

### Supplementary Material 16S rRNA clone library

To investigate the total bacterial community a clone library based on the 16S rRNA gene was performed of the pool *Sphagnum* mosses from Andorra peat, next to *S. magellanicum* some *S. falcatulum* was present in this pool and both these species were analysed. Both 16S clone libraries showed the presence of *Alphaproteobacteria* (17%), *Verrucomicrobia* (13%) and *Gammaproteobacteria* (2%) and since the distribution of bacterial genera among the two species was comparable an average was made. In total a 180 clones were sequenced and analyzed for the phylogenetic trees see Fig. A1 and A2

The 16S clone libraries showed a very diverse set of bacteria to be present inside or on *Sphagnum* mosses. Compared to other studies the microbial community in *Sphagnum* peat soils (Dedysh *et al.*, 2006; Kulichevskaya *et al.*, 2007a; Opelt and Berg, 2004) is comparable to the microbial community found here, inside and attached on the *Sphagnum* mosses of the Patagonian peatlands. Most of the clones showed sequence similarity to isolates or environmental samples originating from peat ecosystems, of which most of them originate from Siberian acidic peat bogs. This indicated that similar bacterial communities can be found in peatlands in the Northern and Southern hemisphere implying there is no big geographical difference in microbial diversity in peat bogs. Four out of five classes of *Proteobacteria* were present in the 16S rRNA clone library; *Alfa*-, *Beta*-, *Gamma* and *Deltaproteobacteria*. 42 % of the clones belonging to the *Alphaproteobacteria* showed a 96-97% to *Acidophaera rubrifaciens*, a member of the *Rhodospirillales* an acidophilic bacteriochlorophyll-producing bacterium isolated from acidic hotspots and mine drainage (Hiraishi *et al.*, 2000). This bacterium is closely related to *Acidosoma sibirica*, an acidophilic bacterium isolated from a *Sphagnum* peat bog (Belova *et al.*, 2009). Other clones also belonged to the *Rhodospirillales* family, of which several showed high homology to isolates from peat bogs, like *Telmatospirillum siberiense* (Sizova *et al.*, 2007). Another 42% of the clones of the *Alfaproteobacteria* belonged to the order of *Rhizobiales*, to which also all isolated methanotrophs belong of which four clones show high homology (98-99%) to the methanotrophic symbiont of *Sphagnum* found in the Mariapeel (Raghoebarsing *et al.*, 2005). Unfortunately this methanotrophic symbiont has not been cultivated yet. Only a few methanotrophs have been isolated from peat ecosystems, all belonging to the *Alphaproteobacteria* but no close relatives to those were found in the clone library. There is a possibility more unknown methanotrophs belong to this order, but so far these 16S rRNA

sequences cannot reveal a metabolic importance of the obtained clones. From other environments methanotrophs have been isolated belonging to the *Gammaproteobacteria* and *Verrucomicrobia*, but so far none from peat ecosystems and none of the clones showed high homology to other isolates methanotrophs of these classes. The clones belonging to the *Verrucomicrobia* were almost all highest related to *Opititus* spp. of which some were isolated from rice fields, they have never been demonstrated to oxidize methane (Janssen et al., 1997). Only three verrucomicrobial methanotrophs are known and all are thermophilic and originating from volcanic regions, none of the clones were closely related to these methanotrophs. As shown with the microarray more often relatives to thermophilic methanotrophs can be detected in peat ecosystems, which might indicate the presence of new methanotrophic species. Verrucomicrobial methanotrophs are recently discovered and opened new possibilities to find new and unknown methanotrophs in all methane rich ecosystems. Two clones belonged to the *Deltaproteobacteria* being closest relative to *Bdelvibrio bacteriovorus* and *Spirobacillus cienkowskii*, both pathogens. Pathogens have been shown to occur abundantly in *Sphagnum* (Opelt et al., 2007), but so far their presence in these ecosystems has not been understood. Besides these classes an abundance of *Acidobacteria* (28%) and *Betaproteobacteria* (22%) was found, both classes have been found to occur in peat ecosystems, but their role has not been discovered yet. Belova and coworkers (Belova et al., 2006) described the presence of *Burkholderia* species, belonging to the *Betaproteobacteria* in Western Siberian, Canadian and Estonian peat bogs and Opelt and coworkers showed the abundance of the genus *Burkholderia* of endo and ectophytic bacterial populations in bryophytes (Opelt et al., 2007; Opelt and Berg, 2004). These *Burkholderia* species are antagonistic bacteria with antimicrobial activity, which is thought to be used by the *Sphagnum* mosses as a defense strategy against fungi (Opelt et al., 2007). *Acidobacteria* have been detected and isolated from peat (Kulichevskaya et al., 2010; Pankratov et al., 2008), where they most likely grow on various heteropolysaccharides and galacturonic acid, which are released during decomposition of *Sphagnum* moss and vascular plant debris. Three percent of the clones belonged to the *Planctomycetes*, which are often detected in *Sphagnum* dominated peatlands (Dedysh et al., 2006; Kulichevskaya et al., 2006) and several have been isolated (Kulichevskaya et al., 2009; Kulichevskaya et al., 2008; Kulichevskaya et al., 2007b) and several clones show homology to these isolates. A few clones belonged to the *Bacteroidetes*, showing sequence similarity to the *Sphingobacteria* genus containing *Mucilagibacter* spp. which were isolated from a *Sphagnum* peat bog. This species was shown to degrade pectin, xylan and laminarin in peat. The 16S rRNA clone library was able

