesulfovibrio islandicus TSL-P1 (data in columns 1–4 were obtained in this study); 5, Thermodesulfovibrio yellowstonii YP87\textsuperscript{T} [most data obtained from Henry et al. (1994), but some data such as fatty acid composition and substrate range were additionally examined in this study for strain DSM 11347\textsuperscript{T}]; 6, Thermodesulfovibrio islandicus R1Ha3\textsuperscript{T} (data from Sonne-Hansen & Ahring, 1999); 7, ‘Thermodesulfovibrio hydrogenophilus’ Hbr5 (Hauari et al., 2008). All strains give positive results for the utilization of pyruvate, hydrogen (plus acetate) and formate (plus acetate) as electron donors (and carbon source) in the presence of sulfate. All strains give negative results for the utilization of acetate and ethanol as electron donors. All strains are positive for fermentative growth with pyruvate, but negative for fermentative growth with lactate. All strains are positive for utilization of sulfate and thiosulfate as electron acceptors, but negative for elemental sulfur. –, Negative; +, positive; i, iso; ai, anteiso; ND, no data available.
utilization were observed with the following substrates under optimum conditions (60 °C, pH 7.0) with sulfate (20 mM) as electron acceptor: hydrogen (1 atm), formate, \( \text{L-lactate} \) and pyruvate. The following substances did not support growth (1 mM), acetate, propionate and butyrate (all at 20 mM), butanol (all at 20 mM), benzoate (5 mM), phenol (1 mM), acetate, propionate and butyrate (all at 20 mM). Fermentative growth occurred only in the presence of pyruvate. The following substances did not support fermentative growth: Casamino acids (0.1 %), yeast extract (0.1 %), crotonate, betaine, glucose, ribose, xylose, glycerol, malate, fumarate and lactate (all at 20 mM).

Strain TGE-P\textsuperscript{1T} grew in co-culture with the hydrogenotrophic methanogen *Methanotrophobacter thermotrophicus* AH\textsuperscript{T} in the presence of lactate. As shown in Supplementary Fig. S2a, half of the 20 mM DL-lactate was degraded and transformed into acetate and methane within 2 weeks of incubation in co-culture with hydrogenotrophic methanogens (electron recovery 97 %). The strain could degrade the same amount of \( \text{L-lactate} \) completely to acetate in co-culture; hence, it was suggested that strain TGE-P\textsuperscript{1T} is unable to degrade the enantiomer \( \text{D-lactate} \). In pure culture, acetate and hydrogen production from lactate occurred, but very slowly (Supplementary Fig. S2b). Ethanol did not support growth of the strain co-cultured with methanogens.

The following compounds were tested as electron acceptors using lactate medium: 20 mM sulfate, 20 mM nitrate, 2 mM sulfite, 20 mM thiosulfate and 5 mM ferric nitrolritrocate [Fe(III) NTA]. Sulfite, thiosulfate and Fe(III) NTA supported growth of strain TGE-P\textsuperscript{1T}.

The same tests conducted on strain TGE-P\textsuperscript{1T} were also performed on the other three strains (TDV\textsuperscript{T}, TGL-LS\textsubscript{1} and TSL-P\textsubscript{1}) and the physiological differences between the four strains and other *Thermodesulfovibrio* species are summarized in Table 1 (mainly differential data are listed). The doubling times for strains TDV\textsuperscript{T}, TGL-LS\textsubscript{1} and TSL-P\textsubscript{1} on lactate/sulfate medium under optimum conditions (55 °C, pH 7.0) were similar to that of strain TGE-P\textsuperscript{1T}.

Strain TDV\textsuperscript{T} used sulfite as an electron acceptor for growth in addition to the same external electron acceptors used by the other three strains (Table 1). Strain TDV\textsuperscript{T} co-cultured with hydrogenotrophic methanogens in the absence of sulfate did not form methane from lactate nor did it grow, unlike the other strains, indicating that this strain cannot degrade lactate syntrophically, although it was isolated from the enrichment culture capable of methanogenic lactate degradation.

