Oceanographic structure drives the assembly processes of microbial eukaryotic communities

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SI Materials and Methods

Seawater sampling and oceanographic data analyses

Sampling took place aboard the Canadian research icebreaker CCGS *Amundsen* in August 2009, as part of the International Polar Year, project MALINA. At every station, a rosette system equipped with a conductivity-temperature-depth profiler (CTD, Seabird SBE-911+), a fluorometer (Seapoint), and a transmissometer (WetLabs C-Star) was deployed multiple times. Relative nitrate profiles were retrieved from the rosette mounted *in situ* ultraviolet spectrometer probe (ISUS; Satlantic). The rosette system was also equipped with a sensor (Biospherical Instruments) for downwelling photosynthetically active radiation (PAR; 400 to 700 nm, dynamic range from 1.4×10^{-5} to 0.5 $\mu E\ cm^{-2}\ s^{-1}$). A similar deck sensor measured surface PAR during the rosette deployments. The CTD data were calibrated and verified following the Unesco Technical Papers (Crease *et al.* 1988). Periodically, discrete water samples were collected directly from the Niskin bottles for salinity calibration using a Guildline Autosal salinometer. The fluorescence data from the fluorometer were calibrated against *in situ* chlorophyll *a* (Chl *a*) concentrations as described in Forest *et al.* (2013). The transmissivity signal was transformed into c_p using standard equations (Kirk 1994). Verified underwater PAR data were normalized to surface irradiance to compute the percentage of transmitted PAR. All CTD and sensor data were averaged over 1 m bins.

Nutrient samples were collected at 10 to 20 m intervals in the upper water column (Tremblay *et al.* 2008; Martin *et al.* 2010) directly form Niskin-type bottles. Nitrate [NO_3^-] and nitrite [NO_2^-] samples were dispensed into polyethylene tubes, immediately poisoned with mercuric chloride [1 $\mu g\ ml^{-1}$; (Kirkwood 1992)] and stored for subsequent laboratory analysis. [NO_3^-] and [NO_2^-] were measured using a Technicon AutoAnalyzer II following Tréguer and LeCorre (1975). Concentrations in the nanomolar range (detection limit of 3 nmoles l^{-1}) were obtained as in Raimbault *et al.* (1990). Ammonium concentrations [NH_4^+] were measured directly on board using the sensitive fluorescent method of Holmes *et al.* (1999) with a detection limit of 5 nmoles l^{-1}. The reproducibility of nutrient measurements between analyses was assessed using in-house standards compared with commercially available products (OSIL: http://www.osil.co.uk/Products/SeawaterStandards).

Cell abundances were determined using a flow cytometer FACS ARIA (Becton Dickinson, San Jose, CA) on-board the CCGS *Amundsen* as previously described for bacterial (Ortega-Retuerta *et al.*, 2012), pico- and nano-phytoplanktonic cells (Balzano *et al.*, 2012). Bacterial production was measured using ^{3}H-leucine incorporation as in Ortega-Retuerta *et al.* (2012). All physical, biological and nutrient data are available at http://malina.obs-vlfr.fr.

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Titles and legends to SI figures

Figure S1. A. Temperature and **B.** beam attenuation (c_p) profiles. Measures were collected from Beaufort Sea CTD rosette casts from which microbial communities were retrieved. Distinct solid and dashed lines represent the six distinct sampling stations. Stations corresponding to weak SCM are colored in red.

Figure S2. A. Nonmetric multidimensional scaling (NMDS) ordination on unweighted UniFrac distances for the 24 Beaufort Sea microbial communities. Ellipses represent community clusters and 95% confidence intervals. Samples are represented by markers (depths) and numbers (stations). **B.** Procrustes rotations between NMDS ordinations computed on weighted and unweighted UniFrac distances (d_{W5000} and d_{W5000}, respectively). Arrows summarizing the rotations between ordinations are colored based on their corresponding community clusters. **C.** OTU rank abundance curves and, **D.** total sequence numbers for the 50 most abundant OTUs for each Beaufort Sea microbial community clusters.

Figure S3. A. Phylogenetic diversity (Faith's definition) measures for each Beaufort Sea microbial community clusters. Phylogenetic diversity was computed on datasets subsampled 1000 times at en even depth of 5000 sequences. Plotted are mean phylogenetic diversity and error bars are s.e.m. **B.** Relationship between sample depth and phylogenetic diversity. The line represents a least-squares linear regression. Dots are scaled based on corresponding OTU richness.

Figure S4. Relative abundance heatmap of the 25 most abundant taxa (genera, family or 'groups' depending on available taxonomic information) in the Beaufort Sea sequence datasets. Relative abundances were centered-scaled and corresponding z-score scale is displayed as a color gradient (green: abundant; red: rare). Taxonomic lineages of the 25 taxa are indicated by colored dots. Row dendogram represents results from a hierarchical clustering of taxa relative abundances; columns were regrouped based on Beaufort Sea microbial community clusters.

