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Supplementary material

Sulfuriferula thiophila sp. nov., a chemolithoautotrophic sulfur-oxidizing bacterium

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Table S1. Cellular fatty acid content (as percentages of the total) of strain mst6^T and strains of closely related species. Strains: 1, strain mst6^T; 2, *Sulfuriferula multivorans* TTN^T; 3, *Sulfurirhabdus autotrophica* BiS0^T; 4, *Sulfuricella denitrificans* skB26^T.

Fatty acid	1	2	3	4
$C_{8:0}$ 3-OH	–	–	–	2.4
$C_{9:0}$	–	–	0.1	–
$C_{9:0}$ 3-OH	–	–	0.1	–
$C_{10:0}$	2.9	0.4	0.2	–
$C_{10:0}$ 3-OH	1.4	1.5	5.4	–
$C_{11:0}$	0.1	–	–	–
$C_{12:0}$	6.8	5.1	0.5	–
$C_{12:0}$ 2-OH	0.2	0.2	–	–
$C_{12:0}$ 3-OH	1.6	2.7	–	–
$C_{13:1}$ at 12-13	–	–	–	0.1
$C_{14:0}$	0.4	0.2	1.1	0.4
$C_{14:0}$ω5c	0.2	–	–	–
$C_{15:1}$ω8c	–	–	0.1	–
$C_{15:1}$ω6c	0.4	0.2	0.2	–
$C_{16:1}$ω5c	–	–	0.6	1.4
$C_{16:0}$	26.7	33.6	26.4	23.5
$C_{16:0}$ 3-OH	0.2	0.2	0.2	0.3
$C_{17:0}$	0.3	0.6	0.2	–
$C_{17:1}$ ω8c	–	–	0.3	–
$C_{17:1}$ ω6c	0.2	–	0.4	–
cyclo-$C_{17:0}$	–	2.9	–	–
$C_{18:0}$	–	1.1	–	–
$C_{18:1}$ω9c	–	–	0.3	0.9
Summed features*				
3	55.5	44.7	61.8	62.2
4	–	3.7	–	–
8	3.3	3.8	2.0	8.4
$C_{18:1}$ω5c	–	–	–	0.1
$C_{18:0}$	0.3	1.1	0.4	0.4

* Summed features represent groups of two or three fatty acids that could not be separated using the MIDI system. Summed feature 3 comprises $C_{16:1}\omega7c$ and/or $C_{16:1}\omega6c$; summed feature 4 comprises $C_{16:1}\omega7c$ and/or iso-C_{15} 2-OH; summed feature 8 comprises $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$.

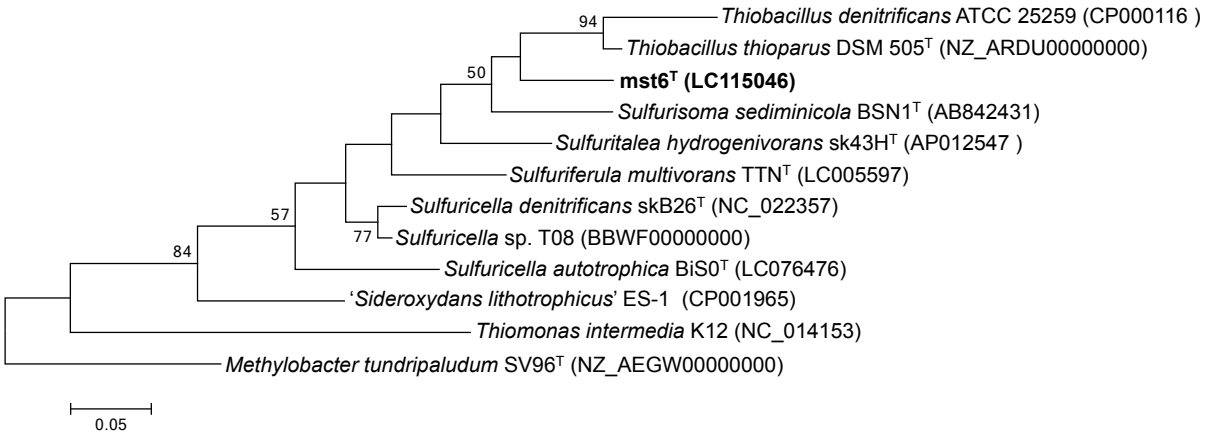


Fig. S1. Phylogenetic position of strain mst6^T within the class *Betaproteobacteria*, based on Sqr amino acid sequences aligned by ClustalW (118 amino acids were used). *Methylobacter tundripaludum* was used as an outgroup. Tree was constructed by the maximum likelihood method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.05 substitutions per amino acid position.

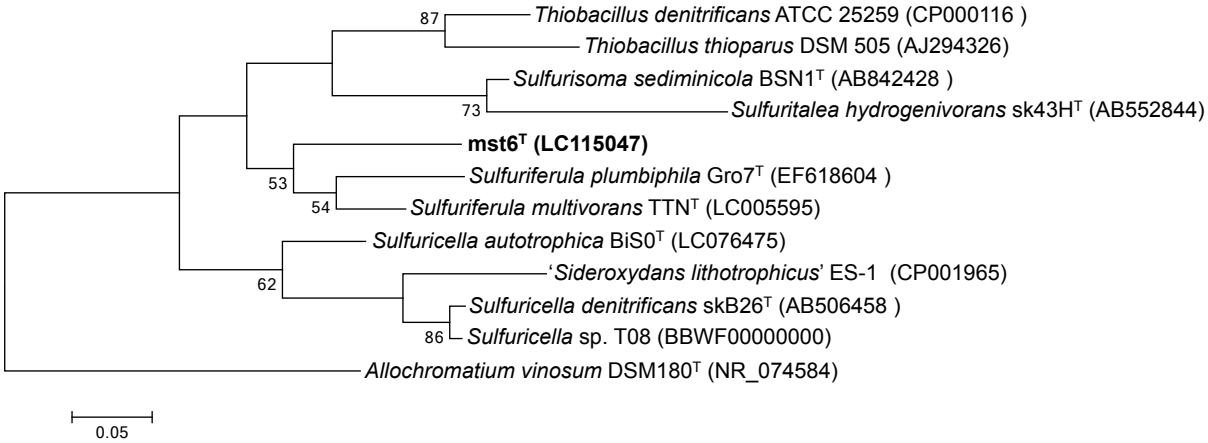


Fig. S2. Phylogenetic position of strain mst6^T within the class *Betaproteobacteria*, based on SoxB amino acid sequences aligned by ClustalW (117 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the maximum likelihood method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.05 substitutions per amino acid position.