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Tepidibacter hydrothermalis sp. nov., a novel anaerobic bacterium isolated from a deep-sea hydrothermal vent

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1 **Supplementary Material Files**

2 ***Tepidibacter hydrothermalis* sp. nov., a novel**
3 **anaerobic bacterium isolated from a deep-sea**
4 **hydrothermal vent**

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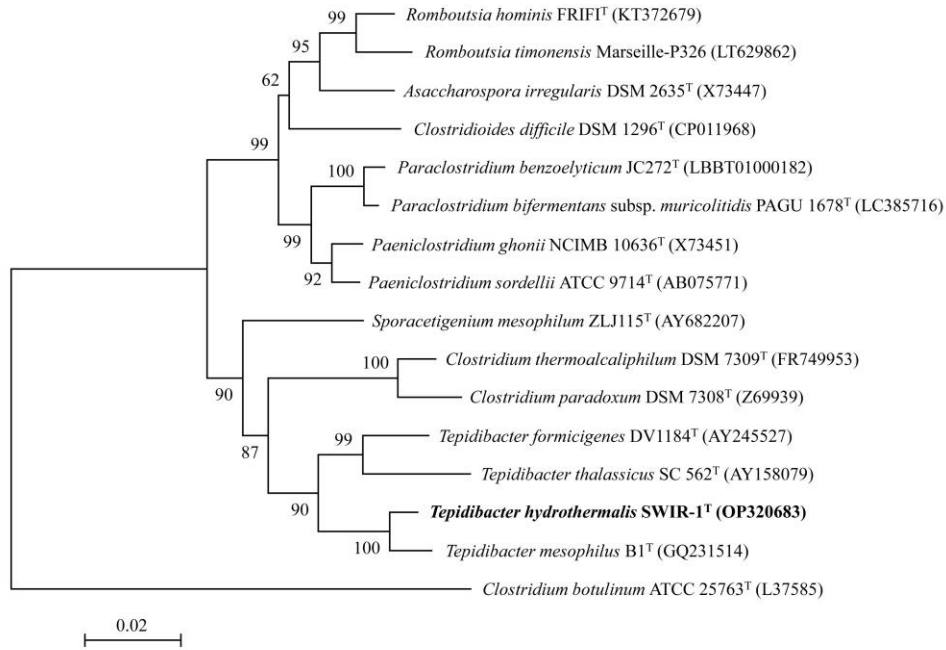
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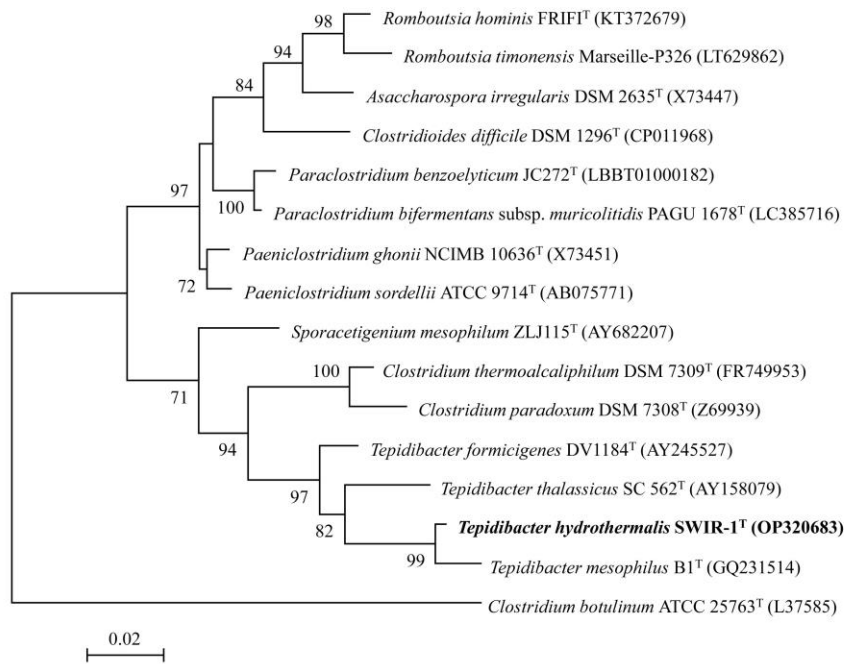
15 Correspondence: Xue-Gong Li: xuegongli@idsse.ac.cn; Long-Fei Wu: wu@imm.cnrs.fr

