

Structuring effects of climate-related environmental factors on Antarctic microbial mat communities

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Supplement. Illustration, table and additional figures showing the taxonomic composition and the difference in microbial mat communities in east Antarctic lakes in relation to environmental and geographical factors



Fig. S1. Microbial mats dominated by *Cyanobacteria* in Kobachi Ike (Lützow-Holm Bay, east Antarctica). The mat is detached as a result of the wind-induced redistribution of melting lake ice, which bulldozes on the shoreline. This physical disturbance is a major factor in shaping the community structure and physiognomy of microbial mats in Antarctic lakes (e.g. Sabbe et al. 2004) and partly underlies the importance of lake water depth in structuring these communities. Inset: Microphotograph of a *Nostoc* sp. colony surrounded by thin oscillatori-ans of the genus *Leptolyngbya*. The picture was taken using a light microscope from a microbial mat sample collected in Lake Reid (Larsemann Hills, east Antarctica)

Table S1. BLAST hits of sequences obtained from DGGE bands. For each DGGE band sequence, the cyanobacterial hits included the first sequence indicated by BLAST; if this sequence was from an uncultivated cyanobacterium, the first strain sequence was added. When the first hit was isolated from an Antarctic environment, the first hit that shared >97.5% similarity with the query and isolated from a non-Antarctic environment was added. For eukaryotes, the closest match is given

DGGE band sequence ^a	Possible taxonomic affiliation	Hit indicated by BLAST ^b	Similarity (%) ^c
E82.8	Eukaryota; Metazoa; Tardigrada; Eutardigrada; Apochela; Macrobiotidae	<i>Ramazzottius oberhauseri</i> (AY582122)	98
E93.54	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales	<i>Carteria</i> sp. UTEX2 (AF182817)	96
E70.3	Eukaryota; Fungi	<i>Chlamydomonas raudensis</i> , isolate CCAP 11/131 from Lake Bonney, Antarctica (AJ781313)	100
E67.1 [20b]	Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae	<i>Pseudodoclonium submarinum</i> (EF591129)	100
E64.72	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas	<i>Chlamydomonas pulsatilla</i> from northwest Spitzbergen (AF514404)	100
E59=58.77=57.73	Eukaryota; Fungi	Uncultured fungus clone F5f2 (AY937464)	95
E80.71	Eukaryota; Fungi; Basidiomycota; Hymenomycetes	<i>Mrakia frigida</i> AFTOL-ID 1818 (DQ831017)	100
E71.2	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Filobasidiales	<i>Filobasidium globisporum</i> (AB075546)	100
E62.51	Eukaryota; Fungi; Ascomycota	Uncultured <i>Pezizomycotina</i> clone Sey062 (AY605205)	99
E90.2	Eukaryota; Fungi; Basidiomycota; Hymenomycetes	Uncultured Sarcosomataceae clone Amb_18S_1472 (EF023999)	100
E51.5	Eukaryota; Alveolata; Apicomplexa; Colpodellidae	<i>Colpodella edax</i> (AY234843)	99
E42.88	Eukaryota; Alveolata; Dinophyceae; Gymnodiniales	Uncultured eukaryote isolate E230 permanently anoxic Cariaco Basin (Caribbean Sea) (AY256288)	100
E53.29	Eukaryota; Cercozoa	Uncultured eukaryote clone Amb_18S_1283 (EF023834)	99
E24.95	Eukaryota; Cercozoa	<i>Spongomonas minima</i> strain ATCC 50404 (AF411280)	97
E36.02	Eukaryota; Cercozoa	Uncultured cercozoan clone LEMD111 (AF372739)	99
E48.32	Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae	Thraustochytriidae sp. MBIC11075 (AB183658)	91
E21.6	Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae	<i>Eolimna minima</i> isolate SNA15 (AJ243063)	95
E52.7	Eukaryota; stramenopiles; oomycetes; Peronosporales	<i>Peronospora corydalis</i> from <i>Corydalis speciosa</i> Max. (AF528564)	100
E37.94	Eukaryota; stramenopiles; Chrysophyceae	Uncultured marine eukaryote clone M4_18F06 (DQ103808)	98
E37.33	Eukaryota; Alveolata; Ciliophora; Intramacronucleata; Colpodea	<i>Bursaria truncatella</i> (U82204)	99
E49.35	Eukaryota; Alveolata; Ciliophora; Intramacronucleata; Spirotrichea; Stichotrichia; Stichotrichida	Oxytrichidae environmental sample clone Amb_18S_1444 (EF023975)	99
E42.25	Eukaryota; Alveolata; Ciliophora; Intramacronucleata; Spirotrichea; Stichotrichia; Stichotrichida	Oxytrichidae environmental sample clone Amb_18S_1444 (EF023975)	99
E49.93=50.5	Eukaryota; Alveolata; Ciliophora; Intramacronucleata; Spirotrichea; Stichotrichia; Stichotrichida; Oxytrichidae	<i>Onychodromopsis flexilis</i> (AY498652)	99

