**Thermoanaerobacter pentosaceus** sp. nov., an anaerobic, extremely thermophilic, high ethanol-yielding bacterium isolated from household waste

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An extremely thermophilic, xylanolytic, spore-forming and strictly anaerobic bacterium, strain DTU01<sup>T</sup>, was isolated from a continuously stirred tank reactor fed with xylose and household waste. Cells stained Gram-negative and were rod-shaped (0.5–2 µm in length). Spores were terminal with a diameter of approximately 0.5 µm. Optimal growth occurred at 70 °C and pH 7, with a maximum growth rate of 0.1 h<sup>−1</sup>. DNA G+C content was 34.2 mol%. Strain DTU01<sup>T</sup> could ferment arabinose, cellobiose, fructose, galactose, glucose, lactate, mannitol, mannose, melibiose, pectin, starch, sucrose, xylan, yeast extract and xylose, but not cellulose, Avicel, inositol, inulin, glycerol, rhamnose, acetate, lactate, ethanol, butanol or peptone. Ethanol was the major fermentation product and a maximum yield of 1.39 mol ethanol per mol xylose was achieved when sulfite was added to the cultivation medium. Thiosulfate, but not sulfate, nitrate or nitrite, could be used as electron acceptor. On the basis of 16S rRNA gene sequence similarity, strain DTU01<sup>T</sup> was shown to be closely related to *Thermoanaerobacter mathanii* A3<sup>T</sup>, *Thermoanaerobacter italicus* Ab9<sup>T</sup> and *Thermoanaerobacter thermocopriae* JT3-3<sup>T</sup>, with 98–99% similarity. Despite this, the physiological and phylogenetic differences (DNA G+C content, substrate utilization, electron acceptors, phylogenetic distance and isolation site) allow for the proposal of strain DTU01<sup>T</sup> as a representative of a novel species within the genus *Thermoanaerobacter*, for which the name *Thermoanaerobacter pentosaceus* sp. nov. is proposed, with the type strain DTU01<sup>T</sup> (=DSM 25963<sup>T</sup>=KCTC 4529<sup>T</sup>=VKM B-2752<sup>T</sup>=CECT 8142<sup>T</sup>).

Extremely thermophilic micro-organisms have in the last few decades been the subject of great interest, not only due to their biological and evolutionary significance, but also for their biotechnological potential. One of the major interesting features is their ubiquitous ability to ferment a large range of carbohydrates, including in many cases those that compose feedstock for second-generation bio-ethanol production. In addition to this, a second-generation ethanologenic process employing an extremely thermophilic micro-organism would be less prone to contamination, and have a facilitated downstream product recovery, compared to a mesophilic process (Taylor et al., 2009).

Thermophilic, anaerobic, saccharolytic bacteria are distributed within the genera *Thermoanaerobacter*, *Thermoanaerobacterium* and *Clostridium*. The latest major phylogenetic revision of these genera occurred in 1994, when Collins *et al.* (1994) following work by Lee *et al.* (1993) and Rainey *et al.* (1993) proposed the reorganization of the genus *Clostridium* and related species, such as strains representing the genus *Thermoanaerobacter*, into several clusters, based on 16S rRNA gene analysis. This resulted in the regrouping of the included micro-organisms into several clusters, of which cluster V comprised old and newly assigned or combined species of the genus *Thermoanaerobacter*. Since then, other species have been added to the genus, most of them isolated from natural thermophilic environments, with the exception of *Thermoanaerobacter thermocopriae*, of which the type strain was isolated from cattle dung compost (Jin *et al.*, 1988). Recently, Verbeke *et al.* (2011a) have reported difficulties in the classification of new isolates representing the genus *Thermoanaerobacter* due to the presence of intervening sequences in some of the copies of the 16S rRNA gene in the bacterial genome. Based on these and previous findings regarding interoperonic diversity in *Thermoanaerobacter pseudethanolicus* and other related species (Fardeau *et al.*, 2004; Pei *et al.*, 2010), Verbeke *et al.* (2011a) suggest that the sole use of 16S rRNA gene similarity for taxonomic

**Abbreviations:** ANIb, average nucleotide identity by BLAST; DSMZ, German Collection of Microorganisms and Cell Cultures.

