

Microbial Ecology and Biogeography

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Southern Ocean

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List of Acronyms

GAAS Genome relative Abundance and Average Size.

AABW Antarctic Bottom Water.

AZ Antarctic Zone.

CFB Cytophaga-Flavobacterium-Bacteroides.

CTD Conductivity, Temperature and Depth.

HMW High Molecular Weight.

KEGG Kyoto Encyclopedia of Genes and Genomes.

nMDS Non-Metric Multidimensional Scaling.

NZ North Zone.

OTU Operational Taxonomic Unit.

POM Particulate Organic Matter.

SZ South Zone.

Acknowledgements

Preliminary analysis of Antarctic Bottom Water (AABW) samples

Abstract

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Introduction and Methods

Three samples of AABW were opportunistically obtained and analysed during the project described in ?? (Fig. 9). Two of these samples (356 and 361) were of newly formed AABW waters on the Antarctic continental shelf, while one (365) was of abyssal AABW from the South Australian basin (Table 8). DNA extraction, sequencing and construction of a taxonomic profile by BLAST comparison to the RefSeq database and processing with Genome relative Abundance and Average Size (GAAS) were performed using the methods described in “Polar Front”. A standardised and log-transformed Bray-Curtis resemblance matrix was constructed including the taxonomic profiles of the AABW samples as well as the North Zone (NZ) and South Zone (SZ) samples described in “Polar Front”. A Non-Metric Multidimensional Scaling (nMDS) plot was then constructed from this matrix. All statistical procedures were performed in PRIMER 6 as described by Clarke and Warwick (2001).

Results and Discussion

Although the three AABW samples were taken in deep, cold and aphotic waters (Table 8) compared to the surface Antarctic Zone (AZ) and SZ samples, the nMDS plot suggested that the two continental shelf AABW samples (356 and 361) were surprisingly similar to those of the AZ, particularly sample 353 (Fig. 10). Further, the indicated the presence of several Operational Taxonomic Units (OTUs) which would not be expected to be present at significant abundance in deep, aphotic waters (Table 9). For example, *Roseobacter denitrificans* OCh 114, a model organism for aerobic anoxygenic photosynthesis, was the fifth most abundant OTU across the three AABW samples. Numerous Cytophaga-Flavobacterium-Bacteroides (CFB) representatives, typically associated with Particulate Organic Matter (POM) and the utilisation of High Molecular Weight (HMW) phytoplankton products, were also unexpectedly high.

A possible explanation for these observations is that the continental shelf samples represent AABW recently formed in the D’Urville sea, and the observed assemblage therefore represents advection

Table 8: Sampling time, location and physicochemical properties of AABW samples used in this preliminary study. All data were retrieved from the CTD (SeaBird, Bellevue, USA) instrument used to collect the samples.

Sample	Date	Latitude	Longitude	Sample Depth (m)	Temperature (°C)	Salinity (PSU)	Volume filtered (L)
356	03/01/08	−66.7617	144.4138	920	−1.9	34.69	230
361	14/01/08	−66.4727	140.5572	1170	−1.8	34.56	225
365	23/01/08	−56.6967	141.9125	3693	0.5	34.69	230

