

Supplementary Material

Unusual genomic traits suggest *Methylocystis bryophila* S285 to be well adapted for life in peatlands

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Table S1. SEED subsystem feature counts for *Methylocystis bryophila* S285, *Methylocystis* sp. SC2 and *Methylocella silvestris* BL2.

Subsystem Feature Counts¹	S285	SC2	BL2
Amino Acids and Derivatives	306	282	299
Carbohydrates	292	265	333
Cell Division and Cell Cycle	26	27	25
Cell Wall and Capsule	113	113	85
Cofactors, Vitamins, Prosthetic Groups, Pigments	274	215	291
DNA Metabolism	97	84	120
Dormancy and Sporulation	1	1	1
Fatty Acids, Lipids, and Isoprenoids	127	105	136
Iron acquisition and Metabolism	5	5	34
Membrane Transport	104	88	118
Metabolism of Aromatic Compounds	14	20	17
Miscellaneous	60	61	54
Motility and Chemotaxis	0	0	75
Nitrogen Metabolism	67	52	81
Nucleosides and Nucleotides	75	74	79
Phages, Prophages, Transposable elements, Plasmids	1	20	2
Phosphorus Metabolism	41	43	49
Photosynthesis	0	0	11
Potassium Metabolism	9	8	12
Protein Metabolism	265	253	277
Regulation and Cell Signaling	84	64	84
Respiration	171	172	172
RNA Metabolism	138	135	148
Secondary Metabolism	9	12	4
Stress Response	127	104	121
Sulfur Metabolism	51	39	58
Virulence, Disease and Defense	137	88	104
Total number of genes	2594	2330	2790

¹ Analysis was done on SEED subsystem level 1.

