

Table S6

Phylogenetic affiliation of 16S rRNA gene sequences representing DGGE bands. Phylogenetic assignments of 16S rRNA gene sequences were performed by using the RDP II Classifier [1] and BLAST [2]. DGGE bands were derived from DGGE patterns generated with *Bacteria* (**EUB**), *Betaproteobacteria* (**Beta**), *Actinobacteria* (**Actino**), or *Sphingomonadaceae* (**SPH**)-specific 16S rRNA gene targeting primer-systems. SW: South-West basin of Lake Grosse Fuchskuhle; **06**, **08**, or **09**: experiments in 2006, 2008, and 2009. Sequence names correspond to those shown in the phylogenetic trees of Fig. 5-9 and the numbers within the sequence names correspond to numbers next to DNA bands in the respective DGGE gels.

Sequence Name	Acc. No.	nt	RDP classifier	Closest related BLAST hit		
				Similarity (%)	Acc.	Sequence name
EUB-SW06-1	JF917134	365	<i>"Chlorobi"[100%] "Chlorobia"[100%] Chlorobiales[100%] Chlorobiaceae[100%] Chlorobium[100%]</i>	100%	GU734037	Lake Grosse Fuchskuhle DGGE band FSW-St05-2
				99%	CP001110	<i>Pelodictyon phaeoclathratiforme</i> BU-1
EUB-SW06-2	JF917135	374	<i>Alphaproteobacteria[95%] Rhizobiales[46%]</i>	100%	HQ420131	Acidic cole mine drainage clone LRE22B42
				95%	EF667926	Uncultured alpha proteobacterium clone Hv(lakePohlsee)_38
EUB-SW06-3	JF917136	388	<i>Gammaproteobacteria[100%] Oceanospirillales[47%] Oleiphilaceae[42%] Oleiphilus[42%]</i>	99%	GU734062	Lake Grosse Fuchskuhle DGGE band FSW-St06-11
				93%	AE017282	<i>Methylococcus capsulatus</i> Bath
EUB-SW06-4	JF917137	452	<i>Alphaproteobacteria[100%] Sphingomonadales[100%] Sphingomonadaceae[100%] Novosphingobium[100%]</i>	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T
EUB-SW09-5	JF917138	408	<i>Cyanobacteria[100%] Cyanobacteria[100%] Chloroplast[100%] Chlorophyta[100%]</i>	100%	EU442895	Nam Co Lake clone N06Jun-31
EUB-SW09-6	JF917139	505	<i>Alphaproteobacteria[99%] Rhizobiales[61%] Bradyrhizobiaceae[20%] Balneimonas[19%]</i>	95%	EF667926	Lake Pohlsee clone Hv(lakePohlsee)_38
EUB-SW09-7	JF917140	367	<i>Firmicutes"[100%] "Bacilli"[98%] Bacillales[98%] "Paenibacillaceae"[87%] Paenibacillus[87%]</i>	100%	GU734065	Acidic mining lake DGGE band B3 Lake Grosse Fuchskuhle DGGE band FSW-St06-14
EUB-SW09-8	JF917141	532	<i>Firmicutes"[100%] "Bacilli"[100%] Bacillales[100%] "Paenibacillaceae"[89%] Paenibacillus[88]</i>	99%	GU734065	Lake Grosse Fuchskuhle DGGE band FSW-St06-14
EUB-SW09-9	JF917142	505	<i>Alphaproteobacteria[100%]</i>	98%	EF520395	Adirondack lake clone ADK-BTe02-51

