

***Acetoanaerobium pronyense* sp. nov., an anaerobic alkaliphilic bacterium isolated from the Prony alkaline Hydrothermal Field in New Caledonia**

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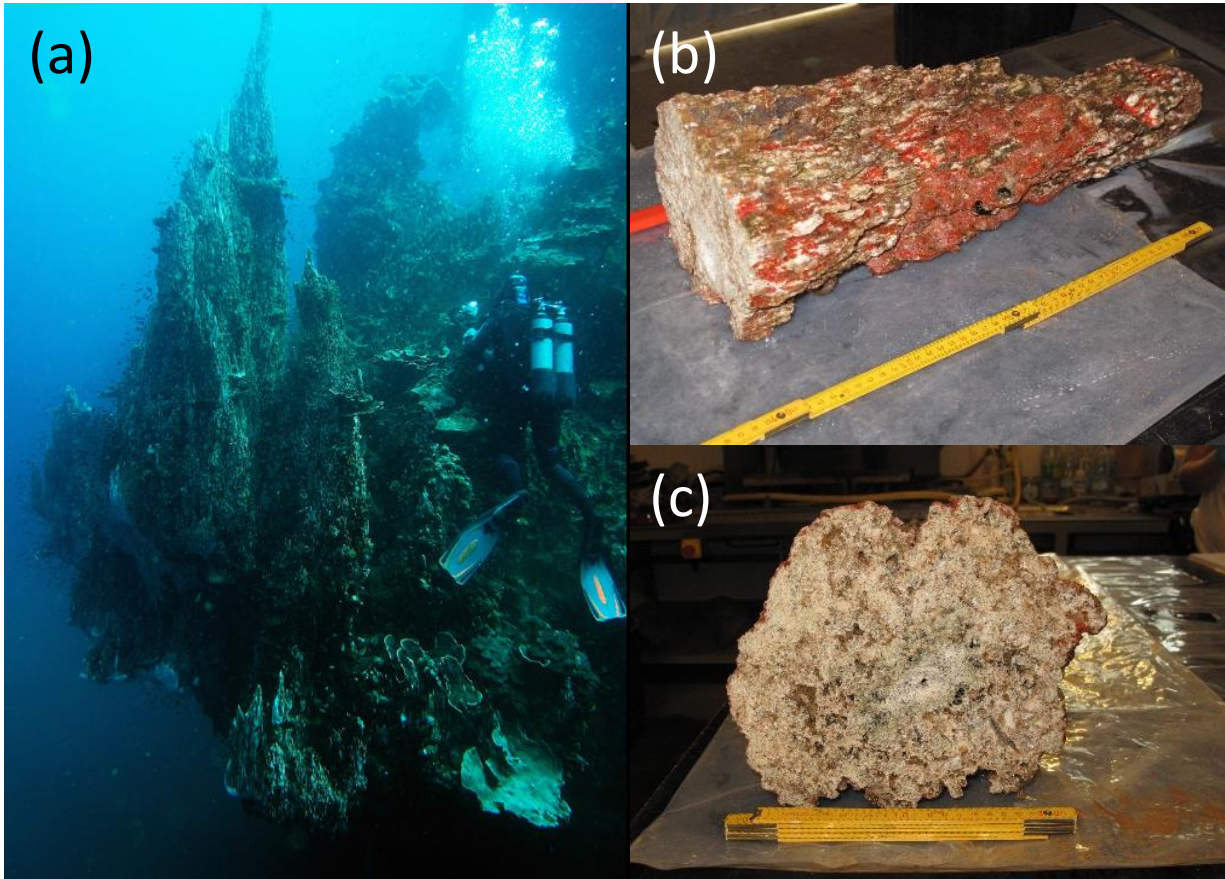