Figure S5. Phylogenetic placements of the Picozoa OTUs. Representative sequences of Picozoa-like OTUs were mapped onto a Picozoa reference tree using RAxML evolutionary placement algorithm. The Picozoa maximum-likelihood reference tree was reconstructed based on an 18S rDNA gene sequence alignment. Picozoa reference sequences were clustered at 99% identity to remove redundancy prior to the phylogenetic reconstruction (number of sequences in a cluster is indicated in parentheses after the Genbank accession of the reference representative sequence). Bootstrap supports are represented by black dots when ≥70%. OTU identifiers are displayed in red; an asterisk after the OTU identifier denotes a phylogenetic placement with a likelihood ≥0.75. Relative abundances of Picozoa OTUs across the Beaufort Sea community clusters are displayed on the right.

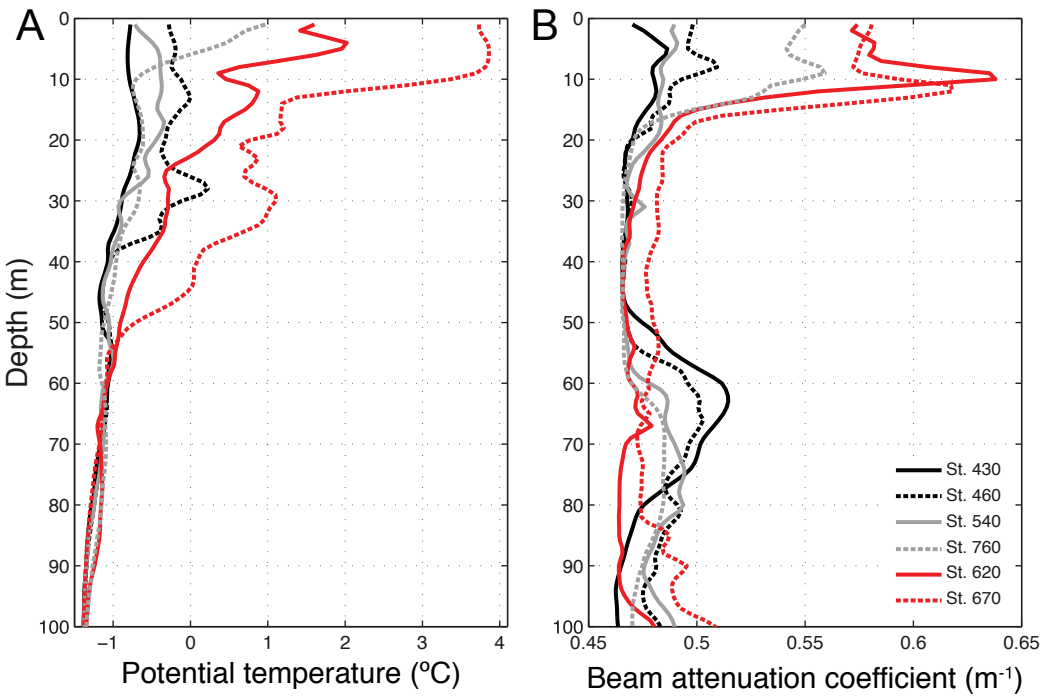
A
B
Depth (m)
Potential temperature (ºC)
Beam attenuation coefficient (m-1)
St. 430
St. 460
St. 540
St. 760
St. 620
St. 670