Table S2. Average nucleotide identity (ANI) calculation based on BLAST+

ANI values and - in parenthesis - aligned percentage ¹	Alphaproteobacteria								Gammaproteobacteria					Verrucomicrobia	
	<i>Mec.</i> ² <i>bryophila</i> S285	<i>Mec. sp.</i> strain SC2	<i>Mec. rosea</i> SV97	<i>Mec. parvus</i> OBBP	<i>Mec. sp.</i> strain SB2	<i>Mec. sp.</i> strain Rockwell	<i>Mec. sp.</i> strain LW5	<i>Ms.</i> <i>trichosporiu</i> <i>m</i> OB3b	<i>Mce.</i> <i>silvestris</i> BL2	<i>Mca.</i> <i>acidiphila</i> B2	<i>Mfe. stellata</i> AR4	<i>Mc.</i> <i>capsulatus</i> Bath	<i>Mmo.</i> <i>methanica</i> MC09	<i>Mm.</i> <i>alcaliphilum</i> 20Z	<i>Ma. inferorum</i> V4
<i>Mec. bryophila</i> S285	*	72.88 [32.40]	72.97 [31.29]	73.13 [33.31]	72.92 [31.14]	73.46 [32.00]	73.19 [33.63]	73.36 [33.60]	70.05 [23.02]	69.95 [25.43]	69.37 [22.89]	65.24 [8.10]	63.70 [5.58]	64.06 [4.33]	63.21 [1.64]
<i>Mec. sp.</i> strain SC2	73.28 [37.25]	*	91.24 [70.96]	76.56 [47.67]	91.19 [70.19]	77.57 [48.39]	74.30 [38.50]	74.70 [38.70]	71.02 [25.40]	70.68 [27.45]	70.58 [24.54]	65.30 [9.35]	63.77 [6.58]	63.59 [5.97]	62.89 [1.63]
<i>Mec. rosea</i> SV97	73.21 [35.61]	90.96 [70.13]	*	76.30 [46.47]	95.24 [78.04]	77.32 [48.62]	73.99 [37.94]	74.43 [37.09]	70.74 [26.48]	70.66 [26.58]	70.24 [24.22]	65.19 [9.22]	63.61 [6.52]	63.51 [5.83]	62.70 [1.58]
<i>Mec. parvus</i> OBBP	73.15 [33.44]	76.40 [40.96]	76.17 [39.96]	*	76.23 [38.95]	78.76 [48.16]	74.31 [36.10]	74.27 [36.05]	70.75 [23.88]	70.54 [24.85]	69.94 [22.69]	65.51 [8.23]	64.22 [5.66]	63.68 [4.88]	62.79 [1.22]
<i>Mec. sp.</i> strain SB2	73.26 [38.63]	91.01 [76.69]	95.63 [85.63]	76.41 [49.45]	*	77.43 [51.02]	74.14 [41.70]	74.50 [40.38]	70.91 [28.23]	70.59 [28.33]	70.41 [26.50]	64.95 [9.67]	63.94 [6.36]	64.04 [5.95]	63.12 [1.54]
<i>Mec. sp.</i> strain Rockwell	73.53 [30.35]	77.10 [39.99]	77.17 [40.99]	78.91 [46.98]	77.16 [38.00]	*	74.76 [33.69]	74.92 [34.00]	70.96 [21.54]	70.78 [24.10]	70.41 [20.38]	65.22 [7.84]	63.79 [5.38]	63.49 [4.91]	62.56 [1.41]