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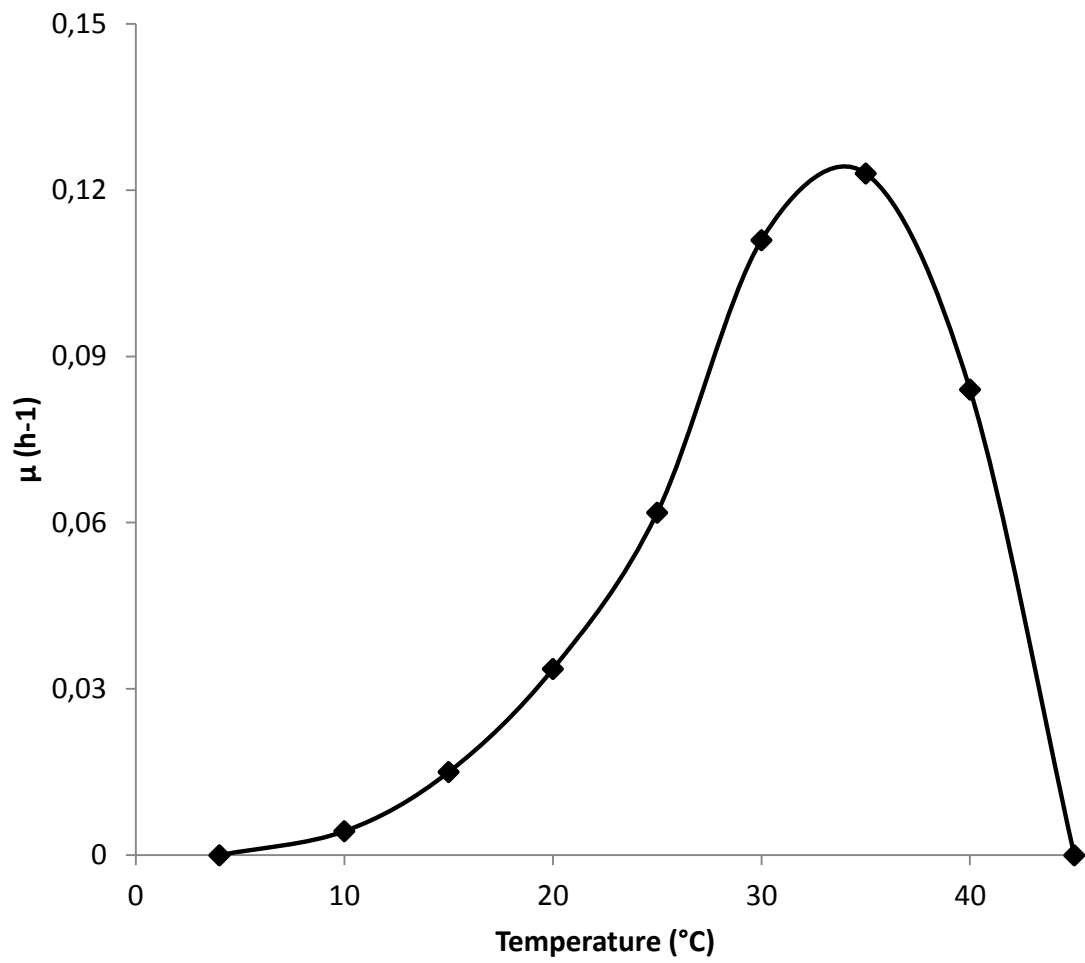
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Supplementary Table S1. Cellular fatty acid profiles as percentage (w/w) of strain ‘*Acetoanaerobium pronyense*’ ST07-YE^T. DMA, dimethyl acetal; ALDE, aldehyde.

