Tepidimicrobium xylanilyticum sp. nov., an anaerobic xylanolytic bacterium, and emended description of the genus Tepidimicrobium

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A novel, xylanolytic, anaerobic, moderately thermophilic bacterium, strain PML14\textsuperscript{T}, was isolated from the sludge of a thermophilic anaerobic digester treating municipal solid waste and sewage in Beijing, China. The strain was a Gram-positive, spore-forming and motile rod. Growth of the novel strain was observed at 25–67 °C (optimum 60 °C) and pH 5.8–9.3 (optimum pH 8.5). Strain PML14\textsuperscript{T} grew on a number of carbohydrates, including xylan, xylose, glucose and cellobiose, and a variety of proteinaceous compounds, including peptone, tryptone, Casamino acids, yeast extract, beef extract, casein hydrolysate, L-cysteine, L-serine, L-lysine, L-glycine, L-threonine, L-methionine and pyruvate. The fermentation products from glucose included acetate, ethanol, butyrate, hydrogen and carbon dioxide. Propionate was produced from xylan in addition to other compounds. Fe(III), 9,10-anthraquinone 2,6-disulfonate and thiosulfate were reduced with peptone as the electron donor. NH\textsubscript{3} was produced. Indole was not produced. Gelatin was not hydrolysed. The DNA G+C content of strain PML14\textsuperscript{T} was 36.2 ± 0.8 mol\% (Tm). Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain PML14\textsuperscript{T} was related to the members of cluster XII of the clostridia, most closely to Tepidimicrobium ferriphilum SB91\textsuperscript{T} with 93.8 % 16S rRNA gene sequence similarity. On the basis of polyphasic evidence from this study, it is suggested that strain PML14\textsuperscript{T} (\text{=CGMCC 1.5080\textsuperscript{T}=JCM 15035\textsuperscript{T}}) represents a novel species of the genus Tepidimicrobium, for which the name Tepidimicrobium xylanilyticum sp. nov., is proposed. An emended description of the genus Tepidimicrobium is also provided.
Strain PML14T grew strictly anaerobically. Growth occurred at 25–67 °C and pH 5.8–9.3, with optimum growth at 60 °C and pH 8.5, respectively. The strain could grow in the presence of 0–4.5 % (w/v) NaCl, with optimum growth at 3.0 % (w/v). The doubling time of strain PML14T was 4.1 h when growing on PYG at 60 °C. The strain used a number of proteinaceous compounds and carbohydrates, including peptone, tryptone, Casamino acids, yeast extract, beef extract and casein hydrolysate (each at 10 g l⁻¹), l-cysteine, l-serine, l-lysine, l-glycine, l-threonine, l-methionine and pyruvate (each at 20 mM), and xylan, xylose, glucose and cellobiose (each at 5 g l⁻¹). The following substrates were not utilized: mannose, lactose, galactose, sucrose, fructose, maltose, l-arabinose, rhamnose, glycerol, lactate, malate, fumarate, l-alanine, l-arginine, l-proline, casein, starch, CM-cellulose, filter paper and chitin. The fermentation products from glucose included hydrogen, carbon dioxide, acetate, ethanol, butyrate and a trace amount of propionate. While growing in xylan, strain PML14T produced substantial amounts of acetate, ethanol, propionate, hydrogen and carbon dioxide. Strain PML14T did not hydrolyse gelatin or curdle milk. NH₃, but not indole, was produced. When using peptone as electron donor, strain PML14T reduced 9,10-anthraquinone-2,6-disulfonate (AQDS) (20 mM) to 9,10-anthrahydroquinone, 2,6-disulfonate and thiosulfate (20 mM) to hydrogen sulfide. Fe(III) citrate and nitrate were also reduced. However, sulfate, selenite and fumarate were not used as electron acceptors with peptone (10 g l⁻¹) as the electron donor. The G+C content of the DNA of strain PML14T was 36.2 ± 0.8 mol% (Tₘ).

To ascertain the phylogenetic position of strain PML14T, an almost-complete 16S rRNA gene sequence (1528 bp) was compared with the most similar sequences and those of the representatives of clostridia retrieved from GenBank. On the basis of a consensus 1345 bp, a 16S rRNA gene sequence phylogenetic tree rooted with Peptostreptococcus hydrogenalis GIFU 7662T was constructed (Fig. 1). Phylogenetic analysis showed that strain PML14T was affiliated to the phylum Firmicutes, and belonged to cluster XII of the clostridia (Collins et al., 1994). The closest relative was T. ferrifilum SB91T with a sequence similarity of 93.8 %. The 16S rRNA gene sequence similarity levels of the novel strain with those of other members of cluster XII ranged between 86.5 and 92.8 %. Phylogenetic trees constructed by the neighbour-joining, UPMGA and minimum-evolution algorithms showed the same topology (Fig. 1).