Figure S1

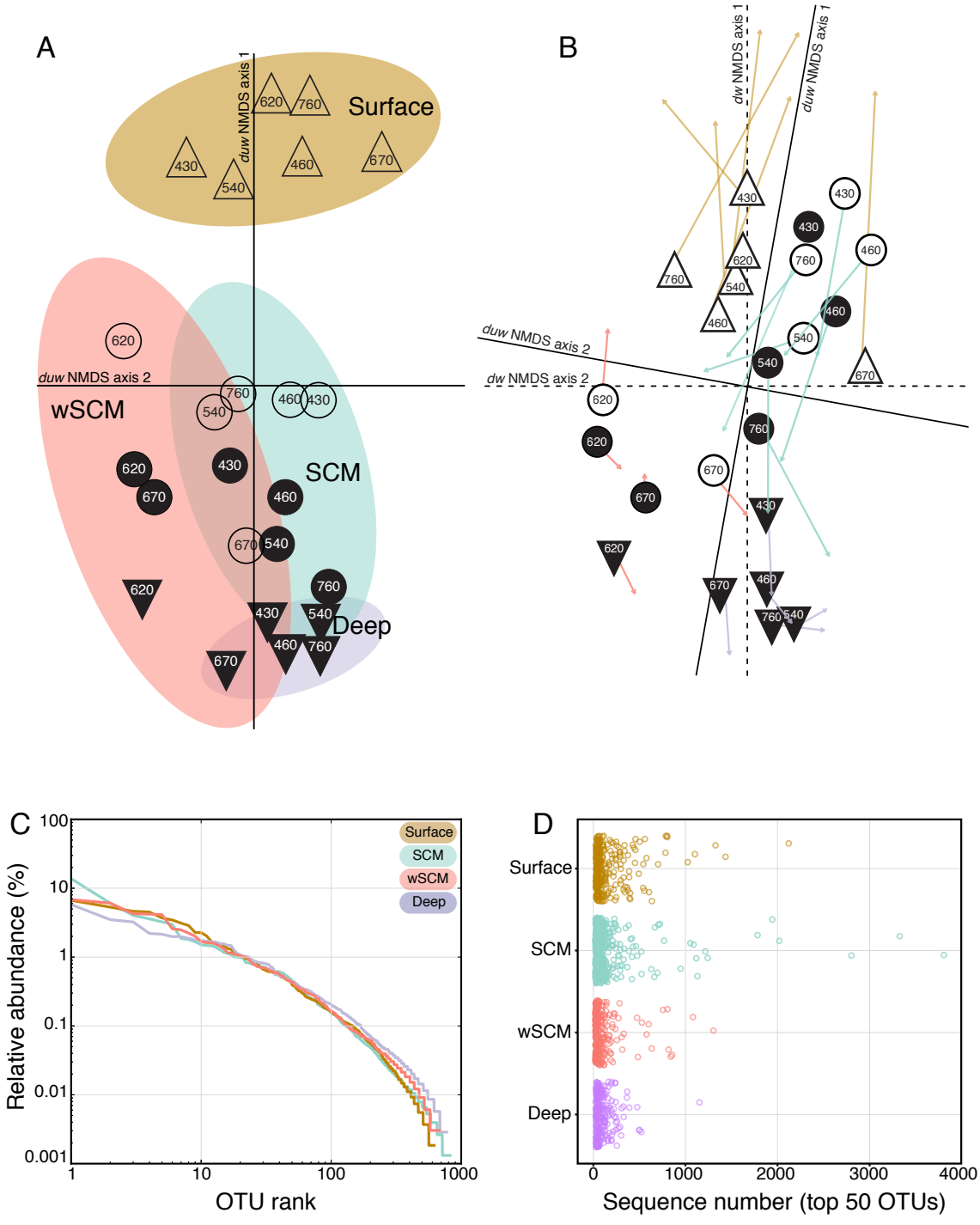
A
duw NMDS axis 1
duw NMDS axis 2
Surface
wSCM
SCM
Deep
B
dw NMDS axis 1
duw NMDS axis 1
duw NMDS axis 2
dw NMDS axis 2
C
Relative abundance (%)
OTU rank
Surface
SCM
wSCM
Deep
D
Surface
SCM
wSCM
Deep
Sequence number (top 50 OTUs)

Figure S2

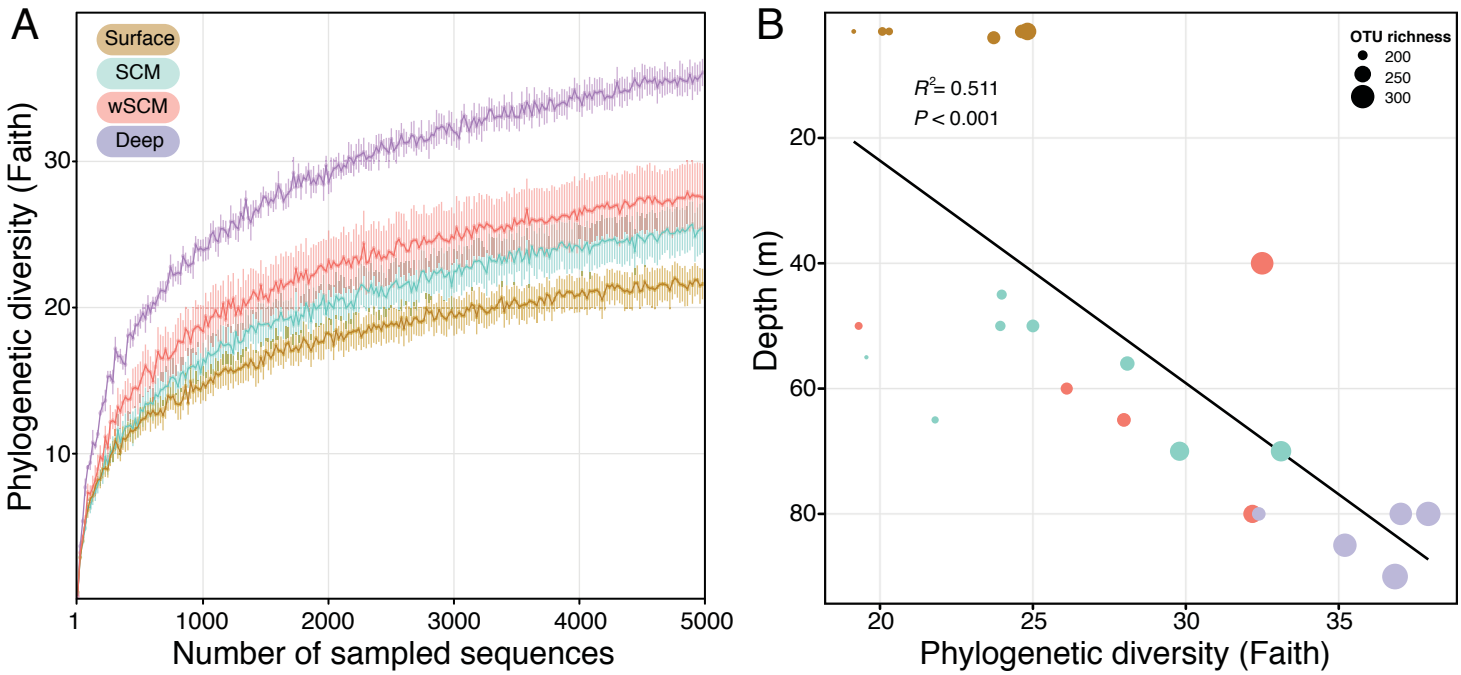
A
Surface
SCM
wSCM
Deep
Phylogenetic diversity (Faith)
10
20
30
1
1000
2000
3000
4000
5000
Number of sampled sequences
B
R^2= 0.511
P < 0.001
OTU richness
200
250
300
Depth (m)
20
40
60
80
20
25
30
35
Phylogenetic diversity (Faith)