<i>Mec. sp.</i> strain LW5	73.71 [30.78]	74.14 [31.40]	74.01 [31.18]	74.60 [34.18]	74.01 [30.73]	75.00 [33.78]	*	80.17 [49.28]	71.19 [24.48]	71.20 [25.16]	70.57 [24.22]	65.75 [8.22]	64.63 [5.79]	64.28 [4.91]	63.54 [1.44]
<i>Ms. trichosporium</i> OB3b	74.08 [29.18]	74.85 [28.90]	74.76 [27.84]	74.69 [31.30]	74.75 [27.29]	75.38 [31.33]	80.45 [45.41]	*	71.55 [22.15]	71.57 [24.18]	70.90 [20.95]	65.87 [7.76]	64.15 [5.78]	64.14 [4.38]	63.16 [1.14]
<i>Mce. silvestris</i> BL2	69.97 [23.55]	70.67 [23.33]	70.41 [23.99]	70.82 [24.81]	70.45 [23.60]	70.68 [24.25]	70.69 [27.06]	71.05 [26.32]	*	73.77 [35.38]	71.89 [32.08]	64.97 [8.54]	63.77 [5.99]	63.71 [5.20]	62.65 [1.49]
<i>Mca. acidiphila</i> B2	70.13 [27.89]	70.47 [26.30]	70.27 [26.11]	70.51 [27.13]	70.27 [24.88]	70.47 [27.99]	70.72 [29.50]	71.06 [29.84]	73.63 [38.26]	*	72.55 [33.56]	65.20 [8.42]	63.40 [6.04]	63.24 [5.28]	62.66 [1.69]
<i>Mfe. stellata</i> AR4	69.16 [25.02]	69.88 [23.61]	69.99 [23.18]	69.71 [25.06]	70.03 [23.06]	69.93 [24.69]	70.07 [28.34]	70.12 [27.40]	71.72 [34.20]	72.37 [33.48]	*	64.81 [8.33]	63.27 [5.96]	63.24 [5.50]	62.79 [1.65]
<i>Mc. capsulatus</i> Bath	64.92 [11.85]	65.00 [11.63]	64.97 [11.24]	65.11 [12.15]	64.88 [11.04]	65.27 [11.89]	65.37 [11.83]	65.28 [12.80]	65.17 [11.33]	65.25 [10.79]	64.76 [10.58]	*	66.61 [26.19]	66.13 [23.34]	62.87 [2.77]
<i>Mmo. methanica</i> MC09	64.03 [5.09]	63.93 [5.47]	63.66 [5.41]	64.01 [5.54]	64.13 [5.08]	63.85 [5.57]	64.25 [5.54]	64.52 [5.62]	63.88 [5.29]	63.76 [5.13]	63.65 [5.17]	66.72 [17.75]	*	69.11 [28.92]	62.96 [1.57]
<i>Mm. alcaliphilum</i> 20Z	63.66 [4.60]	63.84 [4.75]	63.84 [4.85]	63.96 [4.72]	64.08 [4.72]	63.64 [4.85]	64.02 [4.90]	63.95 [4.67]	63.58 [4.88]	63.54 [4.62]	63.48 [4.90]	65.97 [17.45]	69.12 [31.35]	*	62.28 [1.78]
<i>Ma. inferorum</i> V4	62.80 [2.69]	63.00 [2.52]	62.66 [2.55]	62.94 [2.52]	63.02 [2.35]	62.56 [2.73]	63.19 [2.22]	62.82 [2.41]	62.76 [2.66]	62.59 [2.56]	63.27 [2.71]	62.47 [3.44]	62.18 [2.87]	61.56 [2.93]	*

