Appendix 2, List of cyanobacterial sequences analysed in this study (DGGE, clones), corresponding samples and OTUs

sequence	sample	OTU Taton et al. 2006c	OTU This work	Closest relative (BLAST)	Simila-rity %	Accession number	Geographic origin of the closest relative	Distri-bution OTU
WO6_33	WO6 G 0-1	16	1	Uncultured Antarctic cyanobacterium clone LMM1-19	99	EU032364.1	Lac Miers and Beacon Valleys, DV, Ant	A
SH8_28_2a	Stillwell Hills 8	16	1	Uncultured Antarctic cyanobacterium clone Heart lake	1000	DQ181723.1	Lake Heart, Larsemann Hills, EA	A
WO6_31	WO6 littoral East side	16	1	Uncultured Antarctic cyanobacterium clone LMM1-19	100	EU032364.1	Lac Miers and Beacon Valleys, DV, Ant	A
WO8_35(2)	WO8_epilitic littoral	16	1	Uncultured Antarctic cyanobacterium clone LMM1-19	100	EU032364.1	idem	A
WO4LF3(8)	WO4 littoral	16	1	Uncultured Antarctic cyanobacterium clone RJ088	99	DQ181681.1	Lake Reid, Larsemann Hills, EA	A
WO1_30	WO1 littoral	16	1	Uncultured Antarctic cyanobacterium clone LMM1-19	99	EU032364.1	Lac Miers and Beacon Valleys, DV, Ant	A
TMLU4_C30	Lundström lake, littoral mat	17	3	*Phormidium sp*. SAG 37.90	100	AM398795	Endolithic. Pass Bernina, Switzerland	C
SH7_29_1a	Stillwell Hills 7	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	Lake Ace, Vestfold Hills, EA	C
TMFO1D1a1	Forlidas pond, bottom saline slush	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	idem	C
TMFO1S73	Forlidas pond, bottom saline slush	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	idem	C
TMFO1_A5	Forlidas pond, bottom saline slush	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	idem	C
TMFO2H9	Forlidas pond, littoral mat	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	99	AY493589.1	idem	C
WO10_38	WO10 littoral	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	99,035	AY493589.1	idem	C
SH3_23_2a	Stillwell Hills 3 Centre hole	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	99	AY493589.1	idem	C
WO10_39	WO10 littoral	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	idem	C

App. 2 continued

sequence	**Sample**	**OTU Taton et al. 2006c**	**OTU This work**	**Closest relative (BLAST)**	**Simila-rity %**	**Accession number**	**Geographic origin of the closest relative**	**Distri-bution OTU**
WO10_40	WO10 littoral	63	7	*Leptolyngbya antarctica* ANT.ACEV6.1	100	AY493589.1	idem	C
BB164_1a	Belgian basis 164	83	8	*Nostoc sp. 'Stereocaulon exutum cyanobiont'* clone I28958	99	DQ265950.1	Japan	C
BB164_3a	idem	83	8	*Nostoc sp. 'Stereocaulon exutum cyanobiont'* clone I28958	99	DQ265950.1	idem	C
BB164_5b	idem	85	9	Uncultured Antarctic cyanobacterium clone H01_ELL02	96,97	EF220169.1	Ellsworth Mountains, Antarctica	N
BB160_2b	Belgian basis 160	10	11	*Phormidium pristleyi* ANT.LH66.1	99	AY493581.1	Lake Heart, Larsemann Hills, EA	C
TMLU4S7	Lundström lake littoral mat	10	11	*Phormidium pristleyi* ANT.LH66.1	100	AY493581	idem	C
WO1_5	WO1 littoral	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	Chili	C
WO6_8	WO6 littoral East side	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	idem	C
WO8_11	WO8_epilit littoral	33	12	Uncultured Antarctic cyanobacterium isolate DGGE gel band FrF1	98	AY151766.1	Lac Fryxell, DV, Ant	C
WO6_9	WO6 littoral East side	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	Chili	C
WO1_1	WO1 littoral	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	idem	C
WO1_3	WO1 littoral	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	idem	C
WO6_10 (2)	WO6 G 0-1	33	12	*Nostoc sp. 'Pannaria rubiginella cyanobiont*	99	EF536024.1	idem	C
WO1_4	WO1 littoral	33	12	*Nostoc sp. 'Nephroma arcticum cyanobiont*	98	AY333641.1	Arctic	C
TMFO3D1b 1	Forlidas Valley terrestrial	7	16	Uncultured Antarctic cyanobacterium clone Fr121	100	AY151728.1	Lake Fryxell, Ant	C
BB160_8b	Belgian Basis 160	73	17	*Leptolyngbya sp*. ANT.LH52.1	98,2	AY493584.1	Lake Heart, Larsemann Hills, EA	A
BB34_5b	Belgian Basis 34	73	17	*Leptolyngbya sp*. ANT.LH52.1	97.6	AY493584.1	idem	A
WO6_34	WO6 G 0-1	58	18	*Synechococcus sp*. LS0535	99	DQ526409.1	Laurentian Great Lakes (North America)	C

