

Bacterial community structure in a sympagic habitat expanding with global warming: brackish ice brine at 85–90 °N
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Supplementary Tables S1-S5

Table S1. Geographical location and abiotic and biotic variables measured at the 12 sampling stations in the Central Arctic Ocean. Temp = temperature, DIN = dissolved inorganic nitrogen ($\text{NO}_3^- + \text{NO}_2^-$), DIP = dissolved inorganic phosphorus (PO_4^{3-}), DSi = dissolved inorganic silicon (SiO_2), POC = particulate organic carbon, PON = particulate organic nitrogen, POP = particulate organic phosphorus, BACT = bacterial density, Chl*a* = chlorophyll *a* concentration. Ten of these variables (Salinity, Temp, DIN, DIP, DSi, POC, PON, POP, BACT and Chl*a*) were used in the redundancy analysis (**Figure S4**).

Sampling station	Habitat	Date (yy/mm/dd)	Latitude	Longitude	Ice thickness (m)	Snow depth (cm)	Salinity	Temp (°C)	DIN (μM)	DIP (μM)	DSi (μM)	POC (μg L ⁻¹)	PON (μg L ⁻¹)	POP (μg L ⁻¹)	BACT (cells μL ⁻¹)	Chl <i>a</i> (ng L ⁻¹)
IB7	Ice brine	12/08/12	87 50.74°N	59 38.68°W	1.3	5	6.5	-0.5	0.79	0.02	1.80	124	12.1	1.71	141	10.6
IB12	Ice brine	12/08/21	89 56.11°N	73 41.69°W	1.5	10	9.4	-0.5	0.86	0.03	2.57	420	37.2	4.61	65	6.5
IB14	Ice brine	12/08/25	87 58.55°N	122 09.07 °E	1.6	15	2.4	-0.5	1.56	0.01	1.33	117	9.5	0.93	71	30.4
IB15	Ice brine	12/08/28	87 56.55°N	73 29.39 °E	1.7	20	6.7	-0.5	0.98	0.01	0.42	192	21.2	1.24	42	26.0
IB16	Ice brine	12/08/29	88 15.64°N	72 51.76 °E	1.5	15	9.6	-0.5	0.97	0.03	1.15	140	8.3	1.04	60	35.7
IB18	Ice brine	12/08/31	88 42.75°N	55 56.35 °E	1.5	12	3.2	-0.5	1.15	0.01	0.57	154	10.3	1.31	79	3.6
IB21	Ice brine	12/09/04	87 44.35°N	30 05.51 °E	1.4	7.5	5.1	-0.6	1.02	0.01	0.77	145	9.5	0.95	67	14.5
IB23	Ice brine	12/09/07	85 25.63°N	05 15.95 °E	1.5	7.5	4.4	-0.6	1.63	0.01	2.03	159	10.6	1.23	385	46.6
SW4	Immediate sub-ice seawater	12/08/07	87 03.82°N	06 46.67°W	1.5	7.5	34.7	-1.5	4.50	0.77	9.75	68	6.7	0.61	173	30.1
SW6	Immediate sub-ice seawater	12/08/10	87 47.30°N	42 31.82°W	1.5	10	33.8	-1.4	0.91	0.21	2.82	95	13.0	1.62	218	147.9
SW11	Immediate sub-ice seawater	12/08/19	89 11.39°N	70 50.09°W	1.4	10	33.3	-1.5	0.88	0.25	3.63	74	9.9	0.91	100	45.2
SW20	Immediate sub-ice seawater	12/09/03	88 24.37°N	23 50.83 °E	1.5	5	34.9	-1.4	1.42	0.24	1.89	71	9.7	1.27	362	153.4

Table S2. Number of OTUs (singletons and doubletons removed) and mapped reads recovered from the 12 sampling stations in the Central Arctic Ocean analysed in this study. Two IB samples, IB12 at the North Pole and IB23 at the marginal ice zone (southern ice edge) were deep-sequenced.