The GenBank/EMBL/DDJB accession number for the 16S rRNA gene sequence of strain DTU01<sup>T</sup> is GU176611.

A supplementary figure is available with the online version of this paper.
assignment in this genus ‘may not accurately reflect true evolutionary relationships’.

In this work we report the isolation of a new member of the genus *Thermoanaerobacter* that was indirectly isolated from household waste. Household and municipal waste and its deposition sites, such as landfills or composting facilities, are composed of materials coming from the most varied sources. A few studies have been made on the microbial diversity at these sites, mostly with the purpose of addressing problems that occur in the degradation processes (Partanen *et al.*, 2010; Pourcher *et al.*, 2001; Westlake *et al.*, 1995), rather than focusing on isolation of new micro-organisms. Westlake *et al.* (1995) detected cellulolytic bacteria in a landfill, and members of the class *Clostridia* were detected in the thermophilic, poorly aerated late stage of a full-scale composting facility (Partanen *et al.*, 2010). These findings suggest that industrially relevant species can be found in such environments. Recent reports of new isolations from anthropogenic habitats include isolates from compost (Yabe *et al.*, 2011), household waste (Yassin *et al.*, 2009), or animal faeces (Morotomi *et al.*, 2012).

An extreme thermophilic enrichment culture previously achieved 0.49 g ethanol g xylose$^{-1}$ under specific cultivation conditions (Zhao *et al.*, 2010). This culture had been enriched from a hydrogen-producing reactor, operating at 70 °C and using xylose as the main carbon source (Kongjan *et al.*, 2009). The inoculum for this reactor had been in turn obtained from a laboratory scale hydrogen-producing continuously stirred tank reactor fed with household waste, with an operating temperature of 70 °C and a hydraulic retention time of 3 days (Liu *et al.*, 2008).

This high-yielding ethanol-producing culture was used as the inoculum for the isolation process, which was carried out following the roll-tube technique (Hungate, 1969; Macy *et al.*, 1972). A series of dilutions of the enrichment cultures were transferred into a modified basic anaerobic (BA) medium (Angelidaki *et al.*, 1990): cysteine hydrochloride was omitted, 1 g yeast extract l$^{-1}$ was added, and it was supplemented with 11 g Gelrite l$^{-1}$ and 2 g MgCl$_2$ l$^{-1}$ to ensure that the medium remained solid at the incubation temperature of 70 °C (Lin & Casida, 1984). Except where noted, 5 g xylose l$^{-1}$ was used as the carbon source throughout the experiments. Colonies were picked with sterile Pasteur pipettes, diluted in fresh liquid medium and transferred to new roll tubes when grown. This procedure was repeated until only one colony type was present and then three times more to ensure purity.

After two weeks of incubation, 0.5–1 mm diameter, beige, flat colonies were visible in the tubes. Cell morphology was examined using a bright-field microscope (Axioskop; Zeiss). Photomicrographs were taken with a camera (DCF220; Leica) connected to the microscope. Cells were rod-shaped (0.5–2 μm) and appeared singly, in pairs or in chains (Fig. 1a). No active mobility was observed. Gram-negative staining was observed during both exponential and stationary growth phases, although the organism was phylogenetically Gram-positive (Wiegel & Ljungdahl, 1981). Spore staining was performed according to Schaeffer & Fulton (1933). Sporulation of cells into round, terminal spores was observed in the stationary phase of growth (Fig. 1b). Sporulating cultures survived autoclaving for 1 h at 120 °C, showing that the spores were heat-resistant.