As strain PML14T was found to be phylogenetically related to T. ferrifilum SB91T, the phenotypic characteristics of the two strains were determined in parallel. The phenotypic characterization (Table 1) revealed that strain PML14T could represent a novel species of the genus Tepidimicrobium. Morphologically, strain PML14T formed spores in PY medium, while T. ferrifilum did not. Strain PML14T also differed from T. ferrifilum by producing hydrogen and utilizing glucose, pyruvate and xylan. In

![Fig. 1. Phylogenetic dendrogram of strain PML14T and related species, based on 16S rRNA gene sequences and constructed using the neighbour-joining method. Percentages at nodes (≥50%) represent levels of bootstrap support based on 1000 resamplings. Solid circles indicate that the corresponding nodes were also recovered with UPMGA and minimum-evolution methods. Peptostreptococcus hydrogenalis GIFU 7662T was used as the outgroup. Bar, 2% sequence divergence.](http://ijs.sgmjournals.org)
addition, the optimum growth temperature of strain PML14T differed by 10 °C from that of *T. ferriphilum* (Slobodkin *et al.*, 2006 and this study). Therefore, we propose strain PML14T as the type strain of a novel species of the genus *Tepidimicrobium*, *Tepidimicrobium* xylanilyticum *sp.* nov. Accordingly, the description of the genus *Tepidimicrobium* is emended.

**Emended description of the genus *Tepidimicrobium* (Slobodkin *et al.* 2006)**

The genus description is the same as that given by Slobodkin *et al.* (2006) except that abilities to form spores and to reduce elemental sulfur, fumarate and selenite are variable.

**Description of *Tepidimicrobium xylanilyticum* sp. nov.**

*Tepidimicrobium* xylanilyticum (xy.la.ni.ly*’*ti.cum. N.L. n. xylanum xylan, a plant polymer; Gr. adj. lytikos able to loosen, able to dissolve; N.L. adj. lyticus -a -um dissolving; N.L. neut. adj. xylanilyticum xylan-dissolving). Cells are Gram-positive, straight or slightly curved rods with slightly pointed ends, 0.4–0.5 μm in diameter and 4.0–10.0 μm in length. Cells occur singly or in pairs and exhibit twitching motility due to peritrichous flagella. Occasionally, terminal spherical spores are formed. Colonies on PYG agar are white, round and 0.5 mm in diameter after cultivation at 60 °C for 72 h. Growth occurs at 25–67 °C (optimum 60 °C) and pH 5.8–9.3 (optimum pH 8.5). Growth occurs in the range of 0.4–5.0 % (w/v) NaCl, with optimum growth at 3.0 % (w/v). Utilizes a variety of substrates, including peptone, tryptone, Casamino acids, yeast extract, beef extract, casein hydrolysate, L-cysteine, L-serine, L-lysine, L-glycine, L-threonine, L-methionine, pyruvate, xylan, xylose, glucose and cellobiose. Acetate, ethanol, butyrate and hydrogen are the main products when glucose is available as the sole substrate, and a trace amount of propionic acid is also produced. The following substrates are not used: L-histidine, L-leucine, L-phenylalanine, L-valine, L-glutamine, L-tyrosine, tryptophan, L-isoleucine, L-proline, aspartate, L-alanine, L-arginine, ribose, fructose, mannose, lactose, galactose, L-arabinose, rhamnose, sucrose, maltose, melibiose, raffinose, aesculin, glycochen, inulin, casein, starch, glycerol, lactate, malate, fumarate, salicin, sorbose, trehalose, adonitol, amygdalin, dulcitol, erythritol, inositol, mannitol, sorbitol, ribitol, methanol, ethanol, 1-propanol, citrate, fumarate, malate, malonate, hippurate, sodium gluconate, butane diacid, β-hydroxybutyric acid, phenylacetic acid, CM-cellulose, chitin and filter paper. Milk is not curdled and gelatin is not liquefied. Produces NH₃ from PYG and H₂S from thiosulfate. Indole is not produced.

The type strain, PML14T (=CGMCC 1.5080T=JCM 15035T), was isolated from the sludge of a thermophilic anaerobic digester treating municipal solid waste and sewage in Beijing, China. The G+C content of the genomic DNA of the type strain is 36.2 ± 0.8 mol% (T_m).

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**References**