App.2 continued

sequence	sample	OTU Taton et al. 2006c	OTU This work	Closest relative (BLAST)	Simila-rity %	Accession number	Geographic origin of the closest relative	Distri-bution OTU
TMLU4_F10	idem	79	22	Uncultured cyanobacterium clone D1F08	99	EU753629	idem	C
TMFO3S2	Forlidas pond, littoral mat	80	23	*Synechococcus* PCC7335	97,24	AB015062	Marine	N
TMFO2S1	Forlidas Valley, terrestrial	80	23	*Synechococcus* PCC7335	96,94	AB015062	idem	N
TMLU4_E5	Lundström lake littoral mat	79	24	Uncultured cyanobacterium clone D1F08	99	EU753629.1	Dry stromatolite, Spain	C
TMLU4_F12	idem	79	24	Uncultured cyanobacterium clone D1F08	99	EU753629	idem	C
BB196_8a	Belgian Basis 196	79	24	Uncultured cyanobacterium clone D1F08	99	EU753629	idem	C
TMLU4G9	Lundström lake littoral mat	57	25	Uncultured Antarctic cyanobacterium clone RD017	100	DQ181674	Lake Reid, Larsemann Hills, EA	A
BB196_3a	Belgian Basis 196	44	28	Uncultured Antarctic cyanobacterium clone c47	99	DQ533828.1	King George Island, Antarctic Peninsula	C
BB196_2b	idem	44	28	Uncultured Antarctic cyanobacterium clone c47	99	DQ533828.1	King George Island, Antarctic Peninsula	C
BB33_1b	Belgian Basis 33	44	28	*Phormidium autumnale* Arct-Ph5	99	DQ493873.2	Arctic	C
TMLU42a1	Lundström lake littoral mat	44	28	*Phormidium autumnale* Arct-Ph5	99	DQ493873.2	idem	C
BB33_1a (3)	Belgian Basis 33	44	28	*Phormidium autumnale* Arct-Ph5	99	DQ493873.2	idem	C
SH8_28_1a	Stillwell Hills 8	19	29	*Leptolyngbya antarctica* ANT.LH18.1	100	AY493607.1	Lake Heart, Larsemann Hills, EA	C