EUB-SW09-10	JF917143	530	<i>Caulobacterales</i> [100%] <i>Caulobacteraceae</i> [100%] <i>Phenylobacterium</i> [86%] <i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [98%] <i>Acidovorax</i> [34%]	99%	GU734044 DQ501302	Lake Grosse Fuchskuhle DGGE band FSW-St05-9 Lake Grosse Fuchskuhle clone FNE11-10
Beta-SW06-1	JF917144	285	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [98%] <i>Simplicispira</i> [58%]	100% 99% 95%	GU734058 EF520440 AF435948	Lake Grosse Fuchskuhle DGGE band FSW-St06-7 Adirondack Lake clone ADK-BMe02-21 <i>Rhodoferax ferrireducens</i> T118 ^T
Beta-SW06-2	JF917145	287	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Burkholderiaceae</i> [100%] <i>Polynucleobacter</i> [100%]	100%	AJ879783	<i>P. necessarius</i> ssp. <i>asymbioticus</i> QLW-P1DMWA-1 ^T
Beta-SW06-3	JF917146	279	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [100%] <i>Simplicispira</i> [14%]	100% 99% 96%	GU734044 DQ501302 AF285414	Lake Grosse Fuchskuhle DGGE band FSW-St05-9 Lake Grosse Fuchskuhle clone FNE11-10 <i>Xenophilus azovorans</i> KF46F ^T
Beta-SW06-4	JF917147	276	<i>Betaproteobacteria</i> [100%] <i>Methylophilales</i> [100%] <i>Methylophilaceae</i> [100%] <i>Methylophilus</i> [99%]	99% 96%	GU734054 GQ175365	Lake Grosse Fuchskuhle DGGE band FSW06-St06-3 <i>Methylophilus</i> sp. Tobacco-planted soil isolate CS3
Beta-SW06-5	JF917148	281	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [100%] <i>Curvibacter</i> [56%]	99% 96%	GU734088 AB109889	Lake Grosse Fuchskuhle DGGE band FSW06-Lt06-1 <i>Curvibacter gracilis</i> 7-1 ^T
Beta-SW06-6	JF925282	173	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Burkholderiaceae</i> [100%] <i>Polynucleobacter</i> [100%]	100%	AJ879783 GU734064	<i>P. necessarius</i> ssp. <i>asymbioticus</i> QLW-P1DMWA-1 ^T Lake Grosse Fuchskuhle DGGE band FSW-St06-13
Beta-SW08-7	JF917149	277	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Burkholderiaceae</i> [54%] <i>Polynucleobacter</i> [54%]	99% 98%	HM128455 FM208182	Tanggulha Lake clone SINN1071 <i>Polynucleobacter rarus</i> MT-CBb6A5 ^T
Beta-SW08-8	JF917150	285	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [99%] <i>Comamonadaceae</i> [99%] <i>Simplicispira</i> [45%]	100% 99% 95%	GU734058 EF520440 AF435948	Lake Grosse Fuchskuhle DGGE band FSW-St06-7 Adirondack Lake clone ADK-BMe02-21 <i>Rhodoferax ferrireducens</i> T118 ^T
Beta-SW08-9	JF917151	279	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [99%] <i>Simplicispira</i> [24%]	100% 99% 96%	GU734044 DQ501302 AF285414	Lake Grosse Fuchskuhle DGGE band FSW-St05-9 Lake Grosse Fuchskuhle clone FNE11-10 <i>Xenophilus azovorans</i> KF46F ^T
Beta-SW09-10	JF917152	292	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Comamonadaceae</i> [100%] <i>Simplicispira</i> [61%]	100% 99% 95%	GU734058 EF520440 AF435948	Lake Grosse Fuchskuhle DGGE band FSW-St06-7 Adirondack Lake clone ADK-BMe02-21 <i>Rhodoferax ferrireducens</i> T118 ^T
Beta-SW09-11	JF917153	271	<i>Betaproteobacteria</i> [100%] <i>Burkholderiales</i> [100%] <i>Burkholderiaceae</i> [100%] <i>Polynucleobacter</i> [100%]	100%	AJ879783	<i>P. necessarius</i> ssp. <i>asymbioticus</i> QLW-P1DMWA-1 ^T