The DNA G + C contents (mean ± SD) of strains TGE-P\textsuperscript{1T}, TDV\textsuperscript{T}, TGL-LS\textsubscript{1} and TSL-P\textsubscript{1} were calculated to be 35.2 ± 0.3, 34.0 ± 0.1, 34.4 ± 0.2 and 34.5 ± 0.3 mol %, respectively. Fatty acid methyl ester analysis showed that the major fatty acids of the strains were iso-C\textsubscript{17} : 0, iso-C\textsubscript{16} : 0, C\textsubscript{16} : 0 and anteiso-C\textsubscript{15} : 0 (Table 2). For all the strains isolated, >1450 nt of the 16S rRNA genes were sequenced and used for phylogenetic analyses to determine their phylogenetic position in the domain *Bacteria*. Phylogenetic analyses based on gene sequences revealed that the strains belonged to the phylum *Nitrospira*, in which their closest relatives were *Thermodesulfovibrio yellowstonii*, *Thermodesulfovibrio islandicus* and *Thermodesulfovibrio hydrogenophilus* (Fig. 1). The 16S rRNA gene sequence similarities of strain TGE-P\textsuperscript{1T} with *Thermodesulfovibrio yellowstonii* DSM 11347\textsuperscript{T}, *Thermodesulfovibrio islandicus* R1HA3\textsuperscript{T} and *Thermodesulfovibrio hydrogenophilus* Hbr5 were 95.9, 95.8 and 95.9 %, respectively, indicating the novelty of strain TGE-P\textsuperscript{1T} at least at the species level (Stackebrandt & Goebel, 1994). The 16S rRNA gene sequence similarities of strain TDV\textsuperscript{T} with *Thermodesulfovibrio yellowstonii* DSM 11347\textsuperscript{T}, *Thermodesulfovibrio islandicus* R1HA3\textsuperscript{T} and *Thermodesulfovibrio hydrogenophilus* Hbr5 were 95.5, 95.5 and 93.7 %, respectively. Strain TDV\textsuperscript{T} was also relatively distant from strain TGE-P\textsuperscript{1T} (94.1 % similarity).

The DNA G + C contents (mean ± SD) of strains TGE-P\textsuperscript{1T}, TDV\textsuperscript{T}, TGL-LS\textsubscript{1} and TSL-P\textsubscript{1} were calculated to be 35.2 ± 0.3, 34.0 ± 0.1, 34.4 ± 0.2 and 34.5 ± 0.3 mol %, respectively. Fatty acid methyl ester analysis showed that the major fatty acids of the strains were iso-C\textsubscript{17} : 0, iso-C\textsubscript{16} : 0, C\textsubscript{16} : 0 and anteiso-C\textsubscript{15} : 0 (Table 2). For all the strains isolated, >1450 nt of the 16S rRNA genes were sequenced and used for phylogenetic analyses to determine their phylogenetic position in the domain *Bacteria*. Phylogenetic analyses based on gene sequences revealed that the strains belonged to the phylum *Nitrospira*, in which their closest relatives were *Thermodesulfovibrio yellowstonii*, *Thermodesulfovibrio islandicus* and *Thermodesulfovibrio hydrogenophilus* (Fig. 1). The 16S rRNA gene sequence similarities of strain TGE-P\textsuperscript{1T} with *Thermodesulfovibrio yellowstonii* DSM 11347\textsuperscript{T}, *Thermodesulfovibrio islandicus* R1HA3\textsuperscript{T} and *Thermodesulfovibrio hydrogenophilus* Hbr5 were 95.9, 95.8 and 95.9 %, respectively, indicating the novelty of strain TGE-P\textsuperscript{1T} at least at the species level (Stackebrandt & Goebel, 1994). The 16S rRNA gene sequence similarities of strain TDV\textsuperscript{T} with *Thermodesulfovibrio yellowstonii* DSM 11347\textsuperscript{T}, *Thermodesulfovibrio islandicus* R1HA3\textsuperscript{T} and *Thermodesulfovibrio hydrogenophilus* Hbr5 were 95.5, 95.5 and 93.7 %, respectively. Strain TDV\textsuperscript{T} was also relatively distant from strain TGE-P\textsuperscript{1T} (94.1 % similarity). On the basis of these observations, strains TGE-P\textsuperscript{1T} and TDV\textsuperscript{T} should be classified as a representative of novel species of the genus *Thermodesulfovibrio*. Two novel species of the genus *Thermodesulfovibrio* are therefore proposed: *Thermo-