to detect a broad variety of bacteria, which is comparable to other studies. However, no clones were found to be related to isolated methanotrophs and only a few clones were related to the symbiotic methanotroph from *Sphagnum* moss. The used primer set is a general primer set, that however does not always anneal to DNA isolated from methanotrophs (Kip, personal communication), which could explain why methanotrophs were not represented in this clone library. It could be that the used primer set does not detect methanotrophs in environmental samples or is biased against methanotrophs. Described 16S rRNA clone libraries performed on peat also showed only a few clones with homology to known methanotrophs (Dedysh et al., 2006; Raghoebarsing, 2006). Another explanation for the lack of methanotrophic sequences in this clone library could be that there are more unknown methanotrophs present that are not detected by the primer set or the DNA isolation technique is not able to extract methanotrophic DNA as easily as DNA of other bacteria. The primer set does anneal to Verrucomicrobial methanotrophs, which were neither found within these clone libraries.

## **Materials and Methods**

### *16S rRNA gene and pmoA gene clonelibraries*

PCR amplification of the 16S rRNA gene was performed with two general bacterial 16S rRNA gene primers: 616F and 630R (Juretschko et al., 1998). All PCRs were performed in a gradient from 50 to 60 degrees and PCR products were combined. All PCR products were purified using the QIAquick PCR Purifications Kit (Qiagen). DNA sequencing was performed with the primers used in the PCR and for the 16S rRNA gene also the universal bacterial primer 612R (Ehrmann et al., 2003) was used. The pGEM-T Easy Vector System Kit (Promega) was used for ligation of the *pmoA* and 16S rRNA gene amplifications. Ligation was performed as prescribed by the manufacturer. 16S rRNA gene ligation mix was transformed to Top10 competent *E. coli* cells (Invitrogen™) by heat shock exposure (30-45 seconds at 42°C). Plasmid DNA with ligated 16S rRNA gene was isolated with the FastPlasmid Mini Kit (Eppendorf) following the instructions of the manufacturer. pDNA with ligated *pmoA* gene was isolated with the E.Z.N.A.™ Plasmid Miniprep Kit (EZNA™). Partial 16S rRNA gene fragments were sequenced with M13 forward and reverse primers (Invitrogen™), targeting vector sequences adjacent to the multiple cloning site. pDNA sequencing was performed by the sequencing facility of the UMC Sint Radboud, Nijmegen. Clone library sequences and their closes relatives were analyzed using MEGA version 4 (Tamura et al., 2007). All sequences were aligned automatically using the alignment tool of MEGA4 (ClustalW).

