

*The following supplement accompanies the article*

## **Microbial biogeography during austral summer 2007 in the surface waters around the South Shetland Islands, Antarctica**

**Lasse Mork Olsen<sup>1\*</sup>, Murat Van Ardelan<sup>2</sup>, Christopher D. Hewes<sup>3</sup>, Osmund Holm-Hansen<sup>3</sup>, Christian Reiss<sup>4</sup>, Nihayet Bizsel<sup>5</sup>, Egil Sakshaug<sup>1</sup>, Olav Vadstein<sup>6</sup>**

<sup>1</sup>Department of Biology, and <sup>2</sup>Department of Chemistry, Norwegian University of Science and Technology (NTNU), Trondheim 7491, Norway

<sup>3</sup>Polar Research Program, Marine Biology Research Division, Scripps Institution of Oceanography, University of California-San Diego, La Jolla, California 92093-0202, USA

<sup>4</sup>NOAA Fisheries, Antarctic Ecosystem Research Division, La Jolla, California 92037, USA

<sup>5</sup>Institute of Marine Sciences and Technology, Dokuz Eylul University, Baku Bulvari No. 100 Inciralti, 35340 Izmir, Turkey

<sup>6</sup>Department of Biotechnology, Norwegian University of Science and Technology (NTNU), Trondheim 7491, Norway

\*Email: lasse.mork.olsen@ntnu.no

*Aquatic Microbial Ecology 70:131–140 (2013)*

---

**Supplement.** Table S1 shows all the environmental data collected at all sampling stations for the present study. Also listed are the Antarctic Marine Living Resources (AMLR) station ID and the geographical positions for the stations. Average values for the variables for 3 defined water types are also shown. See the main article for a more detailed description of the water types. Table S2 shows the Pearson correlation coefficient ( $r$ ) values for the matrix of all environmental variables. Table S3 shows the sequences and crude taxonomic affiliation obtained from the Ribosomal Database Project (<http://rdp.cme.msu.edu>) to identify tentative chloroplast bands on the DGGE gel for 16S. The sequenced DGGE bands are shown in Fig. S1, which shows the DGGE band pattern for the 16S rDNA. Fig. S2 shows the DGGE bands used for the analysis of the 18S rDNA fingerprints

Table S1. Data for temperature (T, °C), chlorophyll *a* (chl *a*, mg m<sup>-3</sup>), salinity (S, psu), iron (Fe, nM), nitrate (NO<sub>3</sub>, μM), silicate (Si, μM), phosphate (PO<sub>4</sub>, μM) and upper mixed layer depth (Z<sub>UML</sub>, m) for all sampling stations. Average (Avg.) values ± SD are given. All environmental variables were measured at 20 m depth except iron and chl *a*, which were measured in samples from 25 m depth. Three water types (WT) were defined from temperature/salinity depth profile diagrams: WSSW: Weddell Sea and continental shelf water, ACCW: Antarctic Circumpolar Current water, MIXW: mixed water. Our station numbers (Stn), Antarctic Marine Living Resources (AMLR) station ID and position as latitude (°S) and longitude (°W) are shown. nd: no data

Stn	AMLR ID	°S	°W	WT	T	Chl <i>a</i>	S	Fe	NO <sub>3</sub>	Si	PO <sub>4</sub>	Z <sub>UML</sub>
s1	A08-12	62.67	57.30	WSSW	-0.55	0.73	34.45	5.16	28.00	73.00	2.07	146.00
s2	A11-13	63.01	58.60	WSSW	0.04	1.04	34.40	0.74	27.60	59.00	2.38	23.00
s3	A12-14	63.24	59.10	WSSW	-0.03	0.94	34.44	0.96	29.30	76.00	2.15	37.00
s4	A14-14	63.25	60.03	WSSW	0.52	1.13	34.37	1.18	nd	nd	nd	26.00
s5	A17-13	63.00	61.50	MIXW	1.21	1.74	34.10	0.39	28.50	62.00	1.87	38.00
s6	A15-05	61.00	60.50	ACCW	1.99	0.18	33.88	0.14	25.80	49.00	1.88	56.00
s7	A09-04	60.75	57.50	ACCW	1.78	0.06	33.79	0.29	26.50	23.00	2.14	86.00
s8	A07-05	60.99	56.50	ACCW	1.50	1.54	33.95	0.14	25.50	50.00	2.11	48.00
s9	A05.5-01	60.00	55.75	ACCW	1.28	0.61	33.95	0.12	26.60	43.00	2.21	36.00
s10	A04-04	60.75	55.01	MIXW	0.55	0.57	34.11	1.41	29.40	77.00	2.57	40.00
s11	A04-08	61.75	54.99	MIXW	1.22	1.12	34.20	0.48	28.20	66.00	2.44	53.00
s12	A02-01	60.00	53.99	MIXW	0.96	1.62	34.32	0.93	28.40	72.00	2.45	67.00
s13	A02-05	60.99	54.00	MIXW	0.28	1.14	34.38	0.99	28.50	72.00	2.00	142.00
s14	A02-10	62.25	54.00	MIXW	-0.29	0.94	34.11	1.13	nd	nd	nd	nd
Avg.				WSSW	0.00±0.44	0.96±0.17	34.41±0.04	2.01±2.11	28.30±0.89	69.33±9.07	2.20±0.16	58.00±58.97
Avg.				MIXW	0.66±0.59	1.19±0.43	34.21±0.12	0.89±0.39	28.60±0.46	69.80±5.85	2.27±0.31	68.00±42.97
Avg.				ACCW	1.64±0.31	0.60±0.67	33.89±0.07	0.17±0.08	26.10±0.54	41.25±12.55	2.09±0.14	56.50±21.32