¹Percentage values relate to the genomic regions that could be aligned.

²*Mec.* = *Methylocystis*, *Ms.* = *Methylosinus*, *Mce.* = *Methylocella*, *Mca.* = *Methylocapsa*, *Mfe.* = *Methyloferula*, *Mc.* = *Methylococcus*, *Mmo.* = *Methylomonas*, *Mm.* = *Methylomicrobium*, *Ma.* = *Methylacidiphilum*

Table S3. Comparison of gene traits between *Methylocystis* spp.

Number of common traits		II							
		<i>Mec.</i> ¹ <i>bryophila</i> S285	<i>Mec. sp.</i> strain SC2	<i>Mec. rosea</i> SV97	<i>Mec. parvus</i> OBBP	<i>Mec. sp.</i> strain SB2	<i>Mec. sp.</i> strain Rockwell	<i>Mec. sp.</i> strain LW5	<i>Mce. silvestris</i> BL2
I	<i>Mec. bryophila</i> S285	–	–	–	–	–	–	–	–
	<i>Mec. sp.</i> strain SC2	1959 (2222, 88.2%)	–	–	–	–	–	–	–
	<i>Mec. rosea</i> SV97	1969 (2291, 85.9%)	2083 (2211, 94.2%)	–	–	–	–	–	–
	<i>Mec. parvus</i> OBBP	1918 (2280, 84.1%)	1994 (2243, 88.9%)	1985 (2283, 86.9%)	–	–	–	–	–
	<i>Mec. sp.</i> strain SB2	1918 (2218, 86.5%)	2025 (2145, 94.4%)	2092 (2146, 97.5%)	1936 (2226, 87.0%)	–	–	–	–
	<i>Mec. sp.</i> strain Rockwell	1924 (2295, 83.8%)	1970 (2228, 88.4%)	1979 (2275, 87.0%)	2074 (2278, 91.0%)	1939 (2221, 87.3%)	–	–	–
	<i>Mec. sp.</i> strain LW5	1949 (2357, 82.7%)	1959 (2320, 84.4%)	1985 (2365, 83.9%)	1918 (2280, 84.1%)	1919 (2292, 83.7%)	2029 (2368, 85.7%)	–	–
	<i>Mce. silvestris</i> BL2	1858 (2471, 75.2%)	1820 (2464, 73.9%)	1874 (2495, 75.1%)	1911 (2518, 75.9%)	1817 (2416, 75.2%)	1890 (2516, 75.1%)	1999 (2577, 77.6%)	–
Number of unique traits ²		II							
		<i>Mec. bryophila</i> S285	<i>Mec. sp.</i> strain SC2	<i>Mec. rosea</i> SV97	<i>Mec. parvus</i> OBBP	<i>Mec. sp.</i> strain SB2	<i>Mec. sp.</i> strain Rockwell	<i>Mec. sp.</i> strain LW5	<i>Mce. silvestris</i> BL2
I	<i>Mec. bryophila</i> S285	–	148 (2222, 6.7%)	169 (2291, 7.4%)	160 (2280, 7.0%)	172 (2218, 7.8%)	184 (2295, 8.0%)	174 (2357, 7.4%)	224 (2471, 9.2%)
	<i>Mec. sp.</i> strain SC2	115 (2222, 5.2%)	–	55 (2211, 2.5%)	90 (2243, 4.0%)	64 (2145, 3.0%)	110 (2228, 4.9%)	130 (2320, 5.6%)	222 (2464, 9.0%)
	<i>Mec. rosea</i> SV97	153 (2291, 6.7%)	73 (2211, 3.3%)	–	122 (2283, 5.3%)	40 (2146, 1.9%)	140 (2275, 6.2%)	148 (2365, 6.3%)	216 (2495, 8.7%)
	<i>Mec. parvus</i> OBBP	195 (2280, 8.6%)	159 (2243, 7.1%)	176 (2283, 7.7%)	–	185 (2226, 8.3%)	118 (2278, 5.2%)	160 (2280, 7.0%)	239 (2518, 9.5%)
	<i>Mec. sp.</i> strain SB2	128 (2218, 5.8%)	56 (2145, 2.6%)	14 (2146, 0.7%)	105 (2226, 4.7%)	–	118 (2221, 5.3%)	132 (2292, 5.8%)	190 (2416, 7.9%)
	<i>Mec. sp.</i> strain Rockwell	187 (2295, 8.1%)	148 (2228, 6.6%)	156 (2275, 6.9%)	86 (2278, 3.8%)	164 (2221, 7.4%)	–	139 (2368, 5.9%)	232 (2516, 9.2%)
	<i>Mec. sp.</i> strain LW5	234 (2357, 9.9%)	231 (2320, 10.0%)	232 (2365, 9.8%)	189 (2280, 8.3%)	241 (2292, 10.5%)	200 (2368, 8.4%)	–	237 (2577, 9.2%)
	<i>Mce. silvestris</i> BL2	389 (2471, 15.7%)	422 (2464, 17.1%)	405 (2495, 16.2%)	368 (2518, 14.6%)	409 (2416, 16.9%)	394 (2516, 15.7%)	341 (2577, 13.2%)	–