## References

- Belova, S. E., Pankratov, T. A., and Dedysh, S. N.: Bacteria of the genus *Burkholderia* as a typical component of the microbial community of Sphagnum peat bogs, *Microbiology*, 75, 90-96, 2006.
- Belova, S. E., Pankratov, T. A., Detkova, E. N., Kaparullina, E. N., and Dedysh, S. N.: *Acidisoma tundrae* gen. nov., sp. nov. and *Acidisoma sibiricum* sp. nov., two acidophilic, psychrotolerant members of the *Alphaproteobacteria* from acidic northern wetlands, *International journal of systematic and evolutionary microbiology*, 59, 2283-2290, 10.1099/ijs.0.009209-0, 2009.
- Dedysh, S. N., Pankratov, T. A., Belova, S. E., Kulichevskaya, I. S., and Liesack, W.: Phylogenetic analysis and in situ identification of Bacteria community composition in an acidic *Sphagnum* peat bog, *Applied and environmental microbiology*, 72, 2110-2117, 2006.
- Ehrmann, M. A., Muller, M. R. A., and Vogel, R. F.: Molecular analysis of sourdough reveals *Lactobacillus mindensis* sp. nov., *International journal of systematic and evolutionary microbiology*, 53, 7-13, 10.1099/ijs.0.02202-0, 2003.
- Hiraishi, A., Matsuzawa, Y., Kanbe, T., and Wakao, N.: *Acidisphaera rubrifaciens* gen. nov., sp. nov., an aerobic bacteriochlorophyll-containing bacterium isolated from acidic environments, *International journal of systematic and evolutionary microbiology*, 50, 1539-1546, 2000.
- Janssen, P. H., Schuhmann, A., Morschel, E., and Rainey, F. A.: Novel anaerobic ultramicrobacteria belonging to the Verrucomicrobiales lineage of bacterial descent isolated by dilution culture from anoxic rice paddy soil, *Applied and environmental microbiology*, 63, 1382-1388, 1997.
- Juretschko, S., Timmermann, G., Schmid, M., Schleifer, K. H., Pommerening-Roser, A., Koops, H. P., and Wagner, M.: Combined molecular and conventional analyses of nitrifying bacterium diversity in activated sludge: *Nitrosococcus mobilis* and *Nitrospira*-like bacteria as dominant populations, *Applied and environmental microbiology*, 64, 3042-3051, 1998.
- Kulichevskaya, I., Pankratov, T., and Dedysh, S.: Detection of representatives of the *Planctomycetes* in *Sphagnum* peat bogs by molecular and cultivation approaches, *Microbiology*, 75, 329-335, 2006.
- Kulichevskaya, I., Belova, S., Kevbrin, V., Dedysh, S., and Zavarzin, G.: Analysis of the bacterial community developing in the course of *Sphagnum* moss decomposition, *Microbiology*, 76, 621-629, 2007a.
- Kulichevskaya, I. S., Ivanova, A. O., Belova, S. E., Baulina, O. I., Bodelier, P. L., Rijkstra, W. I., Sinninghe Damste, J. S., Zavarzin, G. A., and Dedysh, S. N.: *Schlesneria paludicola* gen. nov., sp. nov., the first acidophilic member of the order *Planctomycetales*, from *Sphagnum*-dominated boreal wetlands, *International journal of systematic and evolutionary microbiology*, 57, 2680-2687, 2007b.
- Kulichevskaya, I. S., Baulina, O. I., Bodelier, P. L. E., Rijkstra, W. I. C., Damste, J. S. S., and Dedysh, S. N.: *Zavarzinella formosa* gen. nov., sp. nov., a novel stalked, *Gemmata*-like *planctomycete* from a Siberian peat bog, *International journal of systematic and evolutionary microbiology*, 59, 357-364, 2009.
- Kulichevskaya, I. S., Suzina, N. E., Liesack, W., and Dedysh, S. N.: *Bryobacter aggregatus* gen. nov., sp. nov., a peat-inhabiting, aerobic chemo-organotroph from subdivision 3 of the *Acidobacteria*, *International journal of systematic and evolutionary microbiology*, 60, 301-306, 10.1099/ijs.0.013250-0, 2010.
- Opelt, K., and Berg, G.: Diversity and antagonistic potential of bacteria associated with bryophytes from nutrient-poor habitats of the Baltic Sea coast, *Applied and environmental microbiology*, 70, 6569-6579, 2004.

Opelt, K., Berg, C., and Berg, G.: The bryophyte genus *Sphagnum* is a reservoir for powerful and extraordinary antagonists and potentially facultative human pathogens, *Fems Microbiology Ecology*, 61, 38-53, 2007.