Station	Habitat	Number of OTUs	Number of reads	Number of OTUs per read
IB15	Ice brine	122	6 239	0.020
IB18	Ice brine	171	6 777	0.025
IB16	Ice brine	390	18 748	0.021
IB14	Ice brine	328	19 658	0.017
IB7	Ice brine	503	26 403	0.019
IB21	Ice brine	901	99 079	0.009
IB12	Ice brine	1 436	222 860	0.006
IB23	Ice brine	1 826	279 189	0.007
SW20	Immediate sub-ice seawater	200	8 995	0.022
SW4	Immediate sub-ice seawater	246	31 994	0.008
SW6	Immediate sub-ice seawater	509	40 106	0.013
SW11	Immediate sub-ice seawater	518	79 357	0.007
Total		7 150	839 405	0.009

Table S3. Comparison of community composition in ice brine (IB) and immediate sub-ice seawater (SW) from the Central Arctic Ocean for the 26 OTUs with relative abundance ≥ 1.0 % in IB, SW or both habitats. The values represent means for the sampling stations \pm standard deviation. The taxonomy is based on the results of the phylogenetic analysis (**Figures 2 and S3**). * = nearly all species were reclassified as *Pseudoalteromonas* (Gauthier G, Gauthier M, Christen, 1995: Phylogenetic analysis of the genera *Alteromonas*, *Shewanella*, and *Moritella* using genes coding for small-subunit rRNA sequences and division of the genus *Alteromonas* into two genera, *Alteromonas* (emended) and *Pseudoalteromonas* gen. nov., and proposal of twelve new species combinations. Int. J. Syst. Bacteriol. 45:755-61), ** = the genus *Persicivirga* (**Figure S3**) was merged with the genus *Nonlabens* (Xi H, Chun J, 2012: Unification of the genera *Nonlabens*, *Persicivirga*, *Sandarakinotalea* and *Stenothermobacter* into a single emended genus, *Nonlabens*, and description of *Nonlabens agnitus* sp. nov. Syst. Appl. Microbiol.35:150-5).

OTU ID	Phylotype	Bacterial class	Relative abundance within the IB habitat (%) n = 8 sampling stations	Relative abundance within the SW habitat (%) n = 4 sampling stations
AO-22161	<i>Halomonas</i>	Gammaproteobacteria	13.1 \pm 11.3	24.7 \pm 24.8
AO-29203	<i>Polaribacter</i>	Flavobacteriia	6.2 \pm 4.4	3.2 \pm 2.8
AO-11040	<i>Shewanella</i>	Gammaproteobacteria	2.8 \pm 2.8	6.8 \pm 8.8
AO-30973	<i>Candidatus Aquiluna</i>	Actinobacteria	18.7 \pm 8.2	0.274 \pm 0.237
AO-4702	<i>Flavobacterium</i>	Flavobacteriia	13.6 \pm 9.3	0.145 \pm 0.103
AO-19850	BAL58	Betaproteobacteria	5.9 \pm 5.2	0.056 \pm 0.056
AO-5	<i>Pseudoalteromonas</i> *	Gammaproteobacteria	5.3 \pm 5.8	0.019 \pm 0.032
AO-13315	<i>Polaromonas</i>	Betaproteobacteria	4.7 \pm 3.3	0.023 \pm 0.027
AO-21669	<i>Loktanella</i>	Alphaproteobacteria	3.8 \pm 4.8	0.689 \pm 0.938
AO-6488	<i>Psychrobacter</i>	Gammaproteobacteria	2.4 \pm 5.7	0.016 \pm 0.019
AO-10331	<i>Glaciecola</i>	Gammaproteobacteria	2.4 \pm 1.8	0.203 \pm 0.075
AO-34590	<i>Nonlabens</i> **	Flavobacteriia	1.8 \pm 1.4	0.004 \pm 0.005
AO-2823	<i>Shewanella</i>	Gammaproteobacteria	1.5 \pm 2.2	0.181 \pm 0.129
AO-21339	Unknown BP	Betaproteobacteria	1.4 \pm 3.4	0.002 \pm 0.002
AO-9457	<i>Pseudomonas</i>	Gammaproteobacteria	1.1 \pm 2.6	0.056 \pm 0.066
AO-3408	<i>Balneatrix</i>	Gammaproteobacteria	0.147 \pm 0.223	21.5 \pm 13.1
AO-36354	GP ZD0405	Gammaproteobacteria	0.070 \pm 0.162	9.1 \pm 7.4
AO-18446	<i>Balneatrix</i>	Gammaproteobacteria	0.032 \pm 0.065	3.8 \pm 1.3
AO-37058	SAR92 clade (HTCC2207)	Gammaproteobacteria	0.189 \pm 0.327	2.6 \pm 1.7
AO-37423	NS9 marine group	Flavobacteriia	0.022 \pm 0.037	2.2 \pm 3.7
AO-5041	<i>Candidatus pelagibacter ubique</i> (SAR11 clade)	Alphaproteobacteria	0.028 \pm 0.064	1.9 \pm 1.1
AO-1486	<i>Pseudospirillum</i>	Gammaproteobacteria	0.019 \pm 0.034	1.7 \pm 1.5
AO-19648	<i>Planktomarina</i>	Alphaproteobacteria	0.247 \pm 0.240	1.7 \pm 1.4
AO-21539	SAR86 clade	Gammaproteobacteria	0.021 \pm 0.029	1.5 \pm 1.2
AO-8052	Unknown BP	Betaproteobacteria	0.007 \pm 0.009	1.3 \pm 0.8
AO-1882	SAR86 clade	Gammaproteobacteria	0.019 \pm 0.040	1.1 \pm 1.2
Total			85.5	84.8