¹*Mec.* = *Methylocystis*, *Mce.* = *Methylocella*.

²The reciprocal numbers (= unique gene traits) in up- and down-triangle were calculated by two-way comparison.

Table S4. Unusual genomic features of *Methylocystis bryophila* S285. Detection of particular gene traits is based on RAST/SEED annotation complemented with manual survey for the presence of particulate methane monooxygenases (pMMO1, pMMO2).

Gene loci in the genome of strain S285	Features ¹	Alphaproteobacteria									Gammaproteobacteria				Verrucomicrobia	
		<i>Mec.</i> ² <i>bryophila</i> S285	<i>Mec. sp.</i> strain SC2	<i>Mec. rosea</i> SV97	<i>Mec. parvus</i> OBBP	<i>Mec. sp.</i> strain SB2	<i>Mec. sp.</i> strain Rockwell	<i>Mec. sp.</i> strain LW5	<i>Ms. tricho-</i> <i>sporium</i> OB3b	<i>Mce.</i> <i>silvestris</i> BL2	<i>Mca.</i> <i>acidiphila</i> B2	<i>Mfe.</i> <i>stellata</i> AR4	<i>Mc.</i> <i>capsulatus</i> Bath	<i>Mmo.</i> <i>methanica</i> MC09	<i>Mm.</i> <i>alcaliphilum</i> 20Z	<i>Ma. infernorum</i> V4
Particulate methane monooxygenase (pMMO) and related enzymes																
B1812_14770	Particulate methane monooxygenase PmoC1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes	Yes
B1812_18675	Particulate methane monooxygenase PmoA1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes	Yes
B1812_14780	Particulate methane monooxygenase PmoB1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes	Yes
B1812_13455	Particulate methane monooxygenase PmoC2	Yes	Yes	No	Yes	No	No	Yes	No	No	No	No	No	No	No	No
B1812_13465	Particulate methane monooxygenase PmoA2	Yes	Yes	No	Yes	No	No	Yes	No	No	No	No	No	No	No	No
B1812_13470	Particulate methane monooxygenase PmoB2	Yes	Yes	No	Yes	No	No	Yes	No	No	No	No	No	No	No	No
B1215_00565	Cu-MMO protein family PxmA	Yes	No	Yes	No	Yes	No	No	No	No	No	No	No	No	No	No
B1215_00560	Cu-MMO protein family PxmB	Yes	No	Yes	No	Yes	No	No	No	No	No	No	No	No	No	No
B1215_00555	Cu-MMO protein family PxmC	Yes	No	Yes	No	Yes	No	No	No	No	No	No	No	No	No	No
Soluble methane monooxygenase (sMMO)																
B1812_14125	Soluble methane monooxygenase MmoZ	Yes	No	No	No	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No
B1812_14135	Soluble methane monooxygenase MmoY	Yes	No	No	No	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No
B1812_14140	Soluble methane monooxygenase MmoX	Yes	No	No	No	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No
B1812_14130	Soluble methane monooxygenase MmoB	Yes	No	No	No	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No
B1812_14115	Soluble methane monooxygenase MmoC	Yes	No	No	No	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	No
B1812_14120	Soluble methane monooxygenase MmoD	Yes	No	No	No	No	No	Yes	No	No	No	No	Yes	Yes	No	No
Alternative carbon assimilation pathway																
B1812_15125	Acetate permease ActP (sodium:solute symporter) ³	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	(Yes)	(Yes)	(Yes)	(No)	(No)	(No)	(No)
B1812_18345	Alcohol dehydrogenase	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
B1812_21160	Aldehyde dehydrogenase	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No ⁴	Yes
B1812_21445	Nitrogenase (vanadium group)	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06645	Nitrogenase (iron-iron) transcriptional regulator	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06630	Nitrogenase (vanadium-iron) alpha chain	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06640	Nitrogenase (vanadium-iron) beta chain	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06635	Nitrogenase (vanadium-iron) delta chain	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06605	Nitrogenase vanadium-cofactor synthesis protein VnfE	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No
B1812_06600	Nitrogenase vanadium-cofactor synthesis protein VnfN	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
B1812_06595	Nitrogenase vanadium-cofactor synthesis protein VnfX	Yes	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No

¹Six of these 15 methanotroph genomes - *Methylocystis bryophila* S285, *Methylocystis sp.* strain SC2, *Methylocella silvestris* BL2, *Methylomonas methanica* MC09, *Methylomicrobium alcaliphilum* 20Z, and *Methylacidiphilum infernorum* V4 - are completely finished and other nine genomes are reported as draft genomes containing a number of contigs or partial genome sequences, which may lead to negative results for certain particular genes in this survey.

²*Mec.* = *Methylocystis*, *Ms.* = *Methylosinus*, *Mce.* = *Methylocella*, *Mca.* = *Methylcapsa*, *Mfe.* = *Methyloferula*, *Mc.* = *Methylcococcus*, *Mmo.* = *Methylomonas*, *Mm.* = *Methylomicrobium*, *Ma.* = *Methylacidiphilum*.

³Categorization according to the symporter gene tree (Fig. S2). Yes = acetate permease present (sodium:solute symporter sequence clusters coherently within the family *Methylocystaceae*). (Yes) = acetate permease present, but sodium:solute symporter sequence groups on a branch separate from that of the family *Methylocystaceae*. (No) = symporter present but unclear whether it functions as acetate permease.