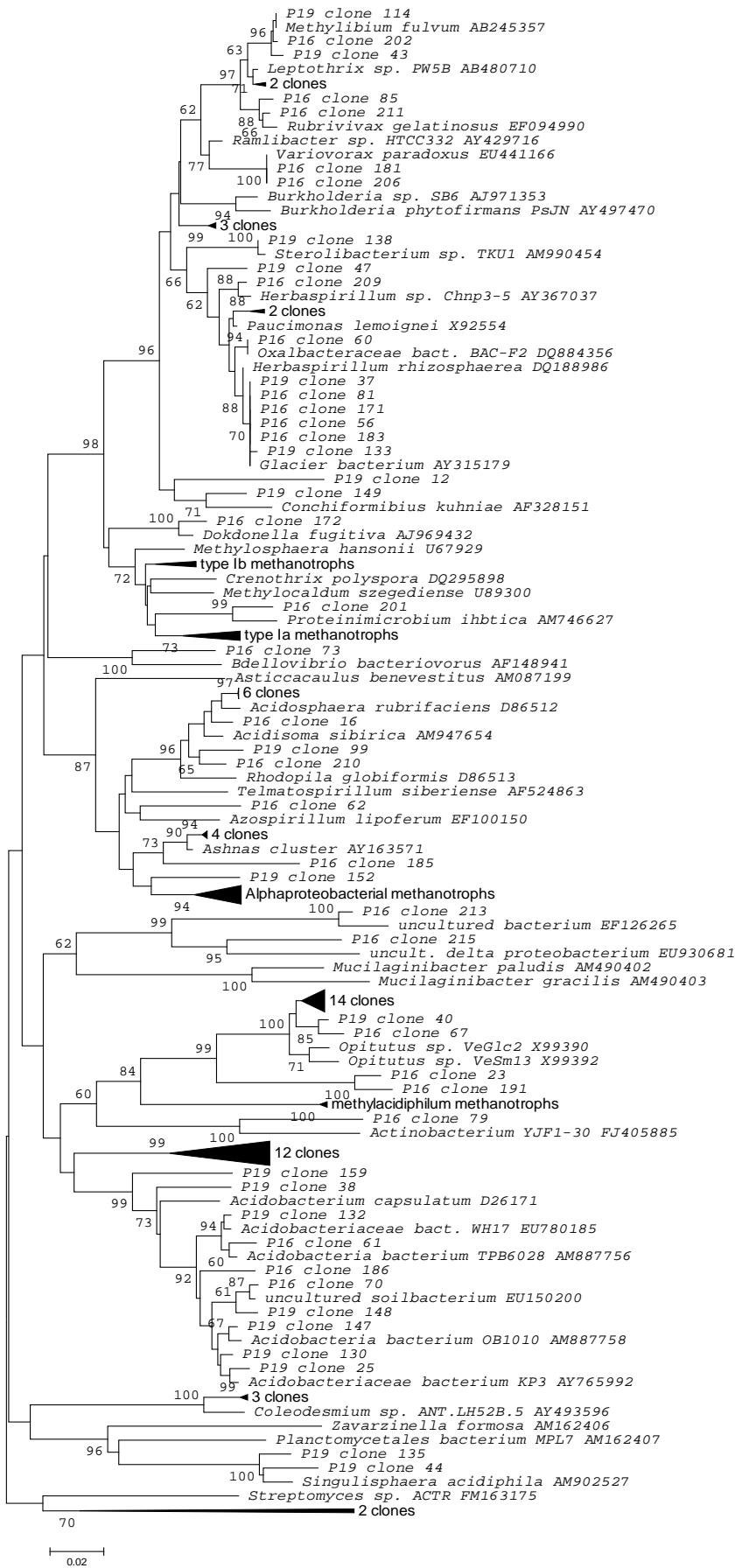
Pankratov, T. A., Serkebaeva, Y. M., Kulichevskaya, I. S., Liesack, W., and Dedysh, S. N.: Substrate-induced growth and isolation of Acidobacteria from acidic *Sphagnum* peat, *ISME Journal*, 2, 551-560, 10.1038/ismej.2008.7, 2008.

Raghoebarsing, A. A., Smolders, A. J., Schmid, M. C., Rijpstra, W. I., Wolters-Arts, M., Derksen, J., Jetten, M. S., Schouten, S., Sinninghe Damsté, J. S., Lamers, L. P., Roelofs, J. G., Op den Camp, H. J., and Strous, M.: Methanotrophic symbionts provide carbon for photosynthesis in peat bogs, *Nature*, 436, 1153-1156, 2005.