The variation of OD$_{600}$ was measured using a Spectronic 20D+ (Thermo Scientific) and correlated with cell dry-weight using a calibration curve obtained under corresponding cultivation conditions. This method was used throughout the experiments to detect and quantify growth of the micro-organism. All batch tests and sampling were performed in triplicate. The doubling time under optimal conditions was 3.6 h. For pH range determination experiments, four different buffers were used in the media, at a final concentration of 50 mM: MES sodium salt, NaHCO$_3$, Tris (Trizma base) and Na$_2$CO$_3$. The temperature range for growth at pH 7 was 45–80 °C, with an optimum of 70 °C, and the pH range for growth at 70 °C was 5.36–8.92. Incubation at temperatures and pH higher than the growth range resulted in browning of the medium, caused by caramelization of xylose or the Maillard reaction (Buera *et al.*, 1987; Hill & Patton, 1947). Strain DTU01$^T$ was strictly anaerobic, with no detectable growth in aerobic or microaerophilic conditions.

Yeast extract was not required, but it stimulated growth. Using 1 g yeast extract l$^{-1}$ as the sole substrate led only to

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**Fig. 1.** Photomicrographs of vegetative cells (a) and sporulating cells (b) of strain DTU01$^T$. In (b), spores are stained green. Bars, 5 μm.
limited growth. The ability of strain DTU01T to utilize other substrates was determined using BA medium, but with 2 g test substrate l\(^{-1}\) instead of 5 g xylose l\(^{-1}\). Utilization was considered positive when variation in OD\(_{600}\) was twice or more than that of control cultures (containing 1 g yeast extract l\(^{-1}\) as sole carbon source), and weakly positive when the variation was only 10% higher. In the case of insoluble substrates, utilization was assessed by comparing the concentration of metabolite products present in the medium for each substrate with controls supplied only with 1 g yeast extract l\(^{-1}\) as a carbon source. Strain DTU01T grew on xylose, glucose, arabinose, fructose, galactose, cellobiose, lactose, mannitol, mannose, melibiose, pectin, soluble starch, sucrose and xylan from beechwood; but not on cellulose, Avicel, inulin, inositol, glycerol, rhamnose, acetate, lactate, ethanol, butanol or peptone.

Fermentation end products were determined using standard HPLC and GC techniques as described previously (Zhao et al., 2009). The major metabolic products after 24 h of cultivation, when using 5 g xylose l\(^{-1}\) as a carbon source, were ethanol, hydrogen, lactate and acetate.

The micro-organism was able to tolerate 4% (w/v) salinity. The use of the electron acceptors Na\(_2\)SO\(_4\), Na\(_2\)SO\(_3\), Na\(_2\)S\(_2\)O\(_3\), NaNO\(_3\), and NaNO\(_2\) (20, 5 and 2.5, 20 and 5 mM, respectively) was tested in medium that contained 0.5 g cysteine-HCl l\(^{-1}\) instead of Na\(_2\)S as the reducing agent. It was found that NaNO\(_2\) inhibited growth, that Na\(_2\)SO\(_4\) and Na\(_2\)SO\(_3\) had no effect, and that Na\(_2\)S\(_2\)O\(_3\) greatly increased the growth rate: after 18 h, the concentration of cells was, respectively, 1.2 and 1.5 times higher than when no electron acceptor was added. Accordingly, sulfide was detected in the medium when sulfite and thiosulfate were used. Interestingly, the use of Na\(_2\)S\(_2\)O\(_3\) led to a shift of the metabolic pathway to acetate production rather than ethanol: the ethanol:acetate ratio decreased from 4.76 (when no electron acceptor was used) to 0.35. In contrast, the use of Na\(_2\)SO\(_3\) resulted also in increased ethanol yields. In fact, previously, a yield of 1.28 mol ethanol per mol xylose had been achieved with this isolate (Tomás et al., 2011); this had been the highest ethanol yield from pentoses to be reported for a non-genetically modified strain. With the addition of 2.5 mM Na\(_2\)S\(_2\)O\(_3\) to a cultivation medium supplied with 5 g xylose l\(^{-1}\), 1.39 mol ethanol mol xylose l\(^{-1}\) was obtained, which is 83% of the theoretical ethanol yield from xylose. This result confirms that strain DTU01T is a promising candidate for a thermophilic industrial ethanol producer.

Chemotaxonomic analysis, such as detection of respiratory quinones, peptidoglycan structure, fatty acid composition and polar lipids, were performed by the Identification Service of the German Collection of Microorganisms and Cell Cultures (DSMZ; Braunschweig, Germany). Cells were grown overnight in liquid BA medium as described above, at 70°C and pH 7, then centrifuged, resuspended in a 10% (w/v) sucrose solution, and freeze-dried, before being sent to DSMZ.