Table 2. Cellular fatty acid compositions of the strains isolated in this study and the type strains of *Thermodesulfovibrio yellowstonii* and *Thermodesulfobacterium commune*

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Genus Thermodesulfovibrio</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>C\textsubscript{14} : 0</td>
<td>0.1</td>
<td>0.8</td>
<td>ND</td>
<td>ND</td>
<td>0.4</td>
<td>0.1</td>
</tr>
<tr>
<td>iso-C\textsubscript{15} : 0</td>
<td>0.5</td>
<td>ND</td>
<td>2.0</td>
<td>1.7</td>
<td>0.6</td>
<td>0.3</td>
</tr>
<tr>
<td>anteiso-C\textsubscript{15} : 0</td>
<td>5.8</td>
<td>13.4</td>
<td>8.3</td>
<td>7.8</td>
<td>8.1</td>
<td>0.2</td>
</tr>
<tr>
<td>C\textsubscript{15} : 0</td>
<td>0.0</td>
<td>0.8</td>
<td>ND</td>
<td>ND</td>
<td>0.1</td>
<td>ND</td>
</tr>
<tr>
<td>iso-C\textsubscript{16} : 0</td>
<td>20.5</td>
<td>11.9</td>
<td>25.0</td>
<td>37.1</td>
<td>57.6</td>
<td>13.1</td>
</tr>
<tr>
<td>C\textsubscript{16} : 0</td>
<td>2.4</td>
<td>17.3</td>
<td>2.0</td>
<td>1.4</td>
<td>5.9</td>
<td>3.4</td>
</tr>
<tr>
<td>Branched C\textsubscript{17} : 0</td>
<td>3.0</td>
<td>2.4</td>
<td>12.7</td>
<td>6.7</td>
<td>1.1</td>
<td>5.7</td>
</tr>
<tr>
<td>iso-C\textsubscript{17} : 0</td>
<td>63.4</td>
<td>49.4</td>
<td>48.1</td>
<td>43.2</td>
<td>25.4</td>
<td>46.1</td>
</tr>
<tr>
<td>C\textsubscript{17} : 0</td>
<td>ND</td>
<td>1.6</td>
<td>ND</td>
<td>ND</td>
<td>0.1</td>
<td>0.1</td>
</tr>
<tr>
<td>iso-C\textsubscript{18} : 0</td>
<td>4.1</td>
<td>1.4</td>
<td>1.9</td>
<td>1.9</td>
<td>0.4</td>
<td>5.0</td>
</tr>
<tr>
<td>C\textsubscript{18} : 0</td>
<td>0.2</td>
<td>1.0</td>
<td>ND</td>
<td>0.2</td>
<td>0.3</td>
<td>26.0</td>
</tr>
</tbody>
</table>