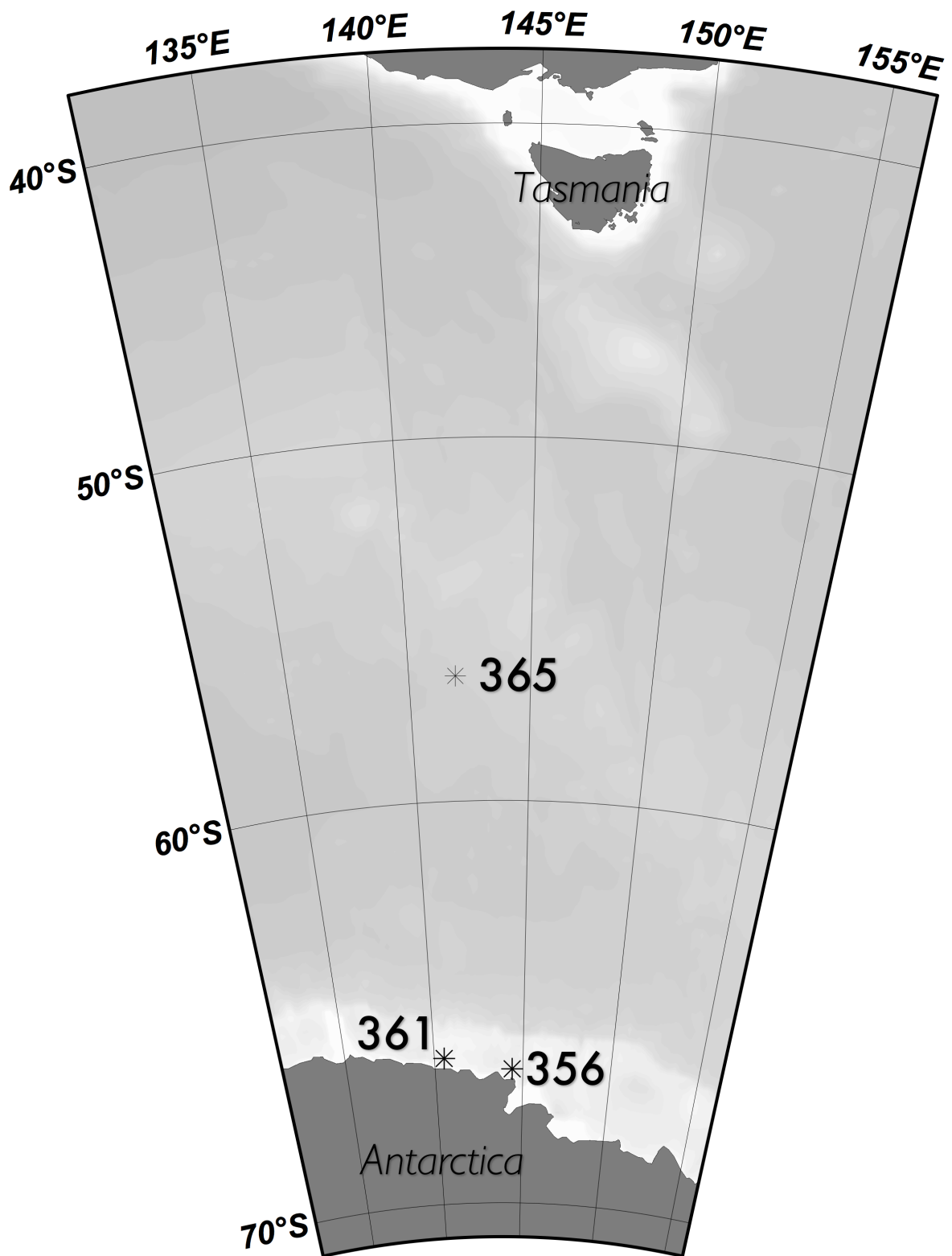


Figure 9: Sites of preliminary AABW samples.

Table 9: Relative abundances (as percentages) of the twenty most abundant OTUs identified in the preliminary study of AABW samples.

OTU	Sample 356			Sample 365		
	0.1 μm	0.8 μm	3.0 μm	0.1 μm	0.8 μm	3.0 μm
<i>"Candidatus Pelagibacter ubique"</i> HTCC1062	48.40	32.32	32.85	19.02	22.31	3.880
<i>Nitrosopumilus maritimus</i> SCM1	11.92	9.289	13.99	30.17	7.790	22.74
<i>"Candidatus Ruthia magnifica"</i> str. Cm (<i>C. magnifica</i>)	3.780	4.563	2.356	2.844	1.504	0.2599
<i>"Candidatus Vesicomysocius okutanii"</i> strain HA	2.349	2.757	1.396	1.859	0.8025	0.08227
<i>Roseobacter</i> sp. OCh 114	0.1412	1.166	0.6845	0.08564	0.6662	0.4851
<i>"Candidatus Puniceispirillum marinum"</i> IMCC1322	0.3180	1.103	0.6403	0.4218	0.8223	0.4202
<i>M. hydrocarbonoclasticus</i> VT8	0.06999	0.4091	0.3976	0.2476	1.050	2.338
<i>S. pomeroyi</i> DSS-3	0.1081	0.8406	0.4996	0.1290	0.4630	0.3621
<i>R. biformata</i> strain HTCC2501	0.2813	0.6433	0.7417	0.1769	0.2739	0.4978
<i>P. haloplanktis</i> strain TAC125	0.02530	0.4540	0.1958	0.2836	2.817	0
<i>A. borkumensis</i> strain SK2	0.09262	0.3163	0.4281	0.1049	0.5674	1.985
<i>G. forsetii</i> strain KT0803	0.3096	0.6465	0.7405	0.1254	0.2670	0
<i>Colwellia</i> sp. 34H	0.04289	0.4512	1.020	0.07200	0.4532	0.7727
<i>F. psychrophilum</i> strain JIP02/86	0.2417	0.4722	0.6353	0.07943	0.1645	0.5072
<i>P. staleyi</i> strain DSM 6068	0.003149	0.2477	0.3093	0.08767	1.401	0.7732
<i>Jannaschia</i> sp. DFL-12	0.07995	0.6770	0.3841	0.03865	0.2030	0.1025
<i>P. atlantica</i> strain T6c	0.02312	0.1653	0.1941	0.03856	0.3235	1.728
<i>Z. profunda</i> strain SM-A87	0.1830	0.3499	0.4826	0.1036	0.1362	0.3825
<i>Silicibacter</i> sp. TM1040	0.09568	0.5448	0.3455	0.03477	0.2014	0.1740
<i>C. ochracea</i> strain DSM 7271	0.1251	0.2916	0.4491	0.03893	0.1542	0.5332