Figure S3

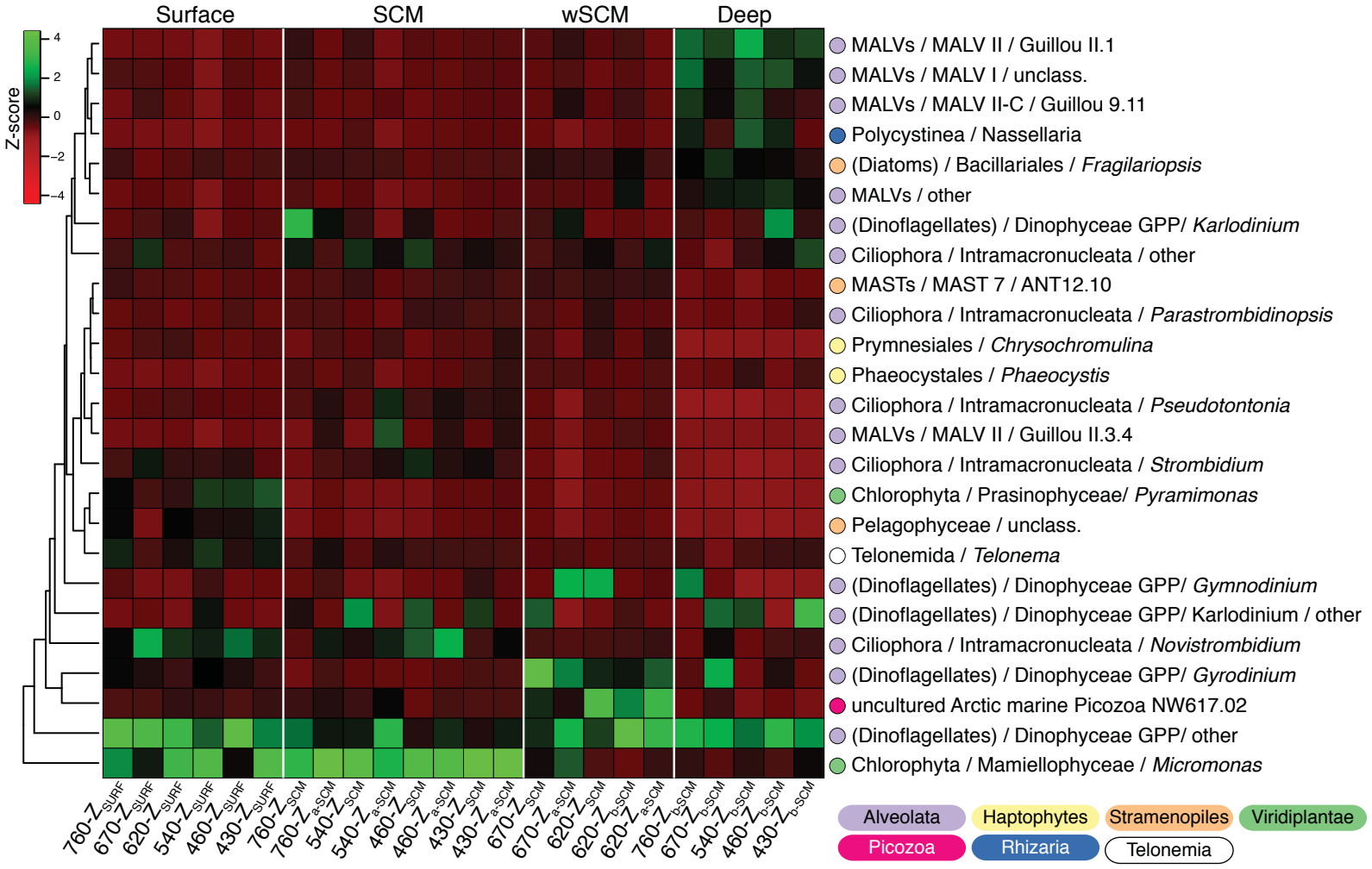
Surface
SCM
wSCM
Deep
Z-score
4
2
0
−2
−4
MALVs / MALV II / Guillou II.1
MALVs / MALV I / unclass.
MALVs / MALV II-C / Guillou 9.11
Polycystinea / Nassellaria
(Diatoms) / Bacillariales / Fragilariopsis
MALVs / other
(Dinoflagellates) / Dinophyceae GPP/ Karlodinium
Ciliophora / Intramacronucleata / other
MASTs / MAST 7 / ANT12.10
Ciliophora / Intramacronucleata / Parastrombidinopsis
Prymnesiales / Chrysochromulina
Phaeocystales / Phaeocystis
Ciliophora / Intramacronucleata / Pseudotontonia
MALVs / MALV II / Guillou II.3.4
Ciliophora / Intramacronucleata / Strombidium
Chlorophyta / Prasinophyceae/ Pyramimonas
Pelagophyceae / unclass.
Telonemida / Telonema
(Dinoflagellates) / Dinophyceae GPP/ Gymnodinium
(Dinoflagellates) / Dinophyceae GPP/ Karlodinium / other
Ciliophora / Intramacronucleata / Novistrombidium
(Dinoflagellates) / Dinophyceae GPP/ Gyrodinium
uncultured Arctic marine Picozoa NW617.02
(Dinoflagellates) / Dinophyceae GPP/ other
Chlorophyta / Mamiellophyceae / Micromonas
760-Z SURF
670-Z SURF
620-Z SURF
540-Z SURF
460-Z SURF
430-Z SURF
760-Z SCM
760-Z a-SCM
540-Z SCM
540-Z a-SCM
460-Z SCM
460-Z a-SCM
430-Z SCM
430-Z a-SCM
670-Z SCM
670-Z a-SCM
620-Z SCM
620-Z b-SCM
620-Z a-SCM
760-Z b-SCM
670-Z b-SCM
540-Z b-SCM
460-Z b-SCM
430-Z b-SCM
Alveolata
Haptophytes
Stramenopiles
Viridiplantae
Picozoa
Rhizaria
Telonemia