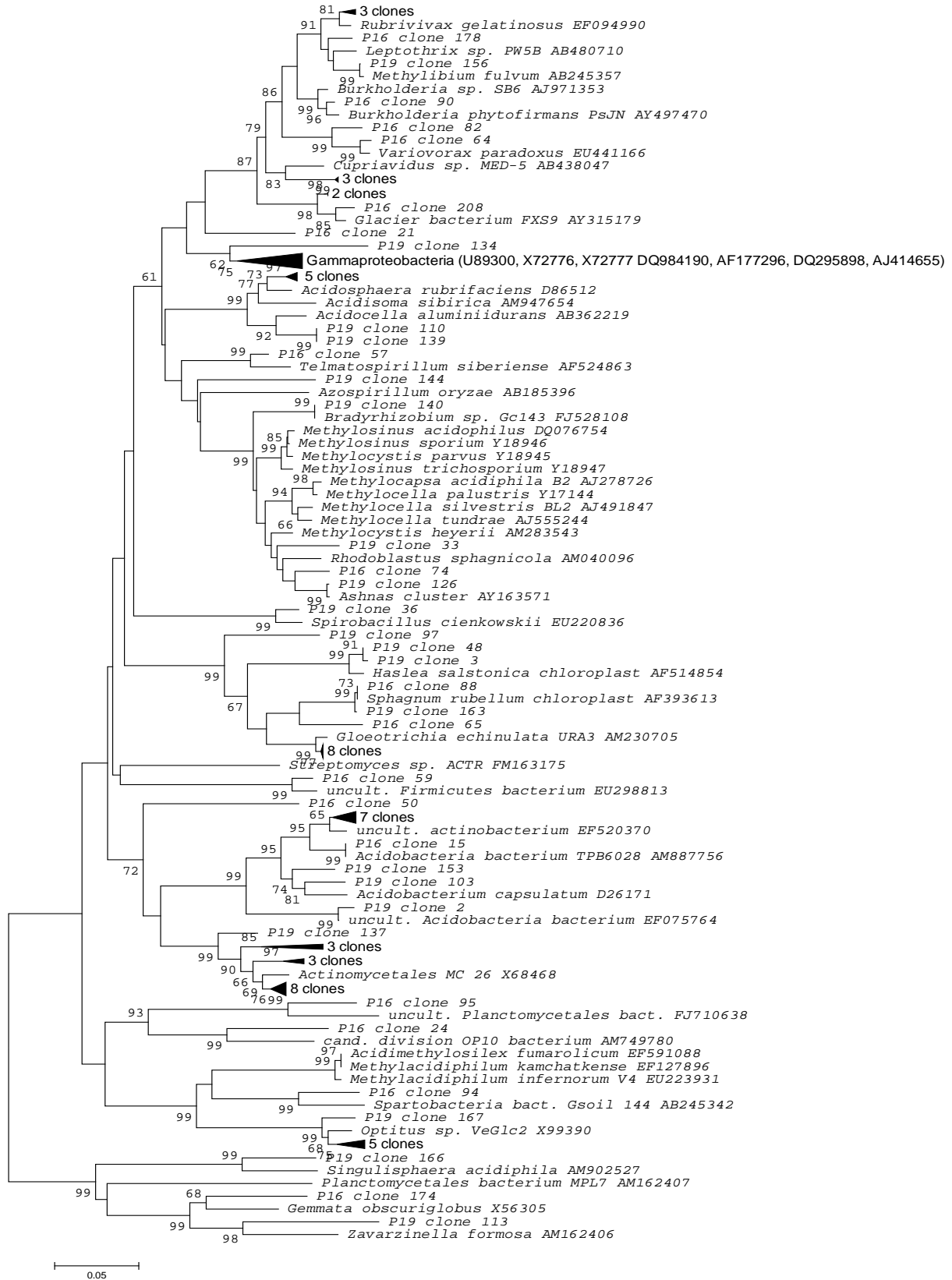
Raghoebarsing, A. A.: New directions in microbial methane oxidation, *Microbiology*, Radboud University, Nijmegen, 2006.

Sizova, M. V., Panikov, N. S., Spiridonova, E. M., Slobodova, N. V., and Tourova, T. P.: Novel facultative anaerobic acidotolerant *Telmatospirillum siberiense* gen. nov. sp. nov. isolated from mesotrophic fen, *Systematic and Applied Microbiology*, 30, 213-220, 2007.

Tamura, K., Dudley, J., Nei, M., and Kumar, S.: MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0, *Mol Biol Evol*, 24, 1596-1599, 2007.