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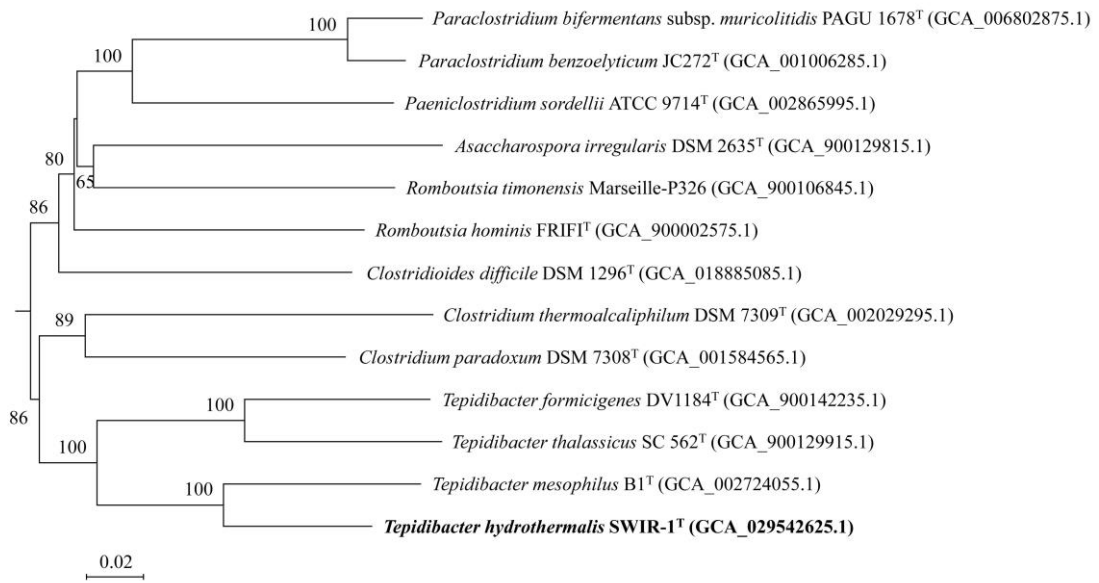
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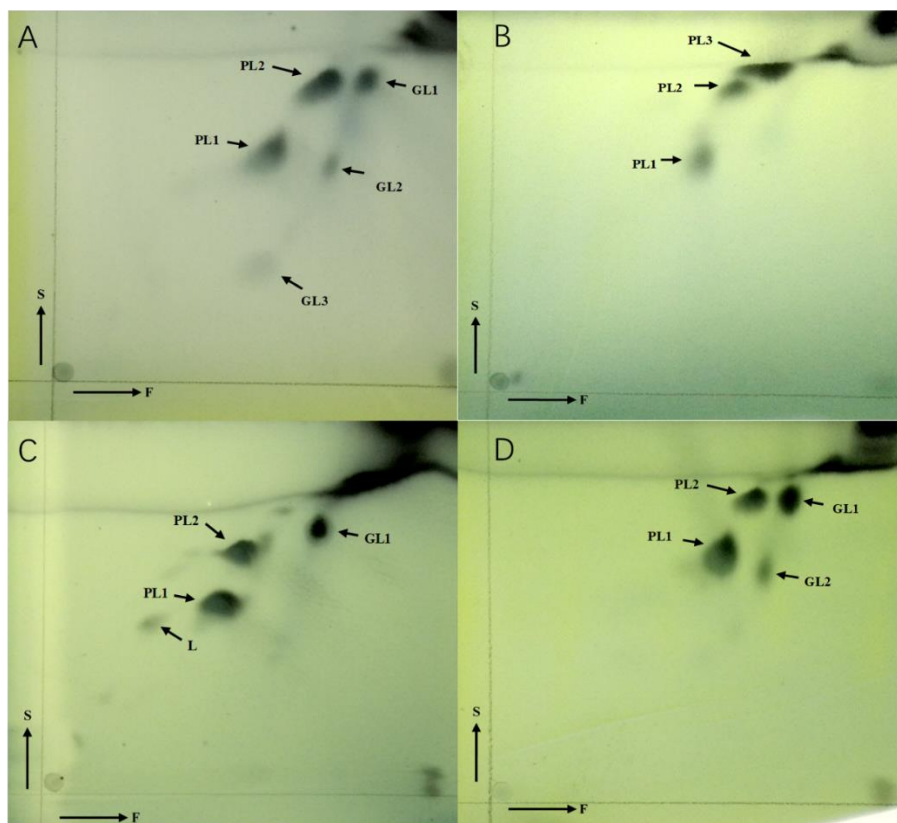
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B