Figure S4


JX988767 PICOBI02F–L52R-He
DQ222874 HE001005.148
EU368021 FS04GA46-01Aug05-5m
AY426835 BL000921.8
otu664*
DQ222875 (10) OR000415.159
BP2
HQ869075 (3) SHAX587
HQ156832 100609-15
otu544
otu4*
otu670*
otu78*
otu240
P9
HQ868882 (2) SHAX1135
otu342*
otu1117
DQ060527 (4) NOR50.52
HQ222462 (4) CB1901S20
HM561172 CFL119DB12
otu669
otu40
HM561171 CFL161DA18
otu111
otu25
otu364
P8
DQ222879 (16) RA000907.18
HQ868776 SHAX1019
HQ868497 SHAX724
HQ868690 (3) SHAX927
HQ868797 SHAX1043
0.01
>70%
HM858787 MO.011.150m.00003
EU368037 (5) EN351CTD039-30mN9
HQ869605 SHBF578
HM561168 (2) CFL146DB13
DQ060523 (3) NOR46.29
HQ869692 SHBF671
HQ869099 (4) SHAX616
JQ222911 (6) SHAU435
otu463
otu777
otu762
otu452
BP3.1
GU822951 (7) AI5F15RM3A09
HQ867420 SHAC744
HQ867337 SHAC623
HQ867354 SHAC648
DQ060524 (3) NW414.27
HQ869362 SHBA707
HQ869261 (13) SHBA597
JN693069 EMC-2G08
JQ226352 SHAA389
HM595055 FS01A-3-3Nov08-1m
DQ060525 (39) NW617.02
otu133*
otu26*
otu464*
otu151*
otu366*
P5
DQ222877 (12) RA000907.54
JX988766 PICOBI01F–L52R-14
JX988761 PICOBI01F–L52R-12
JX988760 PICOBI01F–L52R-7
JX988763 PICOBI01F–L52R-8
JX988764 PICOBI01F–L52R-10
JX988765 PICOBI01F–L52R-18
JX988762 PICOBI01F–L52R-9
AY343928 (4) He000803–72
JF791041 7532
DQ222876 (2) RA000907.33
EU368003 (3) FS01AA11-01Aug05.5m
JX988758 (20) Picomonas judraskeda
JX988759 PICOBI01F–L52R-11
EU368020 (2) FS04GA95-01Aug05.5m
EU368004 (6) FS01AA94-01Aug05.5m
Surface
SCM
wSCM
Deep
0.44%
0.42%
4.26%
0.37%
1%
relative abundance

Figure S5

Table S1. Ancillary data for the Beaufort Sea sampling stations. The data, along with those presented in Figure 2, were used for BEST selection of environmental parameters. Additional ancillary data for the MALINA project are available at http://malina.obs-vlfr.fr.