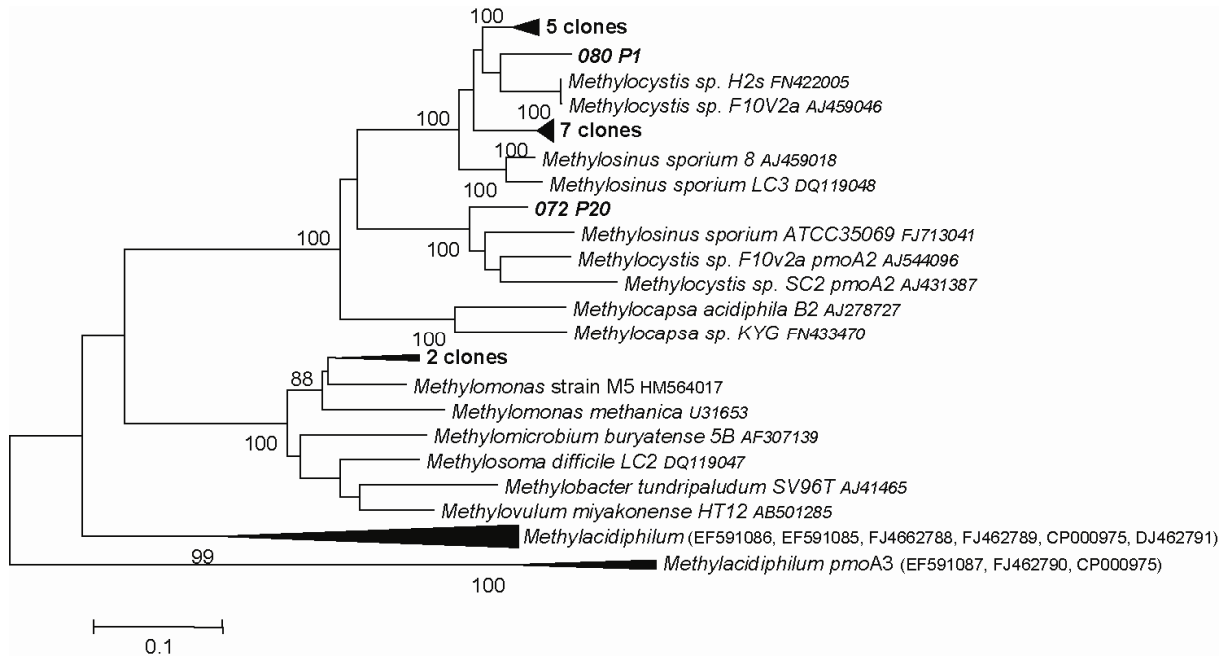


**Fig. A1.** 16S rRNA phylogenetic tree showing relationship of the partial 16S rRNA gene sequences (position 934 to 1408 of the 16S rRNA gene, *E. coli* numbering) to representatives and closest relatives of different bacterial classes. Bootstrap values > 60 are indicated.



**Fig. A2.** 16S rRNA phylogenetic tree showing relationship of the partial 16S rRNA gene sequences (position 104 to 495 of the 16S rRNA gene, *E. coli* numbering) to representatives and closest relatives of different bacterial classes. Bootstrap values > 60 are indicated.

**Fig. S1.** *pmoA* gene phylogenetic tree based on DNA showing the relationship of the clones to selected methanotrophs. The tree was based on Neighbour-Joining analysis using a bootstrap test of 500 replicates. Bootstrap values of >60 are indicated at the node of the branch.





**Supplementary Material Table S1.** Probes used for microarray analysis. The order corresponds to the order in which the probes are arranged on the microarray analysis shown in Figure 1.

Order	Name	Intended specificity
1	MbA557	<i>Methylobacter</i>
2	MbA486	<i>Methylobacter</i>
3	Mb460	<i>Methylobacter</i>
4	Mb_LW12-211	<i>Methylobacter</i>
5	Mb_SL#3-300	<i>Methylobacter</i>
6	Mb_SL299	soda lake <i>Methylobacter</i> isolates and clones
7	Mb_SL#1-418	soda lake <i>Methylobacter</i> isolates and clones
8	MmbB284	<i>Mmb. Buryatense</i> - same region as <i>Jpn284</i> , but 3 MM vs. that one <i>Methylobacter</i> and Japanese strain related
9	Jpn284	clone Jpn 07061
10	BB51-302	<i>Methylobacter</i>
11	Mb267	<i>Methylobacter</i>
12	Mb292	<i>Methylobacter</i>
13	Mb282	<i>Methylobacter</i>
14	Mb_URC278	<i>Methylobacter</i>
15	511-436	<i>Methylobacter</i>
16	LP10-424	<i>Methylobacter</i> LP 10 group
17	LF1a-456	<i>Methylobacter</i> LF 1a group
18	Mb_C11-403	<i>Methylobacter</i>
19	Mb380	<i>M.bacter</i> broad group A universal?
20	Mb271	<i>Methylobacter</i>
21	S14m2-270	Marine type Ia cluster, S14m#2
22	S14m2-406	Marine type Ia cluster, S14m#2
23	PS80-291	clone PS-80
24	MS1-440	Marine type Ia cluster, Marine sediment #1
25	Mm_pel467	<i>Methylomicrobium pelagicum</i>
26	Kuro18-205	Marine type Ia cluster, Kuro18
27	DS1-401	Deep sea cluster #1
28	Mm531	<i>Methylomonas</i>
29	Mm_M430	<i>Methylomonas</i>
30	Mm_RS311	<i>Mm.methanica</i> , RS clade(10-286)
31	Mm_ES294	<i>Methylomonas</i>
32	Mm_ES543	<i>Methylomonas</i>
33	Mm_ES546	<i>Methylomonas</i>
34	Mm_MV421	<i>Methylomonas</i>
35	Mm451	<i>Methylomonas</i>
36	Mm275	<i>Methylomonas</i>