⁴A gene encoding aldehyde dehydrogenase is not present in the genome of *Methylomicrobium alcaliphilum* 20Z, but a gene coding for aldehyde oxidoreductase was found in its genome. This gene catalyzes the conversion of aldehyde to acid and may reduce the toxicity of aldehyde to bacterial cells.

Table S5. PCR primers used for detection of *pmoCAB* and their target sites in *pmoA* gene sequence.

Primer	Sequence
A189f	5'-ggngactgggacttctgg-3'
A682r	5'-gaasgcngagaagaasgc-3' (reverse complement: 5'-gcsttctctcngcsttc-3')
Gene	Sequence
<i>pxmA</i>	atgactgcgacagacttgaatccgccgttcaaccctatgccccgaaaaagcgcgcctgagccgggacctatgattatctcatcctcgtcctggcgttcttctctcgtcggagc ctttcatctccatgtcgcgctcacggg ggcgactgggattttgg ttggattggaaagaccgccaatggtggccactcatcacaccgctgatgatcaccttcctgcagcgg tcaagcgggtgctctggccaaactccgcttggcgttggcgcgacgctctgcatctcttcttggatcggaaacctggatcacgcgggtcttcgctaccatctgtgaattactc cccataaacgaggttctcccgaacgatgttggcagcgccttgggtgctcagcagtcctcatgctgagcaacagctgaccatcaccagcatttccggcggcatggccttcg ccttgccttctatccgagcaactggcccattttgcatgtttcacgttccggctgagtagcggcggcgcagctgacggcggcggatctcttcggcttccaatacgtgagagccg ggacgccggagtatctcgttggatcagagggggcacgttacgcacttacggccaatacgaacgcctctgtcggcctttg cggtcttctctgcacgc ctgatgtaccgctg tgggtggtgcttggcaaaagcttccaccacgaaatacgtcaaaaatatctaa
<i>pmoA2</i>	atgtctgtatcggctgcgcctatcggcaaggcatggaagtcaaaggaggagttctcgggtgcgtcattttgacggactggatcctcctctcgtcctgttcttctgctgctcggct cctaccacatccactatagctgctggcc ggcgactgggacttctgg atcacttcaaagatcggcgcctggtggccgaccgtggcggcggatcgtcggcatgtgcttcgcggcgg ccgcgagctccttctttggactaagttccggctgcccttcggcgcgacggctgacgctggccttctcgtcggcgagtgatgaaccgctacgacaatttctggggttgacc ttctcccgatcagcctggtgttcccctcgcgctgatcccgatggccttctggctcagctcgtgctgctgatctctggcagctggctcgtcaccgcgctgctcggctcgtcggtt ggggcctgttcttctatccgccaactggcctgtgctcgcgcagttaccatcaggccgccgagatcagcggcgtgctgctgaccctcggcgtatctgactggttcaactacgtgcg caccggcacgccggaatacatccgatgatcagcgcggcacgctgcgcaccttcggcaaggatgctgttctcgtcgc gccttctctcgtccttc atctcgtatgctgttactt cctctggtggaagatcgggatgtggttgcggcaccgactatgtgaaggcggagacatctga
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gtctacttcgctggtggtggctgggcccgttctattcgacgacgaaggtcatcaaggaaatctaa

“s” represents nucleotide “g” or “c”, and “n” represents any nucleotides in primer sequences.

The nucleotides in red indicate mismatch positions between primer and target sequences.