Table S1 (continued)

DGGE band sequence ^a	Possible taxonomic affiliation	Hit indicated by BLAST ^b	Similarity (%) ^c
Rauer7-124b* & LH-Pup23-126b*	Cyanobacteria; Uncultured cyanobacterium	Uncultured cyanobacterium clone H-B02**	100
Grovness-11b		Uncultured cyanobacterium isolate DGGE gel band C1	94.5
Rauer7-96a_1*, Pup23-100a*, Pup23-102a*, Pup23-103a* & L70-0-2cm-64a*		Uncultured cyanobacterium clone H-A07**	98.9–100.0
Gentner2-25a		Uncultured soil crust cyanobacterium clone lichen13	98.4
Ace-106a	Cyanobacteria; Oscillatoriales; <i>Phormidium</i> spp.	<i>Phormidium murrayi</i> ANT.ACEV5.2** Uncultured bacterium clone CD29	100 97.6
Ace-129b, Rauer7-123b, Rauer8-48b, Firelight-45b, Sarah-Tarn-121b & Rauer7-96a	Cyanobacteria; Oscillatoriales; <i>Leptolyngbya</i> spp.	<i>Leptolyngbya antarctica</i> ANT.ACEV6.1** <i>Leptolyngbya</i> sp. CCMEE6037 <i>Plectonemia</i> sp. HPC-49	100 98.5 98.8
L11(Reid/Bigj)-13b*		<i>Leptolyngbya antarctica</i> ANT.LH18.1**	99.7
Rauer9-110b		Uncultured cyanobacterium clone R8-B31** LPP-group MBIC10597	100 99
Fold-5b, Fold-6b & Fold-7b		<i>Leptolyngbya frigida</i> ANT.JACK.1** <i>Leptolyngbya</i> sp. CCMEE6119	99.7–100.0 99.4–99.7
Jack-2b*, L67-44b* & Manning-4b		Uncultured cyanobacterium clone H-D28** Uncultured cyanobacterium clone H-C16** Uncultured bacterium Tui1-3 <i>Leptolyngbya frigida</i> ANT.LH52.3**	99.7–100 99.7–100 96.5–97.6 96.0–97.5
Firelight-57a & Manning-28a	Cyanobacteria; Oscillatoriales; <i>Geitlerinema</i> spp.	Uncultured Antarctic cyanobacterium clone BGC-Fr005** <i>Geitlerinema splendendum</i> OES34S4	99.6–100 99.3–99.7
Rauer9-84a	Cyanobacteria; Nostocales; <i>Nodularia harveyana</i>	<i>Nodularia harveyana</i> strain CCAP 1452/1	99.6
Burgess-90a, Burgess-91a & Burgess-92a	Cyanobacteria; Nostocales; <i>Nostoc</i> spp.	<i>Nostoc</i> sp. 152 partial	98.2
L67-49a, L67-50a, L67-51a, L67-54a, L67-52a, Long-146a & L67-53a		<i>Nostoc</i> sp. PC2 partial <i>Nostoc</i> sp. ' <i>Pseudocypbellaria crocata</i> cyanobiont' strain Pcro436	99.2–99.4 98.8–99.4
Sarah-Tarn-94a & Fold-29a		Uncultured Antarctic cyanobacterium DGGE gel band FrF1** <i>Nostoc</i> sp. ' <i>Peltigera canina</i> 2 cyanobiont' <i>Nostoc commune</i> EV1-KK1	99.2–100 99.7–100 99.4–100.0
Jack-26a & Jack-27a	Cyanobacteria; Nostocales; <i>Coleodesmium</i> spp. / <i>Cylindrospermum</i> spp.	<i>Coleodesmium</i> sp. ANT.LH52B.5** <i>Cylindrospermum</i> sp. A1345 Uncultured cyanobacterium clone LV60-CY1-1	99.7 97.9 99.1
Firelight-39b	Cyanobacteria; Chroococcales; <i>Synechococcus</i> sp.	<i>Synechococcus</i> sp. PS845	100
L70-0-2cm-46b	Cyanobacteria; Chroococcales; <i>Chamaesiphon</i> spp.	Uncultured cyanobacterium clone CSC9** <i>C/Nhamaesiphon subglobosus</i> PCC 7430	99.7 98.2