37	Alp7-441	<i>Alpine soil Methylomonas, Alp#7 (10-282)</i>
38	peat_1_3-287	<i>Methylomonas-related peat clones</i>
39	Est514	<i>Methylomicrobium-related clones</i>
40	Mmb259	<i>Methylomicrobium album</i> + Landfill <i>M.microbia</i>
41	Mmb303	<i>Methylomicrobium album</i>
42	Mmb304	<i>Methylomicrobium album</i> + Landfill <i>M.microbia</i> and related
43	LW14-639	<i>Methylomicrobium LW14 group</i>
44	Mmb_RS2-443	<i>Methylomicrobium, Mmb_RS2</i>
45	Mmb562	<i>Mmb. album</i> and <i>Methylosarcina</i>
46	Mm229	<i>Deep-branching M.monas (?) group (WHmb3 related group)</i>
47	MsQ290	<i>M.sarcina quisquiliarum</i> related
48	MsQ295	<i>M.sarcina quisquiliarum</i>
49	LP20-644	<i>Methylomicrobium-related clones</i>
50	LP20-607	<i>LP20 group (Type Ia, deep branching-Mmb?)</i>
51	Ia193	Type I a ( <i>M.bacter-M.monas-M.microbium</i> )
52	Ia575	Type I a ( <i>M.bacter-M.monas-M.microbium-M.sarcina</i> )
53	Bsed516	<i>Marine sediment #2, Bsed</i>
54	SWI1-375	<i>Marine sediment #2, SW#1</i>
55	SWI1-377	<i>Marine sediment #2, SW#1</i>
56	Nc_oce426	<i>Nitrosococcus oceani</i>
57	DS2-287	<i>Deep sea #2, subgroup (N.coccus and Deep sea Type Ia 10-298)</i>
58	AIMS1-442	<i>Deep sea #2, AIMS#1</i>
59	DS2-220	<i>Deep sea #2, subgroup</i>
60	DS2-626	<i>Deep sea #2, subgroup</i>
61	USCG-225	Upland soil cluster Gamma
62	USCG-225b	Upland soil cluster Gamma
63	JR2-409	JR cluster #2 (California upland grassland soil)
64	JR2-468	JR cluster #2 (California upland grassland soil)
65	JR3-505	JR cluster #3 (California upland grassland soil)
66	JR3-593	JR cluster #3 (California upland grassland soil)
67	501-375	<i>Methylococcus-</i> related marine and freshwater sediment clones
68	501-286	<i>Methylococcus-</i> related marine and freshwater sediment clones
69	USC3-305	Upland soil cluster #3
70	Mc396	<i>Methylococcus</i>
71	MclT272	<i>Methylocaldum tepidum</i>
72	MclG281	<i>Methylocaldum gracile</i>
73	MclS402	<i>Methylocaldum szegediense</i>
74	MclS394	<i>Methylocaldum szegediense</i> and related
75	MclS400	<i>Methylocaldum szegediense</i> and related
76	MclE302	<i>Methylocaldum</i> E10
77	Mcl404	<i>Mc.capsulatus-Mcl.tepidum-Mcl. Gracile-Mcl.Szeg</i> and related