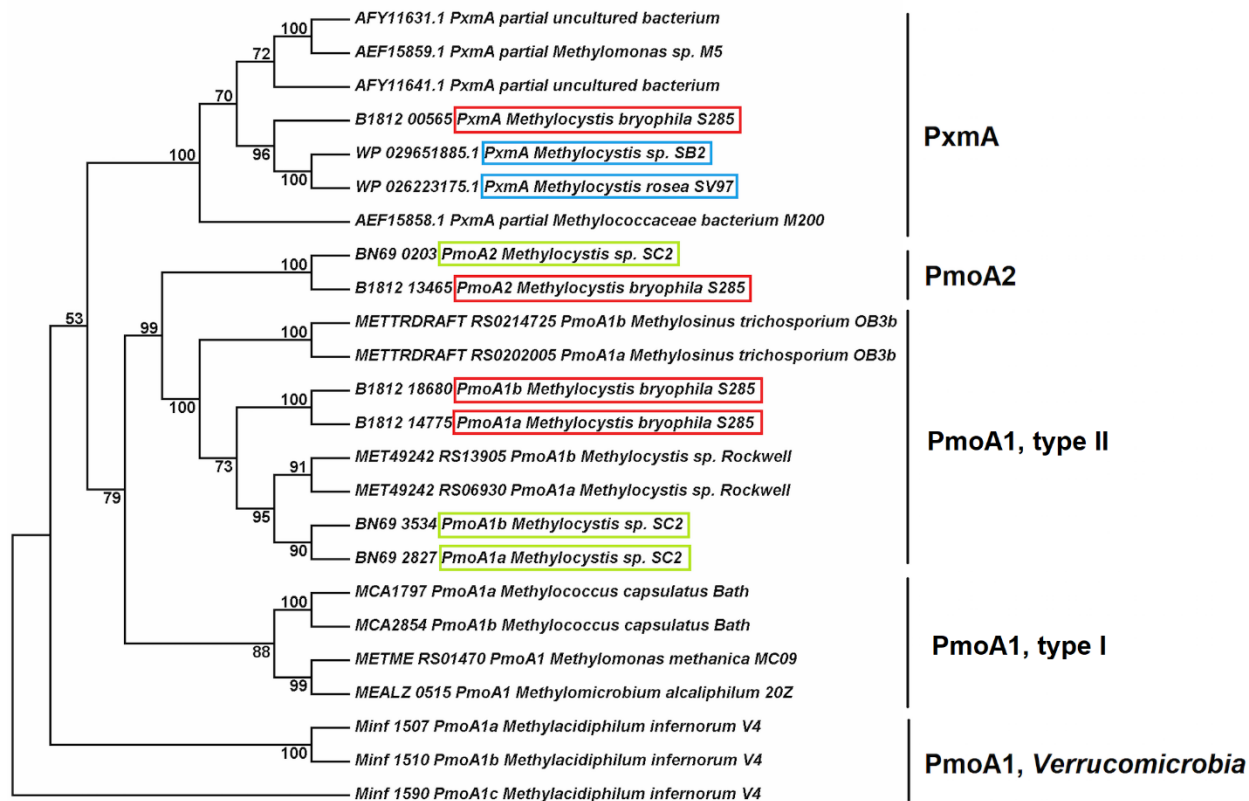


Figure S1. Relationship between the deduced amino acid sequences of *pmoA1*, *pmoA2*, and *pxmA* of type I and type II MOB. Branches defined by *Methylocystis bryophila* S285 and *Methylocystis* sp. SC2 are framed in red and green, respectively. PxmA detected in *Methylocystis rosea* SV97 (isolated from subarctic peatland) and *Methylocystis* sp. strain SB2 (isolated from spring bog) are framed in blue. The tree was constructed using MEGA7 with UPGMA as hierarchical cluster method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) is shown next to the branch points. The scale indicates genetic distance between amino acid sequences.