Table S2. Pearson correlation matrix for environmental variables: temperature (T), chlorophyll *a* (chl *a*), salinity (S), iron (Fe), phosphate (P), nitrate (N), silicon (Si) and upper mixed layer depth ( $Z_{UML}$ ). The *r* values significant after Bonferroni correction are shown in **bold** ( $p < 0.00625$ )

	T	Chl <i>a</i>	S	Fe	N	Si	P
Chl <i>a</i>	-0.164						
S	<b>-0.796</b>	0.423					
Fe	-0.681	-0.072	0.545				
N	-0.653	0.296	<b>0.698</b>	0.326			
Si	<b>-0.718</b>	0.460	<b>0.784</b>	0.460	<b>0.808</b>		
P	-0.178	0.017	0.143	-0.004	0.302	0.244	
$Z_{UML}$	-0.366	-0.147	0.166	0.586	0.032	0.143	-0.207

Table S3. Sequences and crude taxonomic affiliation from the Ribosomal Database Project (<http://rdp.cme.msu.edu>) to identify tentative chloroplast bands on the DGGE gel for 16S. The sequenced bands are shown in Fig. S1

Band no.	Sequence	Affiliation
1	ATCAGCCATGCCGCGTGTGTGAAGAAGGCCTTAGGGTTGTA AA GCTCTTTCTTTGTG	Bacterium
2	GCATACCGCGTGAGGGATGAAGGATTTTGGTCTGTAAACCTCTT TTCTCAAGAAAGAAGTTCTGACGGTACTTGAGGAATAAGCATCG GCTAACTCCGTGCCAGCAGCCGCGGTAATA	Chloroplast
3	TCCAGCCATGCCGCGTGAGTGAAGAAGGCCTTAGGGTTGTA AAAG CTCTTTTTTCAG	Bacterium
4	AAGAATTCTGACGGTACTTGAGGAATAACCATCGGCTAACTCCG TGCCAGCCCCCGCGTAATT	Chloroplast
5	AAGCCTGACGGAGCATAACCGCGTGAGGGAAGACTGCCTATGGGT TGTAACCTCTTTTTTCAGGGAGGAATAAAATGACGTGTACCTGA AGAATAAGCATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATC	Chloroplast
6	GTGCCAGCAGCCGCGGTAATATAAT	Bacterium
7	AAGAAGGCCTGTGGGTTGTAAACCTCTTTTCTCAAGGAAGAAGTT CTGACGGTACTTGAGGAATAAGCATCGGCTAACTCTGTGCCAGCA GCCGCGG	Chloroplast
8	CGTGAGAGAAGAAGGCCTTAGGGTTGTAAACCTCTTTCCTCAGGG AAGAAATTGACAC	Bacterium
9	CAGCCATAACCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCAC TTTAAGCAGGGAGAAAAAGTTATAAGCTAATACCTTATAACCTTG ATGTTACCTGCAGAATAAGCACCGGCTAATTCCGTGCCAGCAGCC GCGGTAAT	Bacterium
10	ATCAGCCATGCCGCGTGCCAGGAAGACTGCCCTATGGGTTGTAAAC TGCTTTTATACAGGAAGAAATATACCTACGTGTAGGTATTTGACG GTACTGTACGAATAAGGATCGGCTAACTCCGTGCCAGCAGCCGCG GTAATA	Bacterium
11	CCATGCCGCGTGAGAGAAGAAGGCCTTCGGGTTGTAAAGCTCTTT CTACGGGGA	Bacterium
12	TTTTCCGGAAAGAAATCGCGCTGGTTA	Bacterium
13	CATGCCGCGTGAAGAAGAAGCCCT	Bacterium

Fig. S1. Band pattern from denaturing gradient gel electrophoresis (DGGE) of 16S rDNA. Sampling stations (St) are indicated. SW is an unrelated seawater sample for reference. The numbered bands were excised for sequencing

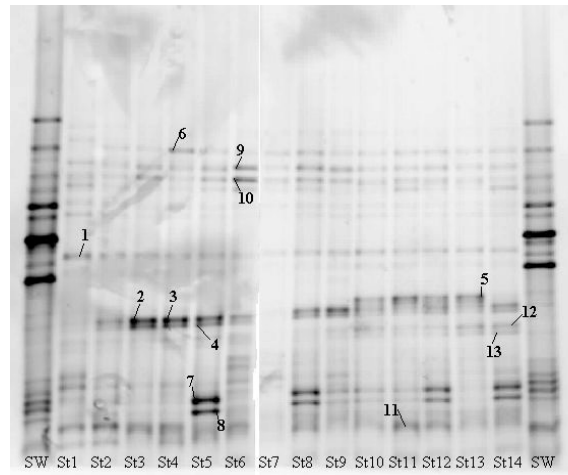


Fig. S2. Band pattern from denaturing gradient gel electrophoresis (DGGE) of 18S rDNA. Sampling stations (St) are indicated. SW is an unrelated seawater sample for reference