78	Mcl408	<i>Methylocaldum</i>
79	fw1-286	fw-1 group: <i>M.coccus-M.caldum</i> related marine and freshwater sediment clones
80	fw1-639	fw-1 group: <i>M.coccus-M.caldum</i> related marine and freshwater sediment clones
81	fw1-641	fw-1 group: <i>M.coccus-M.caldum</i> related marine and freshwater sediment clones
82	JHTY1-267	<i>JH-TY#1</i>
83	JRC4-432	Japanese rice cluster #4
84	OSC220	Finnish organic soil clones and related
85	OSC300	Finnish organic soil clones and related
86	JRC3-535	Japanese Rice Cluster #3
87	LK580	fw-1 group + Lake Konstanz sediment cluster
88	RSM1-419	<i>RSM#1</i>
89	JHTY2-562	<i>JH-TY#2</i>
90	JHTY2-578	<i>JH-TY#2</i>
91	JRC2-447	Japanese Rice Cluster #2
92	LW21-374	LW21 group
93	LW21-391	LW21 group
94	M90-574	<i>M.coccus-M.caldum</i> related marine and freshwater sediment clones
95	M90-253	<i>M.coccus-M.caldum</i> related marine and freshwater sediment clones
96	Mth413	<i>Methylothermus</i>
97	Mha-500	<i>Methylohalobius - M.thermus and related ?</i>
98	DS3-446	Deep sea cluster #3
99	PmoC640	<i>PmoC</i>
100	PmoC308	<i>PmoC</i>
101	Ib453	Type I b ( <i>M.thermus-M.coccus-M.caldum</i> and related)
102	Ib559	Type I b ( <i>M.thermus-M.coccus-M.caldum</i> and related)
103	McyB304	<i>M.cystis B (parvus/echinoides/strain M)</i>
104	Mcy255	<i>M.cystis B (parvus/echinoides/strain M)</i>
105	Mcy459	<i>Methylocystis</i>
106	Mcy264	<i>Methylocystis</i>
107	Mcy270	<i>Methylocystis</i>
108	Mcy413	<i>Methylocystis</i>
109	Mcy522	<i>Methylocystis A + peat clones</i>
110	Mcy233	<i>Methylocystis</i>
111	McyM309	<i>M.cystis strain M and related</i>
112	Peat264	peat clones
113	MsS314	<i>Methylosinus sporium</i>
114	MsS475	<i>Methylosinus sporium</i>
115	Msi263	<i>Methylosinus sporium + 1 Msi.trichosporium subcluster</i>
116	Msi423	<i>Methylosinus</i>
117	Mst214	<i>Methylosinus trichosporium</i> OB3b and rel.

118	Msi520	<i>Methylosinus trichosporium</i>
119	Msi269	<i>Methylosinus trichosporium</i>
120	Msi294	<i>Methylosinus</i>
121	ARC2-518	<i>Deep branching type II clade ARC2 - Methylosinus trichosporium 15-084 group?</i>
122	Msi232	<i>M.sinus</i> + most <i>M.cystis</i> -considered as additional <u>type II</u> probe
123	II509	Type II
124	II630	Type II
125	Alp8-468	<i>Type II novel pmoA, Alpine cluster Alp#8</i>
126	xb6-539	Novel <i>pmoA</i> copy of type II and related environmental clones
127	LP21-190	Novel <i>pmoA</i> copy of type II and related environmental clones
128	LP21-260	Novel <i>pmoA</i> copy of type II and related environmental clones
129	NMcy1-247	Novel <i>pmoA</i> copy of <i>M.cystis</i> #1 (?)
130	NMsi1-469	Novel <i>pmoA</i> copy of <i>M.sinus</i>
131	NMcy2-262	Novel <i>pmoA</i> copy of <i>M.cystis</i> #2 (?)
132	LP21-436	<i>Mcy + Msi novel pmoA #1 groups</i>
133	NMsiT-271	Novel <i>pmoA</i> copy of <i>M.sinus trichosporium</i> (?)
134	LP21-232	Novel <i>pmoA</i> copy of type II and related environmental clones
135	RA14-299	RA14 related clones
136	RA14-594	RA14 related clones
137	RA14-591	RA14 related clones
138	Wsh1-566	Watershed + flodded upland cluster 1
139	Wsh2-491	Watershed + flodded upland cluster 2
140	Wsh2-450	Watershed + flodded upland cluster 2
141	B2rel251	<i>Methylocapsa</i> -related clones
142	B2-400	<i>Methylocapsa</i>
143	B2-261	<i>Methylocapsa</i>
144	B2all343	<i>Methylocapsa</i> and related clones
145	B2all341	<i>Methylocapsa</i> and related clones
146	pmoAMO3-400	clone pmoA-MO3
147	pmoAMO3-486	<i>MO3 group</i>
148	pmoAMO3-511	<i>MO3 group</i>
149	ESR-579	ESR (Eastern Snake River) cluster
150	M84P22-514	environmental clones of uncertain identity
151	TUSC409	Tropical Upland Soil Cluster #2
152	TUSC502	Tropical Upland Soil Cluster #2
153	mtrof173	Universal
154	mtrof362-I	Methanotrophs
155	mtrof661	Methanotrophs
156	mtrof662-I	Methanotrophs
157	mtrof656	Methanotrophs