Station	Date 2009	Z	Z (m)	O_2[a]	Phaeo small[b]	Phaeo large[b]	NO_3+ NO_2[c]	NH_4[c]	PO_4[c]	$SiOH_4$[c]	POC[c]	DOC[c]	DON[c]	DOP[c]	PP[d]	BP[e]	Bacteria[f]	Nano[f]	Pico[f]	CDOM[g]
430	18/09	Z_{SURF}	3	8.63	0.01	0	0.01	0	0.52	2.89	1.76	60.99	5.57	0.19	0.52	3.07	238830	427	5171	0.07
		$Z_{a\text{-}SCM}$	55	8.88	0.33	0.05	2.93	0.02	0.99	8.99	3.11	n.a.	n.a.	n.a.	1.98	3.78	360052	1047	9854	0.08
		Z_{SCM}	65	8.21	0.37	0.04	6.80	0	1.30	14.52	2.38	65.76	6.16	0.10	0.45	3.06	447085	831	13057	0.10
		$Z_{b\text{-}SCM}$	80	7.22	0.03	0.02	12.89	0	1.79	27.88	n.a.	n.a.	n.a.	n.a.	n.a.	0.74	169411	682	974	0.10
460	19/08	Z_{SURF}	4	8.57	0.02	0	0.01	0	0.54	3.04	2.82	57.80	10.14	0.20	0.93	8.70	n.a.	n.a.	n.a.	0.08
		$Z_{a\text{-}SCM}$	45	9.26	0.03	0	0.02	0	0.75	4.04	1.18	59.44	12.24	0.22	0.42	3.85	n.a.	n.a.	n.a.	0.08
		Z_{SCM}	56	8.99	0.28	0.05	1.93	0.02	0.91	7.60	2.82	57.80	9.45	0.22	0.96	2.15	n.a.	n.a.	n.a.	0.09
		$Z_{b\text{-}SCM}$	80	7.32	0.06	0.03	11.50	0.01	1.66	25.21	0.59	63.67	9.47	0.27	n.a.	0.49	n.a.	n.a.	n.a.	0.10
540	17/08	Z_{SURF}	3	8.72	0.01	0.03	0.01	0	0.55	3.09	1.68	62.07	5.73	0.20	0.75	7.39	193087	490	2887	0.07
		$Z_{a\text{-}SCM}$	50	9.13	0.04	0	0.03	0	1.36	3.83	1.40	69.43	5.14	0.15	0.63	2.68	266374	509	2289	0.08
		Z_{SCM}	70	8.26	0.29	0.06	6.17	0.01	2.20	14.04	1.77	83.22	5.77	0.10	0.91	1.34	221987	915	2091	0.09
		$Z_{b\text{-}SCM}$	85	7.15	0.06	0.06	10.28	0.01	2.75	22.43	0.84	77.07	6.32	0.07	0.16	0.64	137003	146	368	0.10
620	11/08	Z_{SURF}	3	8.35	0	0	0	0.03	0.33	7.82	5.61	99.48	4.56	0.11	3.36	14.71	424847	522	4036	0.13
		$Z_{a\text{-}SCM}$	50	9.14	0.02	0.01	0.01	0	0.63	3.60	0.92	60.77	4.34	0.19	0.22	5.44	280552	253	67	0.08
		Z_{SCM}	65	8.90	0	0	2.01	0.16	0.91	8.90	1.15	51.40	4.21	0.14	0.40	4.91	297468	146	108	0.09
		$Z_{b\text{-}SCM}$	80	8.04	0	0.01	6.83	0.05	1.26	18.34	0.92	n.a.	n.a.	n.a.	0.07	2.70	237149	128	0	0.11
670	10/08	Z_{SURF}	3	8.11	0	0	0.01	0.02	0.41	7.76	5.96	94.43	4.43	0.10	2.07	36.95	874089	400	1902	0.14
		$Z_{a\text{-}SCM}$	40	9.28	0	0	0.04	0.02	0.65	3.46	n.a.	74.20	5.65	0.53	n.a.	10.18	399293	190	128	0.09
		Z_{SCM}	60	8.50	0	0.11	0.33	0.07	0.96	8.13	1.95	72.25	14.68	0.76	0.17	2.10	300520	1072	0	0.09
		$Z_{b\text{-}SCM}$	80	7.29	0.02	0.02	6.30	0.03	1.29	15.33	1.15	59.96	3.92	0.11	0.14	1.310	244390	433	1049	0.10
760	12/08	Z_{SURF}	3	8.62	0.01	0	0.01	0.01	0.39	4.86	3.55	108.40	15.83	0.56	1.70	13.87	395137	723	4333	0.11
		$Z_{a\text{-}SCM}$	50	9.22	0.03	0.01	0	0.01	0.68	3.38	1.83	57.57	4.20	0.09	0.11	3.27	366178	743	5000	0.08
		Z_{SCM}	70	8.90	0.18	0.01	2.93	0.01	1	8.43	1.37	62.56	4.66	0.08	0.34	1.22	306567	1174	4423	0.09
		$Z_{b\text{-}SCM}$	90	7.36	0.03	0.02	10.04	0.01	1.54	21.72	0.69	58.72	5.27	0.04	0.10	0.68	162854	406	0	0.10