No respiratory quinones were detected by the two-stage method described by Tindall (1990a, b). This is not unexpected for strictly anaerobic bacteria (Collins & Jones, 1981; Crespo et al., 2012; Kim et al., 2001; Yokoyama et al., 2010) and most new taxonomic descriptions of this type of micro-organism do not include isoprenoid quinone detection in their characterization methods. However, in a study by Yamamoto et al. (1998), menaquinone 7 was found in several thermophilic, anaerobic, Gram-positive bacteria, indicating that perhaps these molecules are more widespread than is currently thought.

Peptidoglycan analysis was performed by subjecting hydrolysate of whole cells of strain DTU01T to TLC on cellulose plates, as described by Schumann (2011). The whole-cell hydrolysate contained meso-diaminopimelic acid as the diagnostic amino acid, indicating that the peptidoglycan type in strain DTU01T is A\(_{1\alpha}\) or A\(_{1\gamma}\), a feature shared with other anaerobic thermophiles (Yamamoto et al., 1998).

For determination of the fatty acid profile, fatty acid methyl esters were obtained by saponification and methylation and extracted using the methods of Miller (1982) and Kuykendall et al. (1988) with minor modifications. The mixtures were further separated using the Sherlock Microbial Identification System (MIDI; Microbial ID). The predominant fatty acid was iso-C\(_{15:0}\) (40.39%), followed by other branched acids such as iso-C\(_{14:0}\) 3-OH (15.79%), iso-C\(_{17:0}\) (15.51%), iso-C\(_{16:0}\) (7.42%), anteiso-C\(_{15:0}\) (5.94%) and anteiso-C\(_{17:0}\) (4.25%). Minor components were iso-C\(_{13:0}\) (1.8%), C\(_{18:0}\) (1.44%), C\(_{14:0}\) (1.38%), C\(_{14:0}\) 2-OH (1.35%) and iso-C\(_{11:0}\) (0.59%). No unsaturated acids were detected. iso-Diabolic acid, an unusual, very long (C32) dimethyl dicarboxylic acid, which has been identified as the most abundant transmembrane fatty acid in some thermophilic strains (Balk et al., 2002; Jung et al., 1994; Lee et al., 2002), has not been detected in strain DTU01T.

Polar lipids were extracted using a chloroform:methanol: 0.3% aqueous NaCl mixture, 1:2:0.8 (by vol.) (Bligh & Dyer, 1959), and then separated by two-dimensional silica gel TLC, as described by Tindall et al. (2007). The profile of strain DTU01T presented eight resolved lipid spots (Fig. S1, available in IJSEM Online), corresponding to phosphatidylglycerol, diphosphatidylglycerol, two unidentified phospholipids and four unidentified polar lipid classes. Phosphatidylglycerol and diphosphatidylglycerol are commonly found in most prokaryotes (da Costa et al., 2011; Lechevalier & Lechevalier, 1988). The remaining unidentified lipids could correspond to plasmogens and sphingolipids, which are common in anaerobic bacteria (Lechevalier & Lechevalier, 1988).

For colony purity assessment and phylogenetic analysis, DNA was extracted using a QIAmp DNA Stool Mini kit (Qiagen, 51504). PCR-DGGE (denaturing gradient gel electrophoresis) was performed as described by Zhao et al. (2009). The PCR product was purified using a GenElute
PCR DNA Purification kit (NA1020; Sigma) and sent for sequencing at DNA Technology (Risskov, Denmark). Primers used for sequencing were universal primer 1492r, bacteria specific primer 24-f and a home-designed primer (5'-GGATTAGATACCTGATGTCGCCAG-3'). The identification of phylogenetic neighbours based on 16S rRNA gene sequence similarity was initially carried out by using the BLAST (Altschul et al., 1997) and megablast (Zhang et al., 2000) programs against the database of type strains with validly published prokaryotic names (Chun et al., 2007). The sequences with the highest scores were then selected for the calculation of pairwise sequence similarity using a global alignment algorithm, which was implemented at the EzTaxon server (http://www.eztaxon.org; Chun et al., 2007). Multiple sequence alignment was performed using the program CLUSTAL X 2 (Larkin et al., 2007) and manually edited in MEGA 5 (Tamura et al., 2011), which was also used for phylogenetic analysis. Consensus trees were inferred from 1000 replicates and were reconstructed using the maximum-likelihood method based on the Jukes–Cantor model (Jukes & Cantor, 1969).