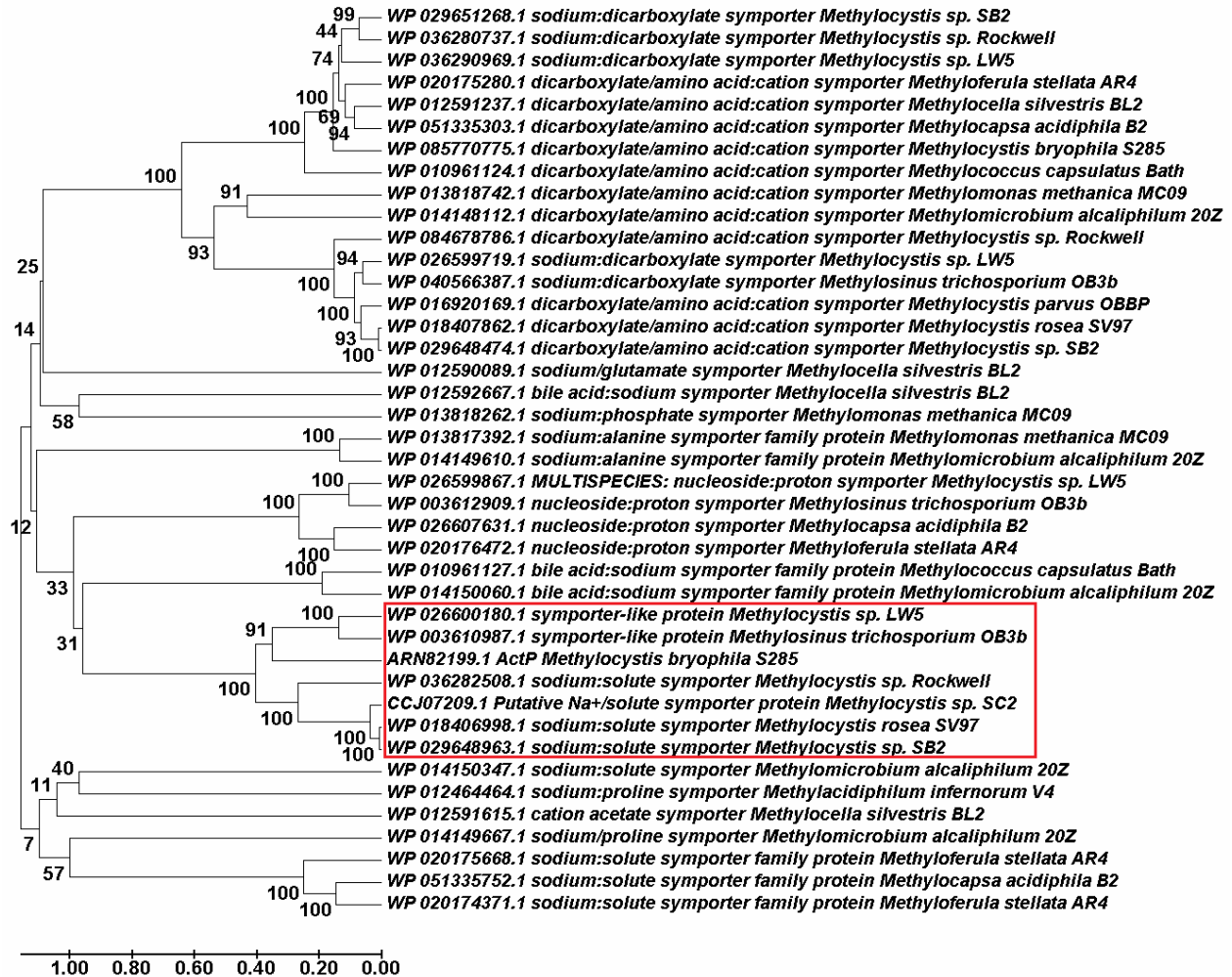


Figure S2. Relationship between symporter genes detected in the 15 methanotroph genomes listed in Table S4. Their annotation is according to the respective GenBank database entry. The tree is based on deduced amino acid sequences (310 to 609 residues). The coherent cluster of sodium:solute symporters within the family *Methylocystaceae* is framed in red. Most likely, they function as acetate permease (ActP). The tree was constructed using MEGA7 with UPGMA as hierarchical cluster method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) is shown next to the branch points. The scale indicates genetic distance between amino acid sequences.