19 Fig. S1. Phylogenetic tree based on 16S rRNA sequences of strain SWIR-1^T and its relatives
 20 according to the minimum evolution (A) and maximum likelihood (B) method. Bootstrap values
 21 above 50 % based on 1,000 replicates are shown at nodes. GenBank accession numbers of 16S
 22 rRNA sequences are given in parentheses. Bar, 2 nucleotide substitutions per 1,000 nucleotide
 23 positions.



24
 25 Fig. S2. Tree inferred with FastME 2.1.6.1 [1] from GBDP distances calculated from genome
 26 sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above
 27 branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average
 28 branch support of 84.3 %. The tree was rooted at the midpoint [2].



29
 30 Fig. S3. Polar lipids composition of strain SWIR-1^T and other *Tepidibacter* species. (A) strain
 31 SWIR-1^T; (B) *T. mesophilus* B1^T; (C) *T. formicigenes* DV 1184^T; (D) *T. thalassicus* SC 562^T.
 32 PL: Phospholipid, GL, glycolipid; L, unknown polar lipid; F-first dimension of TLC; S- second
 33 dimension of TLC.

34

35 **Supplementary Table S1.** Whole genome-based comparisons between strain SWIR-1^T and
 36 closely relatives.

Strains	ANI (%)	DDH (%)	AAI (%)
<i>Tepidibacter mesophilus</i> B1 ^T	87.2	35.7	78.9
<i>Tepidibacter formicigenes</i> DV1184 ^T	76.7	22.1	63.2
<i>Tepidibacter thalassicus</i> SC 562 ^T	77.3	21.5	62.3

37

38 **Supplementary Table S2.** Fatty acid composition of strain SWIR-1^T and its closely related
 39 strains. Strains: 1, Strain SWIR-1^T; 2, *T. mesophilus* B1^T; 3, *T. formicigenes* DV 1184^T; 4, *T.*
 40 *thalassicus* SC 562^T. Values are percentages of total fatty acids. Fatty acids that represented <1 %
 41 in all strains were omitted. TR, Traces (<1 %).

Fatty acid*	Composition (%) in:			
	1	2	3	4
C _{10:0}	TR	TR	1.1	TR
C _{11:0 iso}	1.2	TR	TR	TR
C _{12:0}	3.5	5.3	TR	1.0
C _{13:0 iso}	3.7	TR	1.8	2.1
C _{14:1ω5c}	1.5	TR	TR	TR
C _{14:0}	6.9	9.1	6.3	6.4
C _{13:0 iso 3OH}	1.7	TR	TR	TR
C _{15:1 iso F}	15.4	TR	10.1	5.2
C _{15:0 iso}	28.4	TR	57.5	59.5
C _{15:0 anteiso}	1.2	TR	2.2	1.4
C _{16:0}	9.8	23.8	4.8	5.5
C _{17:0 iso}	TR	TR	1.3	1.4
C _{17:0 cyclo}	TR	6.0	TR	TR
C _{18:1ω9c}	6.0	1.8	2.8	4.4
C _{18:0}	6.7	1.1	2.6	3.0
Summed Feature 1	1.6	TR	TR	TR
Summed Feature 2	TR	7.8	TR	TR
Summed Feature 3	2.2	28.9	1.0	1.3
Summed Feature 8	2.23	13.27	TR	1.45
Summed Feature 9	1.5	TR	TR	TR

42 *Summed Features are fatty acids that cannot be resolved reliably from another fatty acid using the
 43 chromatographic conditions chosen. The MIDI system groups these fatty acids together as one
 44 feature with a single percentage of the total. Summed Feature 1 contained iso-C_{15:1 iso H} and/or
 45 C_{13:0 3-OH}; Summed Feature 2 contained C_{12:0 aldehyde}; Summed Feature 3 contained C_{16:1 ω7c}
 46 and/or C_{16:1 ω6c}; Summed Feature 8 contained C_{18:1 ω7c} and/or C_{18:1 ω6c}; Summed Feature 9
 47 contained C_{17:1 iso ω9c}.

48

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53