Phylogenetic and similarity sequence analysis of the 16S rRNA gene sequence of strain DTU01T revealed that it was affiliated to the genus Thermoanaerobacter of the family Therm anaerobacteraceae (phylum ‘Firmicutes’) (Fig. 2). The calculation of pairwise sequence similarity values revealed that the closest relatives with validly published names were the two subspecies of Thermoanaerobacter mathranii (99.4%; Carlier et al., 2006; Larsen et al., 1997), Thermoanaerobacter italicus Ab9T (98.4%; Kozianowski et al., 1997) and Thermoanaerobacter thermocopiae JT3-3T (97.8%; Jin et al., 1998). Similarity with the remaining members of the genus Thermoanaerobacter was between 92.3 and 95.9%. All species of the genus Caldanaerobacter had 90.4–92.3% 16S rRNA gene similarity with strain DTU01T, while similarity with other bacteria remained below 89.9%. Thermoanaerobacter mathranii A3T and Thermoanaerobacter italicus Ab9T were ordered from the (DSMZ) and initially cultivated using the recommended media. For comparison purposes, both strains were cultivated in the same medium as for strain DTU01T.

All the closest relatives of strain DTU01T are thermophilic, anaerobic microbes that can ferment a wide range of substrates and produce ethanol as one of the products of mixed-acid fermentation, along with lactate, acetate, CO₂ and hydrogen. Despite this, a few morphological and physiological differences remain: Thermoanaerobacter mathranii A3T is not able to ferment pectin, and it can stain Gram-positive, while strain DTU01T always stains Gram-negative. In addition to this, it can use sulfate and thiosulfate as an electron acceptor, while DTU01T can use thiosulfate, but not sulfate. Thermoanaerobacter italicus Ab9T, despite not having the highest 16S rRNA gene similarity with DTU01T, shares more features and is placed on the same branch in the generated phylogenetic tree (Fig. 2). The substrate utilization profile is very similar, except for mannitol and the fact that while Thermoanaerobacter italicus Ab9T is able to degrade pectin and inulin efficiently; growth of strain DTU01T on pectin could only be classified as weakly positive. As for Thermoanaerobacter thermocopiae JT3-3T, this strain has a 10 °C lower temperature optimum and a distinct substrate profile.

Cells of strain DTU01T are generally smaller (0.5–2 μm) than cells of Thermoanaerobacter mathranii A3T, Thermoanaerobacter italicus Ab9T and Thermoanaerobacter thermocopiae JT3-3T. In addition to this, strain DTU01T was isolated from a reactor inoculated with household waste, while the others were isolated from thermophilic, natural environments such as an alkaline hot spring in the case of Thermoanaerobacter mathranii and a thermal spa in the case of Thermoanaerobacter italicus Ab9T. Strain DTU01T yields a higher amount of ethanol from xylose than any other wild-type, thermophilic anaerobe: 1.39 mol ethanol mol xylose⁻¹, which corresponds to 83% of the theoretical yield. When cultivated under the same conditions, strains DTU01T, Thermoanaerobacter mathranii A3T and Thermoanaerobacter italicus Ab9T exhibit distinct fermentation product profiles, and strain DTU01T remains the one with the highest ethanol yield on xylose. Finally, Thermoanaerobacter mathranii has a generation time that is almost twice as fast as that of strain DTU01T and Thermoanaerobacter italicus. A summary of the morphological and physiological differences between these closely related strains is reported in Table 1.