Phaeo: phaeopigments; POC: particulate organic carbon; DOC: dissolved organic carbon; DON: dissolved organic nitrogen; DOP: dissolved organic phosphorus; PP: primary production; BP: bacterial production; CDOM: colored dissolved organic matter.

[a]: µM kg^{-1}.

[b]: in mg m^{-3}; small: 0.7-5 µm, large: 5-20µm.

[c]: in µM.

[d]: in mgC m^{-3} $24h^{-1}$.

[e]: in pmol leu l^{-1} h^{-1}.

[f]: bacterial, nano- and picophytoplanktonic cell abundances in cell ml^{-1} (flow cytometry).

[g]: *in situ* CDOM fluorescence in mg m^{-1}.

Table S2. Sequence, OTU and diversity information for the 24 Beaufort Sea microbial samples.

Station	Depth category	Raw reads	Quality reads[a]	Total OTUs[b,c]	PD[c]	Shannon[c]	Chao1[c]	NRI
430	Z_{SURF}	13077	10495	163	19.14	4.98	204.17	2.38
	$Z_{a\text{-}SCM}$	12905	10609	159	19.55	4.60	167.71	1.31
	Z_{SCM}	11261	9381	181	21.80	4.60	212.05	1.56
	$Z_{b\text{-}SCM}$	11102	8405	278	32.32	6.41	319.00	2.96
460	Z_{SURF}	12600	9591	224	23.71	5.87	246.80	3.06
	$Z_{a\text{-}SCM}$	13723	11123	202	23.97	5.05	235.66	1.47
	Z_{SCM}	13186	10732	234	28.08	5.52	286.00	2.20
	$Z_{b\text{-}SCM}$	8356	6150	293	37.02	6.61	371.08	2.09
540	Z_{SURF}	12454	9900	192	20.07	5.58	244.00	3.32
	$Z_{a\text{-}SCM}$	11105	9138	222	24.99	5.70	260.78	1.91
	Z_{SCM}	12701	9985	269	29.79	5.79	345.66	1.83
	$Z_{b\text{-}SCM}$	10399	7544	300	35.20	6.67	350.83	1.91
620	Z_{SURF}	10128	7557	228	24.63	5.90	314.56	2.54
	$Z_{a\text{-}SCM}$	11323	7722	186	19.30	5.60	305.00	3.50
	Z_{SCM}	10271	6925	229	27.97	5.70	314.55	3.21
	$Z_{b\text{-}SCM}$	8449	5585	262	32.29	6.28	342.37	4.07
670	Z_{SURF}	12790	8348	257	24.82	6.45	289.46	3.47
	$Z_{a\text{-}SCM}$	9380	6859	294	32.49	6.24	338.38	3.75
	Z_{SCM}	9650	5816	217	26.10	5.30	255.02	3.19
	$Z_{b\text{-}SCM}$	9640	5799	307	37.92	6.71	377.03	3.25
760	Z_{SURF}	12130	8319	185	20.29	5.65	250.87	3.35
	$Z_{a\text{-}SCM}$	12009	6569	204	23.93	5.19	350.75	1.57
	Z_{SCM}	12465	8443	278	33.11	6.19	331.03	2.14
	$Z_{b\text{-}SCM}$	11156	6964	317	36.84	6.68	369.48	2.08

OTUs: operational taxonomic units; PD: phylogenetic diversity; NRI: net-relatedness index.
[a]: after quality controls (de-noising, removal of short, low-quality and/or chimeric reads).
[b]: at 98% sequence identity.
[c]: computed on quality read datasets subsampled at an even depth of 5000 sequences.

Table S3. Results of environmental factor fitting on ordination and permutational analyses of variance on distance matrices (EFF and PVM, respectively).