Strains: 1, *Thermodesulfovibrio aggregans* sp. nov. TGE-P\textsuperscript{1T}; 2, *Thermodesulfovibrio thiophilus* sp. nov. TDV\textsuperscript{T}; 3, *Thermodesulfovibrio islandicus* TGL-LS\textsubscript{1}; 4, *Thermodesulfovibrio islandicus* TSL-P\textsubscript{1}; 5, *Thermodesulfovibrio yellowstonii* DSM 11347\textsuperscript{T}; 6, *Thermodesulfobacterium commune* DSM 2178\textsuperscript{T}. Data were obtained in this study, and are shown as percentages of the total fatty acids detected. **ND**, Not detected.
desulfovibrio aggregans sp. nov., with strain TGE-P1T as the type strain, and Thermodesulfovibrio thiophilus sp. nov., with strain TDVT as the type strain. Strains TGL-LS1 and TSL-P1 were very closely related to the type strains of Thermodesulfovibrio yellowstonii and Thermodesulfovibrio islandicus (99.5 % 16S rRNA gene sequence similarity) and were closely related to each other (99.6 % similarity). Therefore, to compare the differences between the strains and related species at the species level, DNA–DNA hybridization tests of respective genomic DNAs were performed. Genomic DNAs from strains TGL-LS1 and TSL-P1 were extracted and labelled as the DNA probe and their relatedness with DNAs from strains TGE-P1T, TDVT, TGL-LS1 and TSL-P1, Thermodesulfovibrio yellowstonii DSM 11347T and Thermodesulfovibrio islandicus DSM 12570T was examined. Genomic DNA from strain TGL-LS1 had high DNA–DNA hybridization values with that of strain TSL-P1 (mean ± SD of 99.1 ± 6.9 %) and Thermodesulfovibrio islandicus DSM 12570T (81.4 ± 9.0 %); DNA–DNA hybridization values with the other strains were lower than 60 %. Similarly, genomic DNA from strain TSL-P1 had a high DNA–DNA hybridization value with DNA from Thermodesulfovibrio islandicus DSM 12570T (74.1 ± 6.8 %); the hybridization values with the other strains were in the same ranges as values obtained with DNA from strain TGL-LS1. On the basis of the recommended cut-off point of 70 % DNA–DNA hybridization for bacterial species delineation (Wayne et al., 1987), it is concluded that strains TGL-LS1 and TSL-P1 should be classified as strains of the species Thermodesulfovibrio islandicus.

On the basis of 16S rRNA gene sequence information, an oligonucleotide probe specific to 16S rRNA of virtually all members of the genus Thermodesulfovibrio was designed (probe TDV1015; see Supplementary Table S1). The probe was used successfully to detect whole cells of Thermodesulfovibrio yellowstonii, Thermodesulfovibrio islandicus and the isolates obtained in this study by FISH. None of the other bacterial strains listed above (seven species) reacted with the probe (data not shown), indicating its specificity. Thin sections of sludge granules obtained from the thermophilic UASB reactor (from which strains TGE-P1T and TGL-LS1 were isolated) were prepared and subjected to FISH analysis using probe TDV1015. The probe detected a number of rod- or vibrio-shaped cells within the sludge granules (Supplementary Fig. S3); these cells were widely distributed within the outer and inner layers of the sludge granules.
This observation indicates that members of the genus *Thermodesulfovibrio* make up a significant population within the methanogenic thermophilic sludge. Indeed, *Thermodesulfovibrio*-type 16S rRNA gene clones [TUG4 (AB011332) and TUG5 (AB011333)] have frequently been retrieved from the same thermophilic sludge (Sekiguchi et al., 1998).

In previous 16S rRNA gene cloning and FISH studies of the same sludge sample (Sekiguchi et al., 1998, 1999), it was observed that the sludge possessed *Methanothrix* (‘*Methanoseta*’)-type cells and *Methanobacterium*-type cells as the major archaeal populations. Under normally adjusted CLSM conditions, double-staining FISH with probes TDV1015 and ARC915 (Stahl et al., 1988) of sections did not clearly show the close juxtaposition between *Thermodesulfovibrio*-type cells and archaeal cells (Supplementary Fig. S3a), because ARC915-positive, thick rod-shaped cells, morphologically similar to *Methanothrix*, fluoresced brightly with the ARC915 probe and consequently hid other weakly fluorescent archaeal cells (such as *Methanobacterium*-like cells) in the CLSM images. However, when the detection level of archaeal signals was increased when observing CLSM fields in order to visualize these weakly fluorescent archaeal cells, a number of slightly thin rod-shaped cells, resembling *Methanobacterium*, were observed as archaeal cells within the outer and middle layers of the sludge granules and some of these thin rod-shaped cells were found within microcolonies of TDV1015-positive cells (Supplementary Fig. S3b). Because the sludge had been used for the treatment of wastewater containing a limited amount of sulfate (160 mg sulfate l⁻¹, 3 % of the total chemical oxygen demand removed attributed to sulfate reduction) (Sekiguchi et al., 1998), most of the *Thermodesulfovibrio*-type cells in the sludge were presumed to thrive without dissimilatory sulfate reduction. Based on these observations in association with the physiological traits of the *Thermodesulfovibrio* strains isolated in this study, a possible ecophysiological role of the *Thermodesulfovibrio* in the sludge could be consumption of lactate in syntrophic association with hydrogenotrophic methanogens. Lactate has been suggested to be one of the most important intermediate compounds in methanogenic degradation of carbohydrates in thermophilic anaerobic wastewater treatment process (Stams & Zehnder, 1990).