With the fast-paced advance of genetic technologies, the ‘gold standard’ for bacterial species definition that is DNA–DNA hybridization (Richter & Rossello-Mora, 2009) is slowly being left behind in favour of newer methods. Whole-genome sequence similarity has been shown to be correlated with DNA–DNA hybridization (Goris et al., 2007; Konstantinidis & Tiedje, 2005), and so has similarity of gene sequences other than the 16S rRNA gene (Verbeke et al., 2011b; Zeigler, 2003). With this in mind, and in order to further clarify the phylogenetic position of strain DTU01T regarding its closest relatives, total genomic DNA was sent to BGI (China) for determination of the DNA G+C content and sequencing. A draft genome (in 143 contigs), with a DNA G+C content of 34.2 mol% was obtained. This sequence was used to determine the average nucleotide identity by BLAST (ANIb) between strains DTU01T, Thermoanaerobacter mathranii subsp. mathranii A3T, Thermoanaerobacter italicus Ab9T and other reference strains representing the genus Thermoanaerobacter whose genome sequences are available from GenBank and the Joint Genome Institute (JGI; http://img.jgi.doe.gov/cgi-bin/w/main.cgi), by using the in silico DNA–DNA hybridization method of the Jspecies software (http://www.imedea.uib-csic.es/jspecies/about.html; Richter & Rosselló-Mora, 2009). Thermoanaerobacterium thermosaccharolyticum DSM 571T was used as a phylogenetically related outgroup for comparison purposes.

Previously, Verbeke et al. (2011a) conducted a similar analysis among species of the genus Thermoanaerobacter.
Since the parameters and genomic data used were the same, and for a better overview, the results of all the calculations are presented in Table 2. If the recommended species-delineating cut-off value of 95% ANIb is taken into account, then *Thermoanaerobacter mathranii* A3\(^T\), *Thermoanaerobacter italicus* Ab9\(^T\) and strain DTU01\(^T\) should be considered as the same species. This had already been pointed out by Verbeke et al. (2011a), based not only

**Fig. 2.** 16S rRNA gene sequence-based phylogenetic dendrogram of strain DTU01\(^T\) and members of the genus *Thermoanaerobacter*, its closest relatives and other selected members of the family *Thermoanaerobacteraceae*. The evolutionary history was inferred by using the maximum-likelihood method based on the Jukes–Cantor model (Jukes & Cantor, 1969). The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analysed (Felsenstein, 1985). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches (Felsenstein, 1985). Initial tree(s) for the heuristic search were obtained automatically as follows: when the number of common sites was <100 or less than one quarter of the total number of sites, the maximum-parsimony method was used; otherwise the BIONJ method with MCL distance matrix was used. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 30 nt sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1842 positions in the final dataset. Evolutionary analyses were conducted in MEGA 5 (Tamura et al., 2011).
on ANIb values, but also on several other well-described and validated genome-relatedness predicting models. However, this is not the only case where micro-organisms that have been classified as different species are shown to have above-threshold similarity values (and vice-versa). Such is the case of infectious disease-related species like *Escherichia coli* and *Shigella flexneri*, or the peculiar case of the species of the genus *Bordetella* (Konstantinidis & Tiedje, 2005). Different subspecies and strains with similar genotypic and/or phenotypic properties are often assigned to a single species when they are isolated from the same, or a very similar, habitat (Fardeau et al., 2004; Verbeke et al., 2011a). However, this is not the case with strain DTU01T and its closest relatives *Thermoanaerobacter mathranii* A3T (Larsen et al., 1997); 3, *Thermoanaerobacter italicus* Ab9T (Kozianowski et al., 1997); 4, *Thermoanaerobacter thermocopriae* JT3-3T (Jin et al., 1988). +, Positive; –, negative; NR, not reported; +W, weakly positive. Doubling time, substrate utilization, fermentation products and electron acceptor data from this study for all strains, except strain 4. All strains produce spores and are able to grow with galactose.

### Description of *Thermoanaerobacter pentosaceus* sp. nov.

*Thermoanaerobacter pentosaceus* (pen.to.sa’ce.us N.L. neut. n. pentosum a pentose sugar; L. masc. suff. -aceus suffix used with the sense of belonging to; N.L. masc. adj. pentosaceus relating to a pentose).