App.2 continued

sequence	**sample**	**OTU Taton et al. 2006c**	**OTU This work**	**Closest relative (BLAST)**	**Simila-rity %**	**Accession number**	**Geographic origin of the closest relative**	**Distri-bution OTU**
WO4LF2(10)	WO4 littoral	19	29	Uncultured Antarctic cyanobacterium clone Fr397	99	AY151735.1	Lake Fryxell, DV, Ant	C
BB195_1b	Belgian Basis 195	86	30	Uncultured bacterium clone NK2_527	97,01	EU376198.1	Lake Kastoria, Greece	N
BB144_1b	Belgian Basis 144	86	30	Uncultured bacterium clone NK2_527	97	EU376198.1	idem	N
WO8_15a	WO8_epipsammic	2	31	Uncultured Antarctic cyanobacterium clone H-C30	98	DQ181727.1	Lake Heart, Larsemann Hills, EA	A
WO8_15	WO8_epipsammic	2	31	Uncultured Antarctic cyanobacterium clone H-A07	97,45	DQ181740.1	idem	A
WO1_28	WO1 littoral	21	34	Uncultured Antarctic cyanobacterium clone H-B02	100	DQ181686.1	idem	C
WO8_35b	WO8_epipsammic	21	34	Uncultured Antarctic cyanobacterium clone H-A01	98	DQ181717.1	idem	C
TMFO2A2	Forlidas pond, littoral mat	49	36	Uncultured Antarctic cyanobacterium clone BGC-Fr005	100	AY151737.1	Lake Fryxell, DV, Ant	C
TMFO2D2a2	idem	49	36	Uncultured Antarctic cyanobacterium clone BGC-Fr005	100	AY151737.1	idem	C
TMFO3A2	Forlidas Valley, terrestrial	49	36	*Geitlerinema carotinosum* AICB 37	99	AY423710	Romanian fishpond	C
TMFO2A9	Forlidas pond, littoral mat	49	36	*Geitlerinema carotinosum* AICB 37	99	AY423710	idem	C
TMFO3D1a1	Forlidas Valley, terrestrial	49	36	*Geitlerinema carotinosum* AICB 37	99	AY423710	idem	C
BA_17_1a	Barkell, edge hole	82	37	*Nostoc sp.* SKS8	98	EU022706.1	Skibotn, Norway	C
TMFO1D1b1	Forlidas pond, bottom saline slush	14	38	Uncultured Antarctic cyanobacterium clone LMM1-4	99	EU032358	Lake Myers mat, DV	C
TMFO2D1	Forlidas pond, littoral mat	14	38	Uncultured Antarctic cyanobacterium clone LMM1-4	99	EU032358	Lake Myers mat, DV	C
WO10_22a(4)	WO10 littoral	47	39	*Phormidium murrayi* ANT.ACEV5.2	100	AY493627.1	Lake Ace, Vestfold Hills, EA	C

App.2 continued

sequence	sample	OTU Taton et al. 2006c	OTU This work	Closest relative (BLAST)	Simila-rity %	Accession number	Geographic origin of the closest relative	Distri-bution OTU
REY_19_5a	Reynolds, microbial mat	47	39	*Phormidium murrayi* ANT.ACEV5.2	99	AY493627.1	idem	C
TMFO2D2a4	Forlidas pond, littoral mat	44	42	Uncultured bacterium clone KuyT-ice-36	98	EU263778.1	Kuytun Glacier, Norway	C
BB160_1b(2)	Belgian Basis 160	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB33_2b_1	Belgian Basis 33	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB34_1b	Belgian Basis 34	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
TMFO3D2a4	Forlidas Valley, terrestrial	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB196_1b(2)	Belgian Basis 196	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
SH1_25_2a	Stillwell Hills	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
TMFO2_H1	Forlidas pond, littoral mat	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
TMFO2S10	Forlidas pond, littoral mat	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB183_1a	Belgian Basis 183	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB195_3a	Belgian Basis 195	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
SH1_22_6a	Stillwell Hills 1	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
SH3_23_1a	Stillwell Hills 3	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
SH7_29_1b	Stillwell Hills 7	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB144_1a	Belgian Basis 144	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
BB34_1a	Belgian Basis 34	44	42	Uncultured bacterium clone KuyT-ice-36	100	EU263778.1	idem	C
TMFO3_B5	Forlidas Valley, terrestrial	44	42	Uncultured bacterium clone KuyT-ice-36	99,70%	EU263778.1	idem	C

A or Ant: Antarctic, sequences found only in Antarctica so far
C : cosmopolitan, OTU containing also non antarctic sequences
N : new, not found so far (no published sequences in Genbank at a level of similarity equal or superior to 97,5 %)
DV: Dry Valleys of Mc Murdo

EA: East Antarctica
WO : samples from the West Ongul region (Schirmacher Oasis, East Antarctica)