^aDGGE band sequences were grouped using the average neighbour-clustering algorithm of the software Dotur (<http://schloss.micro.umass.edu/software>) with a threshold of 97.5% binary similarity according to a similarity matrix made with the software package ARB (www.arb-home.de) and based on an alignment that includes the positions 380 to 730 relative to *Escherichia coli*. Insertion-deletions and ambiguities were not taken into account. * An asterisk denotes sequences that do not have relatives with at least 97.5% binary similarity from a non-Antarctic environment and therefore could potentially be considered as endemic to Antarctica.

^b**Double asterisk denotes sequences isolated from an Antarctic environment.

^cA range of similarities is given when multiple DGGE band sequences were included in the same group. Levels of similarity were determined by the computation of similarity matrices.

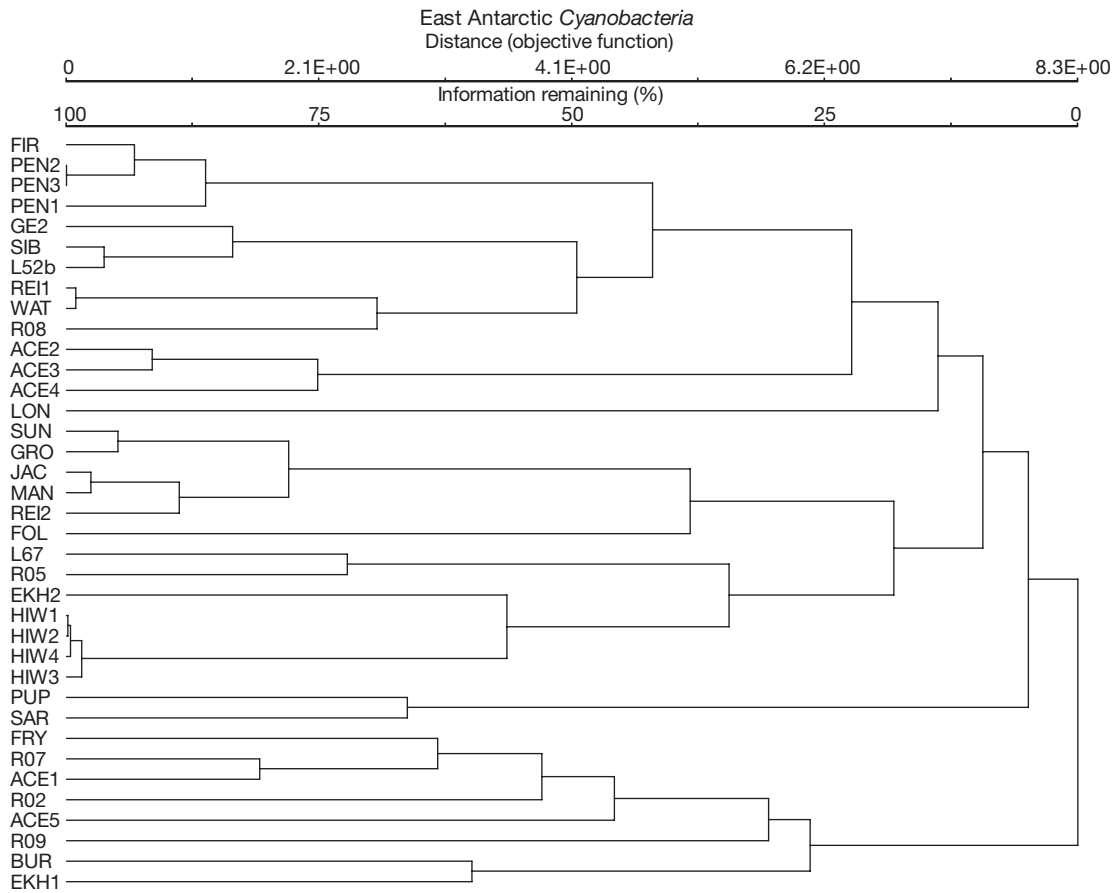


Fig. S2. Cluster analysis of DGGE bands derived using our *Cyanobacteria*-specific primers showing that in-lake variability is generally low, except for Ekho Lake, Lake Reid and 2 samples from Ace Lake (1 of which is a littoral sample). For lake names, see Table 1 in the main article

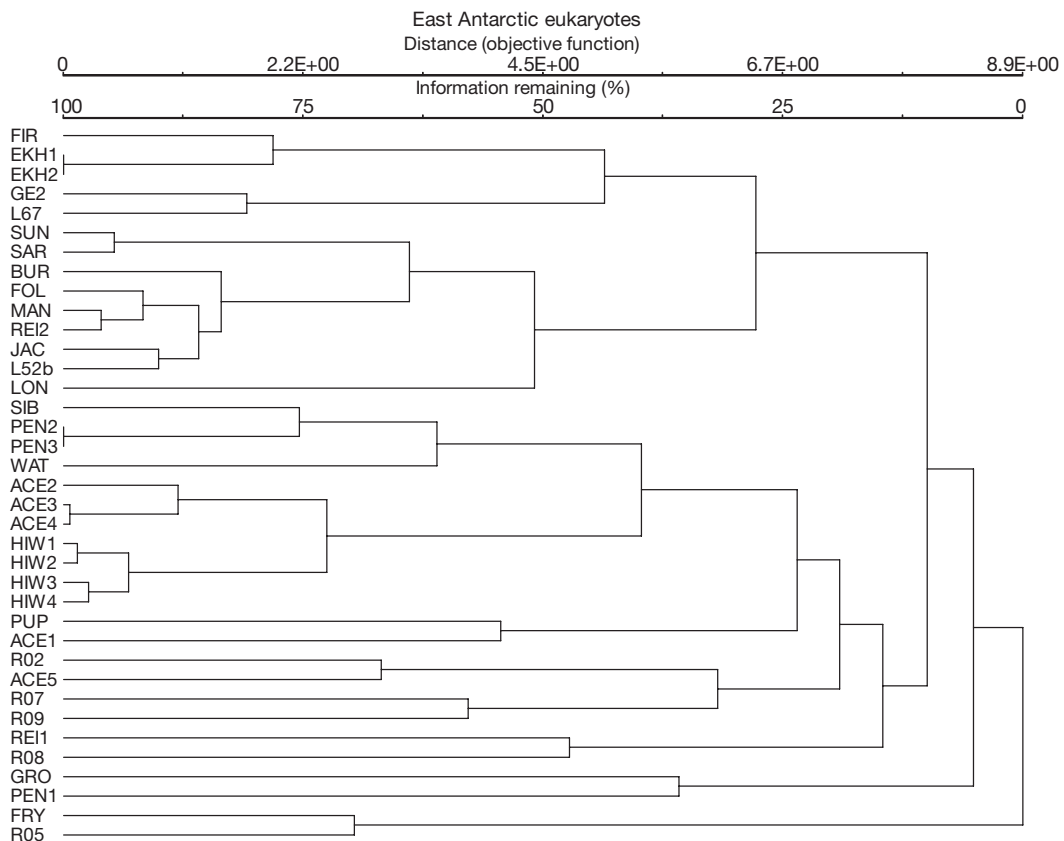


Fig. S3. Cluster analysis of DGGE bands derived using our universal eukaryote primers showing that in-lake variability is generally low, except for the 2 samples from Lake Reid and Ace Lake, which were similarly different in DGGE bands of cyanobacterial sequences, and 1 littoral sample from Pendant Lake. Samples from Ekho Lake are highly similar in contrast to the cyanobacterial sequence composition. For lake names, see Table 1 in the main article