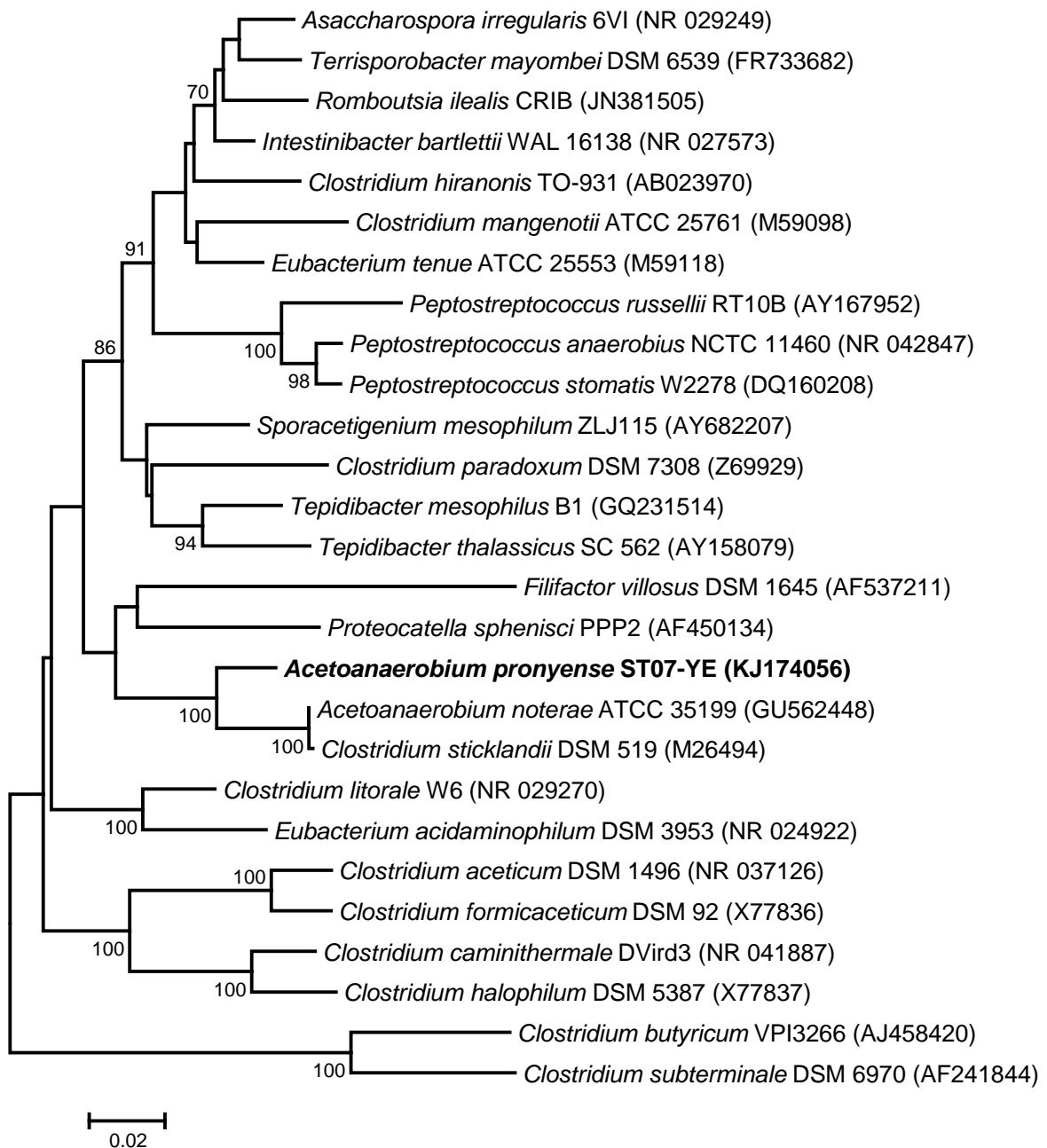
Fatty acids	Strain ST07-YE^T
C_{16:0}	46.4
C_{16:1 cis9}	14.1
C_{14:0}	6.1
C_{16:1 cis7}	5.5
C_{18:1 cis11}	4.2
C_{16:0 DMA}	4.0
C_{14:0 DMA}	3.8
C_{18:0}	2.8
C_{15:0}	2.5
C_{18:1 cis9}	2.0
C_{17:0}	1.9
C_{13:1 cis12}	1.6 (and/or 14 :0 ALDE)
C_{12:0}	1.3



Supplementary Fig. S1. (A) Underwater photograph of an actively venting part of the Needle of Prony (Credit photo: Dr R. Price), (B) photograph of the sampled chimney, (C) transversal cut view of the sampled chimney ((B) and (C) Credit photos: Pr B. Ménez, IPGP).



Supplementary Fig. S2. Temperature range and optimum for growth of strain ST07-YE^T on yeast extract medium with pH 9.5 and NaCl 2 g l⁻¹.



Supplementary Fig. S3. Phylogenetic tree based on 16S rRNA gene sequences showing the position of strain ST07-YE^T among the family *Peptostreptococcaceae* (order *Clostridiales*). A total of 1164 sites were used for the phylogenetic analysis. Accession numbers are indicated in brackets. The topology corresponds to an unrooted tree obtained by the Neighbor-Joining method (Maximum Composite Likelihood as substitution model). Numbers at nodes indicate bootstrap values above 70% from 1500 replications. The scale bar indicates 0.02 substitutions per nucleotide position. The 16S rRNA sequence from *Clostridium butyricum* VPI3266 (AJ458420) and *Clostridium subterminale* DSM 6970 (AF241844), both members of Cluster I, were used as outgroup.