Cells are spore forming rods (0.5–2 μm in length), non-motile, and stain Gram-negative. They can appear singly, in pairs or short chains. Spores are terminal, round and approximately 0.5 μm in diameter. Strictly anaerobic, extremely thermophilic, neutrophilic, growing optimally at 70 °C (and within 50–80 °C) and at pH 7 (no growth tools. Until then, and in order to maintain coherence with the existing classifications within the genus *Thermoanaerobacter*, on the basis of physiological, chemotaxonomic, phylogenetic and environmental characteristics of strain DTU01T, we propose strain DTU01T to be assigned to a novel species of the genus *Thermoanaerobacter*, within the family *Thermoanaerobacteraceae*, order *Thermoanaerobacteriales*, class *Clostridia*, phylum ‘*Firmicutes*’.

#### Table 1. Phenotypic comparison of strain DTU01T and the type strains of its closest relatives

<table>
<thead>
<tr>
<th>Strains: 1, DTU01T (data from this study); 2, <em>Thermoanaerobacter mathranii</em> subsp. <em>mathranii</em> A3T (Larsen et al., 1997); 3, <em>Thermoanaerobacter italicus</em> Ab9T (Kozianowski et al., 1997); 4, <em>Thermoanaerobacter thermocopriae</em> JT3-3T (Jin et al., 1988).</th>
<th>1</th>
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<tr>
<td>16S rRNA gene similarity (%) to strain DTU01T</td>
<td>–</td>
<td>99.4</td>
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<td>DNA G+C (mol%)</td>
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<td>Cell size (μm)</td>
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<td>0.7–3.9</td>
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<td>Motility</td>
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<td>+</td>
<td>–</td>
<td>NR</td>
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<td>Doubling time (h)</td>
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<td>Fermentation products (mol xylose mol⁻¹)</td>
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<td>Ethanol, 0.29; acetate, 0.39; lactate, 0.14; hydrogen, 0.70</td>
<td>Ethanol, 0.41; acetate, 0.06; lactate, 0.34; hydrogen, 0.08</td>
<td>Ethanol, acetate, lactate, hydrogen</td>
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<tr>
<td>Thiosulfate</td>
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<td>+</td>
<td>+</td>
<td>NR</td>
</tr>
<tr>
<td>Source</td>
<td>Household waste (Denmark)</td>
<td>Slightly alkaline hot spring (Iceland)</td>
<td>Thermal spa (Italy)</td>
<td>Cattle dung compost (Japan)</td>
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below pH 5.36 or above pH 8.5). Can tolerate 4\% (w/v) NaCl. Can use arabinose, cellobiose, fructose, galactose, glucose, lactate, mannitol, mannose, melibiose, pectin, starch, sucrose, xylan, yeast extract and xylose, but not cellulose, Avicel, inositol, inulin, glycerol, rhamnose, acetate, lactate, ethanol, butanol or peptone, as carbon and energy source. Sulfite and thiosulfate can be used as terminal electron acceptor, but not sulfate, nitrite or nitrate. The doubling time under optimal conditions is 6.6 h.

The type strain, DTU01\(^T\) (= DSM 25963\(^T\)=KCTC 4529\(^T\)=VKM B-2752\(^T\)=CECT 8142\(^T\)), was isolated from a thermophilic reactor fed with household solid waste from a biogas plant in Grindsted, Denmark. The DNA G+C content of the type strain is 34.2 mol%.

Acknowledgements

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References


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Table 2. ANIb between strain DTU01\(^T\) and selected reference strains, determined using Jspecies (Richter & Rossello-Mora, 2009)
39E to Thermoanaerobacter ethanolicus, Thermoanaerobacter brockii, and Thermoanaerobacter thermohydrosulfuricus and Clostridium thermohydrosulfuricum, isolated from a hot spring in Japan. A cellulolytic thermophile from animal feces, compost, soil, and anaerobes.

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Verbeke, T. J., Sparling, R., Hill, J. E., Links, M. G., Levin, D. & Dumonceaux, T. J. (2011b). Predicting relatedness of bacterial genomes using the chaperonin-60 universal target (cpn60 UT);