	EFF		PVM	
Variable	R^2	P	R^2	P
$SiOH_4$	0.575	0.003	0.370	< 0.001
Picoeuk[a]	0.549	0.001	0.321	< 0.001
NO_3+NO_2	0.519	0.006	0.343	< 0.001
O_2	0.477	0.009	0.341	< 0.001
NH_4	0.338	0.026	0.062	0.204
Light	0.319	0.069	0.191	0.01
DOP	0.264	0.105	0.031	0.576
Bacteria[a]	0.188	0.235	0.096	0.122
Nanoeuk[a]	0.083	0.539	0.109	0.09

DOP: dissolved organic phosphorus; Picoeuk/Nanoeuk: picoeukaryotic and nanoeukaryotic phytoplankton cell counts, respectively.
[a]: Cell counts via flow cytometry; data missing for station 460.
[b]: DOP data missing for samples 430-Z_{aSCM}, 430-Z_{bSCM} and 620-Z_{bSCM}.

Table S4. Taxa differently abundant between SCM and wSCM communities ($P \leq 0.05$).

Eukaryotic clade	Lineage	Taxa	SCM relative abundance[a]	wSCM relative abundance[a]	*P*-value[b]
Alveolata	Ciliate (Intramacronucleata)	*Laboea*	$0.62 \pm 3.5e^{-3}$	$0.02 \pm 2.7e^{-5}$	0.011
		Novistrombidium	8.18±0.3	$2.06 \pm 1.5e^{-3}$	0.008
		Pseudotontonia	3.74±0.04	1.11±0.01	0.005
		Tintinnopsis	$0.05 \pm 2.4e^{-5}$	$2.4e^{-3} \pm 3.4e^{-7}$	0.007
	Dinoflagellates (Dinophyceae GPP)	NOR26.29 group	0	$0.39 \pm 2.2e^{-3}$	0.042
		G. helveticum group	$1.12 \pm 1.5e^{-3}$	10.55±0.7	0.009
		Lepidodinium	1.29±0.01	$0.15 \pm 3.1e^{-4}$	0.013
	Ellobiopsidae	*Thalassomyces*	0	$9.6e^{-3} \pm 5.5e^{-6}$	0.022
	MALVs	IIB / Guillou_II.27*	$0.01 \pm 1.0e^{-6}$	$4.2e^{-3} \pm 4.4e^{-7}$	0.021
		IIB / Guillou II.7.36*	$0.98 \pm 1.6e^{-3}$	$0.49 \pm 6.3e^{-4}$	0.011
		II / Guillou II.3.4*	3.20±0.09	$0.61 \pm 2e^{-3}$	0.029
Cryptophyta	Cryptomonadales	Cryptomonas	0	$9.6e^{-3} \pm 5.5e^{-6}$	0.022
	Unclassified	CCMP2045	$0.03 \pm 8.8e^{-6}$	0	0.006
Picozoa	Picozoa	Arctic NW617.02	2.73±0.02	11.69±0.7	0.018
Rhizaria	Cercozoa	NOR46.14	$6.6e^{-3} \pm 8.1e^{-7}$	$0.08 \pm 4.7e^{-5}$	0.012
		Cryothecomonas	$0.07 \pm 3.2e^{-5}$	$0.01 \pm 4.0e^{-6}$	0.011
		Ebria	0	$0.02 \pm 2.6e^{-6}$	0.0007
		Pseudopirsonia	0	$0.01 \pm 4.3e^{-6}$	0.022
Stramenopiles	Bolidophyceae	*Bolidomonas*	$0.06 \pm 2.9e^{-5}$	$0.13 \pm 1.7e^{-5}$	0.011
	Bacillariophyceae	*Craticula*	0	$0.01 \pm 8.5e^{-6}$	0.022
	Mediophyceae	*Chaetoceros*	$0.04 \pm 4.4e^{-5}$	$0.29 \pm 5.3e^{-4}$	0.014
		Thalassiosira	$0.50 \pm 6.4e^{-4}$	$0.99 \pm 2.4e^{-3}$	0.033
	MAST	MAST-1B	$0.13 \pm 1.4e^{-4}$	$0.75 \pm 4.7e^{-3}$	0.031
		MAST-2	$0.08 \pm 3.1e^{-5}$	$0.03 \pm 4.5e^{-6}$	0.044
		MAST-3	$0.03 \pm 2.9e^{-5}$	$0.24 \pm 4.0e^{-4}$	0.017
		MAST-7	$1.80 \pm 2.5e^{-3}$	$2.50 \pm 1.7e^{-3}$	0.002
		MAST-8	$0.20 \pm 4.9e^{-4}$	$1.15 \pm 3.1e^{-3}$	0.001
Telonemia	Telonemida	*Telonema*	2.57±0.01	$1.34 \pm 2.7e^{-3}$	0.034
Viridiplantae	Mamiellophyceae	*Micromonas* CCMP2099	24.89±0.95	9.44±2.1	0.03

[a] : mean relative abundance ± standard deviation (%).

[b]: significance at $P < 0.05$ (Metastats).

* : Guillou L., *et al.*, *Environmental Microbiology*, 10: 3349–3365. doi: 10.1111/j.1462-2920.2008.01731.x