Actino-SW06-1	JF917154	421	<i>Actinobacteria</i> [92%] <i>Actinobacteridae</i> [89%] <i>Actinomycetales</i> [85%] <i>Micrococcineae</i> [47%] <i>Intrasporangiaceae</i> [26%] <i>Intrasporangium</i> [6%]	99%	DQ316352	Lake Grosse Fuchskuhle clone FSW11-20
Actino-SW06-2	JF917155	421	<i>Actinobacteria</i> [99%] <i>Actinobacteridae</i> [97%] <i>Actinomycetales</i> [90%] <i>Micrococcineae</i> [52%] <i>Intrasporangiaceae</i> [32%] <i>Terracoccus</i> [5%]	100% 99%	EU117631 DQ316352	Crystal Bog Lake clone CB7B1 Lake Grosse Fuchskuhle clone FSW11-20
Actino-SW06-3	JF917156	402	<i>Verrucomicrobia</i> "[100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	98%	AY792311	Crystal Bog Lake clone CystalBoq022E6
Actino-SW06-4	JF917157	388	<i>Actinobacteria</i> "[94%] <i>Actinobacteria</i> [94%] <i>Actinobacteridae</i> [88%] <i>Actinomycetales</i> [86%] <i>Micrococcineae</i> [49%] <i>Intrasporangiaceae</i> [30%] <i>Terracoccus</i> [6%]	100% 99%	HQ532266 DQ316348	Crystal Bog Lake clone CB3D11 Lake Grosse Fuchskuhle clone FSW11-16
Actino-SW06-5	JF917158	402	<i>"Verrucomicrobia"</i> [100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	98%	FJ624906	Boreal pine forest clone HF_C_33
Actino-SW06-6	JF917159	400	<i>Verrucomicrobia</i> "[100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	99%	AY792311	Crystal Bog Lake clone CystalBoq022E6
Actino-SW06-7	JF917160	419	<i>"Verrucomicrobia"</i> [100%] <i>Spartobacteria</i> [98%] <i>Spartobacteria_genera_incertae_sedis</i> [96%]	97%	FJ916701	Twin Valley Lake clone TW1A5
Actino-SW08-8	JF917161	380	<i>Actinobacteria</i> [100%] <i>Actinobacteridae</i> [100%] <i>Actinomycetales</i> [100%] <i>Corynebacterineae</i> [100%] <i>Mycobacteriaceae</i> [100%] <i>Mycobacterium</i> [100%]	100% 98%	FJ544445 AY208856	<i>Mycobacterium</i> sp. S061 <i>Mycobacterium saskatchewanense</i> NRCM 00-250 ^T
Actino-SW08-9	JF917162	414	<i>"Verrucomicrobia"</i> [100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	98%	AY792311	Crystal Bog Lake clone CystalBoq022E6
Actino-SW08-10	JF917163	414	<i>"Verrucomicrobia"</i> [100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	98% 97%	HQ162248 AY792311	Arctic peat soil clone Jun20 Crystal Bog Lake clone CystalBoq022E6
Actino-SW08-11	JF917164	402	<i>"Verrucomicrobia"</i> [100%] <i>Subdivision3</i> [100%] <i>Subdivision3_genera_incertae_sedis</i> [100%]	98%	AY792311	Crystal Bog Lake clone CystalBoq022E6
SPH-SW06-1	JF917165	508	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Acetobacteraceae</i> [100%] <i>Kozakia</i> [24%]	99%	GU734042	Lake Grosse Fuchskuhle DGGE bands FSW-St05-7
SPH-SW08-2	JF917166	505	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [100%] <i>Telmatospirillum</i> [100%]	99% 97%	GQ402757 AF524863	Peat swamp forest soil clone clone PW351 <i>Telmatospirillum siberiense</i> 26-4b1
SPH-SW08-3	JF917167	505	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [98%] <i>Skermanella</i> [81%]	94%	GU256437	<i>Azospirillum amazonense</i> DSM 2787 ^T
SPH-SW08-4	JF917168	505	<i>Alphaproteobacteria</i> [100%] <i>Sphingomonadales</i> [100%]	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T