rather than selection by environmental factors. The project described in "*The advection effect*" was designed to test and explore this hypothesis.

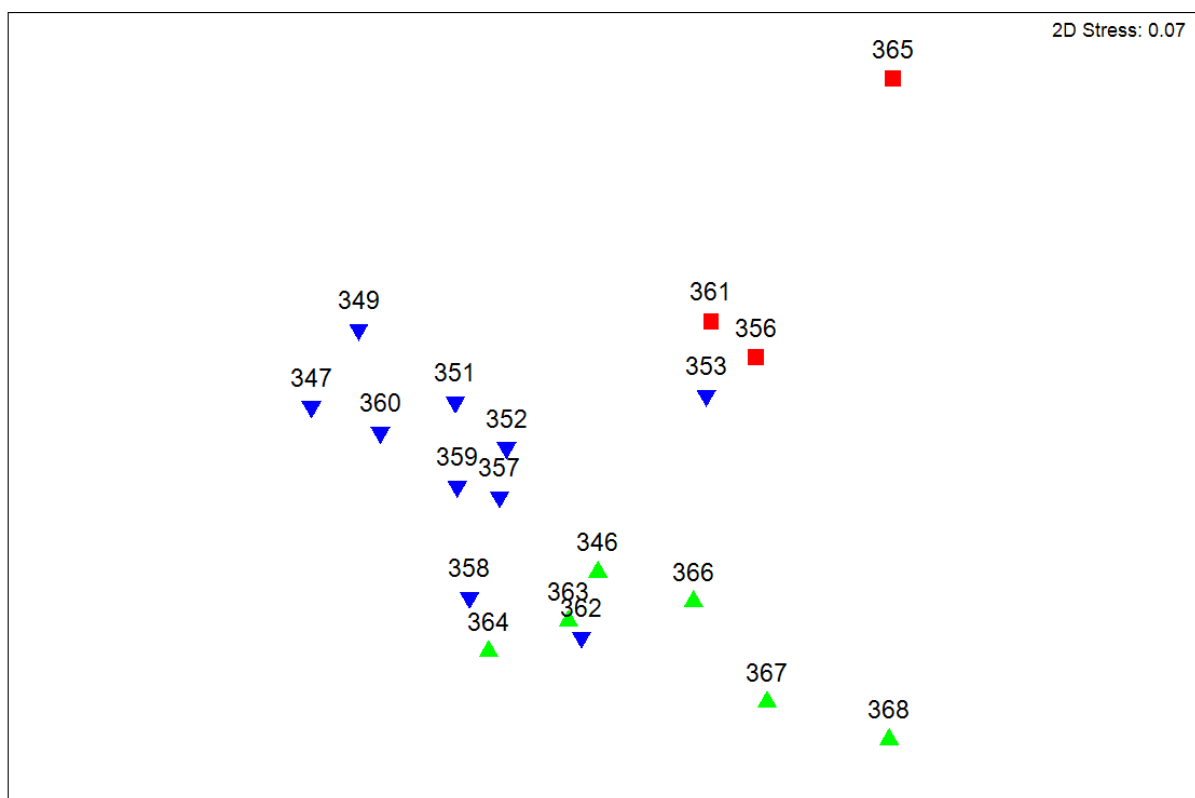


Figure 10: nMDS plot showing distance between AABW, NZ and SZ samples. Green triangles represent samples from the NZ; blue inverted triangles from the SZ; and red squares from AABW.

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