Table S4. Network properties of the sympagic bacterial metacommunity in the Central Arctic Ocean. Two different levels of resolution were used: all 2,715 OTUs and the 180 OTUs with relative abundance $\geq 0.01\%$ across all samples.

Properties	All 2,715 OTUs	180 OTUs with RA $\geq 0.01\%$
Density	0.09	0.05
Modularity	0.85	0.34
Clustering coefficient	0.43	0.83
Centralization	0.18	0.06
Average number of neighbours	17.05	58.52
Characteristic path length	3.03	4.0
Shortest paths (%)	90%	99%
Edges/vertices	1569/184	32976/1125
Heterogeneity	0.79	0.55

Table S5. List of the 28 hubs identified in the network based on OTUs with relative abundance $\geq 0.01\%$ across all samples (Figure 5b). Hubs were defined as the OTUs accounting for $>60\%$ of all edges in the analysis. The taxonomy is based on the results of the phylogenetic analysis (Figures 2 and S3). - = OTU absent

Degree of connectivity	OTU ID	Class	Order (Phylotype)	IB (%)	SW (%)
36	AO-7619	Acidimicrobiia	Acidimicrobiales	-	0.09
37	AO-1095	Alphaproteobacteria	Rickettsiales (SAR11 clade II)	0.01	0.58
45	AO-22454	Alphaproteobacteria	Rickettsiales (SAR11 clade IV)	<0.01	0.06
35	AO-5041	Alphaproteobacteria	Rickettsiales (<i>Candidatus Pelagibacter</i>)	0.03	1.91
48	AO-11707	Alphaproteobacteria	Rickettsiales (<i>Candidatus Pelagibacter</i>)	<0.01	0.32
45	AO-22528	Alphaproteobacteria	Rhodospirillales	<0.01	0.07
36	AO-37615	Alphaproteobacteria	Rhodobacterales (<i>Lentibacter</i>)	<0.01	0.16
41	AO-8052	Betaproteobacteria	Unknown	0.01	1.31
49	AO-37660	Betaproteobacteria	Methylophilales	<0.01	0.26
43	AO-1849	Betaproteobacteria	Methylophilales	0.01	0.84
42	AO-12713	Betaproteobacteria	Methylophilales	<0.01	0.13
45	AO-20775	Cytophagia	Cytophagales	<0.01	0.23
39	AO-15625	Deltaproteobacteria	SAR324 clade	0.01	0.77
40	AO-2729	Flavobacteriia	Flavobacteriales (NS9 marine group)	0.01	0.17
38	AO-7059	Flavobacteriia	Flavobacteriales (NS5 marine group)	0.01	0.12
36	AO-25505	Flavobacteriia	Flavobacteriales (NS5 marine group)	<0.01	0.06
38	AO-10601	Flavobacteriia	Flavobacteriales (NS2b marine group)	<0.01	0.24
42	AO-5876	Flavobacteriia	Flavobacteriales (<i>Flavobacterium</i>)	<0.01	0.04
38	AO-19330	Gammaproteobacteria	Thiotrichales (<i>Thiothrix</i>)	<0.01	0.18
43	AO-36354	Gammaproteobacteria	Oceanospirillales (ZD0405)	0.07	9.06
40	AO-21539	Gammaproteobacteria	Oceanospirillales (SAR86 clade)	0.02	1.52
51	AO-1486	Gammaproteobacteria	Oceanospirillales (<i>Pseudospirillum</i>)	0.02	1.70
36	AO-16331	Gammaproteobacteria	Oceanospirillales (OM182 clade)	0.01	0.31
49	AO-7137	Gammaproteobacteria	Oceanospirillales	<0.01	0.73
38	AO-23732	Gammaproteobacteria	Oceanospirillales	-	0.19
35	AO-23228	Gammaproteobacteria	Oceanospirillales	<0.01	0.03
38	AO-20617	SAR406 clade	AB16, Arctic96B-7	-	0.06
48	AO-20990	Sphingobacteria	Unknown	0.02	0.47