SPH-SW08-5	JF917169	505	<i>Sphingomonadaceae</i> [100%] <i>Novosphingobium</i> [100%] <i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [100%] <i>Telmatospirillum</i> [99%]	96%	AF524863	<i>Telmatospirillum siberiense</i> 26-4b1
SPH-SW08-6	JF917170	503	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [98%] <i>Rhodospirillaceae</i> [78%] <i>Rhodocista</i> [33%]	99% 94%	EU409478 GU256437	Lake Grosse Fuchskuhle isolate Fuku2-ISO-153 <i>Azospirillum amazonense</i> DSM 2787 ^T
SPH-SW08-7	JF917171	506	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [99%] <i>Skermanella</i> [77%]	94%	GU256437	<i>Azospirillum amazonense</i> DSM 2787 ^T
SPH-SW09-8	JF917172	505	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [100%] <i>Telmatospirillum</i> [100%]	99% 97%	GQ402757 AF524863	Peat swamp forest soil clone clone PW351 <i>Telmatospirillum siberiense</i> 26-4b1
SPH-SW09-9	JF917173	505	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [99%] <i>Skermanella</i> [79%]	95%	GU256437	<i>Azospirillum amazonense</i> DSM 2787 ^T
SPH-SW08-10	JF917174	503	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [100%] <i>Rhodospirillaceae</i> [100%] <i>Telmatospirillum</i> [98%]	99% 97%	GQ402757 AF524863	Peat swamp forest soil clone PW351 <i>Telmatospirillum siberiense</i> 26-4b1
SPH-SW09-11	JF917175	495	<i>Gammaproteobacteria</i> [99%] <i>Methylococcales</i> [96%] <i>Methylococcaceae</i> [96%] <i>Methylobacter</i> [87%]	94% 93%	AJ290055	<i>Methylobacter</i> Lake Grosse Fuchskuhle clone Fuku N33
SPH-SW09-12	JF917176	506	<i>Alphaproteobacteria</i> [100%] <i>Sphingomonadales</i> [100%] <i>Sphingomonadaceae</i> [100%] <i>Novosphingobium</i> [100%]	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T
SPH-SW09-13	JF917177	498	<i>Alphaproteobacteria</i> [100%] <i>Sphingomonadales</i> [100%] <i>Sphingomonadaceae</i> [99%] <i>Novosphingobium</i> [98%]	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T
SPH-SW09-14	JF917178	506	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [99%] <i>Rhodospirillaceae</i> [90%] <i>Rhodocista</i> [38%]	99% 94%	EU409478 GU25643	Lake Grosse Fuchskuhle isolate Fuku2-ISO-153 <i>Azospirillum amazonense</i> DSM 2787 ^T
SPH-SW09-15	JF917179	530	<i>Gammaproteobacteria</i> [100%] <i>Methylococcales</i> [100%] <i>Methylococcaceae</i> [100%] <i>Methylobacter</i> [100%]	95%	AJ290055	Lake Grosse Fuchskuhle clone FukuN13

SPH-SW09-16	JF917180	506	<i>Alphaproteobacteria</i> [100%] <i>Sphingomonadales</i> [100%] <i>Sphingomonadaceae</i> [100%] <i>Novosphingobium</i> [99%]	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T
SPH-SW09-17	JF917181	506	<i>Alphaproteobacteria</i> [100%] <i>Sphingomonadales</i> [100%] <i>Sphingomonadaceae</i> [100%] <i>Novosphingobium</i> [99%]	99%	EU336977	<i>N. acidiphilum</i> FSW06-204d ^T
SPH-SW09-18	JF917182	506	<i>Alphaproteobacteria</i> [100%] <i>Rhodospirillales</i> [99%] <i>Rhodospirillaceae</i> [92%] <i>Rhodocista</i> [30%]	99% 94%	EU409478 GU256437	Lake Grosse Fuchskuhle isolate Fuku2-ISO-153 <i>Azospirillum amazonense</i> DSM 2787 ^T

Reference

1. Wang Q, Garrity GM, Tiedje JM, Cole JR (2007) Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl Environ Microbiol* 73: 5261-5267.
2. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. *J Mol Biol* 215: 403-410.