**Description of Thermodesulfovibrio aggregans sp. nov.**

*Thermodesulfovibrio aggregans* (ag’gre.gans. L. part. adj. aggregans aggregating, aggregate-forming).

Curved rods or vibrios, 0.3–0.4 μm long and 2.0–7.0 μm wide. Non-motile. Gram-reaction-negative. Obligate anaerobe. Growth occurs between 45 and 70 °C, with optimum at 60 °C. The pH range is 6.0–8.5. Optimum growth occurs at pH 6.5–7.0. With sulfate as electron acceptor, the electron donors are lactate, hydrogen (in the presence of acetate), formate (in the presence of acetate) and pyruvate. Organic substrates are oxidized incompletely to acetate. Malate, fumarate, succinate, methanol, 1-propanol, 1-butanol, benzoate, phenol, acetate, propionate and butyrate are not used as electron donors. With lactate as electron donor, the electron acceptors are sulfate, thiosulfate and Fe(III) NTA. Hydrogenotrophic methanogens can also be used as the electron-accepting system. Nitrate, sulfite, fumarate and sulfur are not used. Fermentative growth occurs with pyruvate. Casamino acids, crotonate, betaine, glucose, ribose, xylose, glycerol, malate, fumarate, succinate, lactate, yeast extract and tryptone do not support fermentative growth.

The type strain is TGE-PIᵀ (=JCM 13213ᵀ =DSM 17283ᵀ), isolated from thermophilic sludge granules treating organic wastewater. The genomic DNA G+C content of the type strain is 35.2 mol%.

**Description of Thermodesulfovibrio thiophilus sp. nov.**

*Thermodesulfovibrio thiophilus* (thi.o’phi.lus. Gr. n. theion sulfur; Gr. adj. philos loving; N.L. masc. adj. thiophilus sulfur-loving).

Curved rods or vibrios, 0.3–0.4 μm long and 2.0–3.0 μm wide. Non-motile. Gram-reaction-negative. Obligate anaerobe. Growth occurs between 45 and 60 °C, with optimum at 55 °C. The pH range is 6.0–8.5. Optimum growth occurs at pH 7.0–7.5. With sulfate as electron acceptor, the electron donors are lactate, hydrogen (in the presence of acetate), formate (in the presence of acetate) and pyruvate. Organic substrates are oxidized incompletely to acetate. Malate, fumarate, succinate, methanol, 1-propanol, 1-butanol, benzoate, phenol, acetate, propionate and butyrate are not used as electron donors. With lactate as electron donor, the electron acceptors are sulfate, sulfite, thiosulfate and Fe(III) NTA. Hydrogenotrophic methanogens can also be used as the electron-accepting system. Fumarate, nitrate and sulfur are not used. Fermentative growth occurs with pyruvate. Casamino acids, crotonate, betaine, glucose, ribose, xylose, glycerol, malate, fumarate, succinate, lactate, yeast extract and tryptone do not support fermentative growth.

The type strain is TDVᵀ (=JCM 13216ᵀ =DSM 17215ᵀ), isolated from thermophilic sewage sludge decomposing organic solid wastes. The genomic DNA G+C content of the type strain is 34.0 mol%.

**Emended description of Thermodesulfovibrio**

*Thermodesulfovibrio*

Henry et al. 1994

In addition to the criteria given by Henry et al. (1994), the genus circumscription is emended as follows. All species may use Fe(III) NTA as the electron acceptor for growth; some species use nitrate as well. Some species can also use hydrogenotrophic methanogens as the electron-accepting system. The main fatty acids are iso-C₁₇:₀, iso-C₁₆:₀, C₁₅:₁ and anteiso-C₁₅:₀. The genomic DNA G+C content is...
29–38 mol%. The phylogenetic position is in a lineage of the phylum ‘Nitrospira’.

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References


