

Microbial Ecology and Biogeography

— OF THE —

Southern Ocean

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Contents

Abstract	iii
List of Figures	ix
List of Tables	xi
List of Acronyms	xiv
Acknowledgements	xv
1 Introduction	1
1.1 Physical oceanography of the Southern Ocean	1
1.1.1 Fronts and zones	1
1.1.2 Water masses and circulation	3
1.1.3 Effect of climate change	4
1.2 Microbial ecology of the Southern Ocean	4
1.2.1 Bacteria	5
1.2.1.1 Alphaproteobacteria	5
1.2.1.1.1 Roseobacter clade	5
1.2.1.1.2 SAR11	6
1.2.1.1.3 SAR116	7
1.2.1.2 Betaproteobacteria	8
1.2.1.3 Gammaproteobacteria	8
1.2.1.3.1 SAR86	8
1.2.1.3.2 OMG group	9
1.2.1.3.3 Ant4D3	9
1.2.1.3.4 GSO-EOSA-1	10
1.2.1.4 Deltaproteobacteria	10
1.2.1.5 CFB	10
1.2.1.6 Cyanobacteria	12
1.2.1.7 Verrucomicrobia	12
1.2.1.8 Other bacteria	12
1.2.2 Archaea	13
1.2.3 Virioplankton	14
1.3 Project aims	15
1.3.1 The Polar Front	15
1.3.1.1 Biogeographic role	15
1.3.1.2 Differences in community composition	15
1.3.1.3 Differences in functional potential	15
1.3.2 The role of advection in microbial biogeography	15

2 MINSPEC	17
2.1 Abstract	17
2.2 Introduction	17
2.2.1 Metagenomic analysis of microbial assemblages	17
2.2.2 The maximum parsimony approach	19
2.3 Methods	20
2.3.1 Implementation of MINSPEC	20
2.3.2 Validation of MINSPEC	21
2.4 Results	22
2.5 Discussion	22
2.6 Conclusions	24
3 The Polar Front	25
3.1 Abstract	25
3.2 Introduction	26
3.3 Methods	27
3.3.1 Sampling and metagenomic sequencing	27
3.3.2 Phylogenetic analysis of metagenomic data	30
3.3.2.1 BLAST comparison to RefSeq database	30
3.3.2.2 OTU abundances and variance between zones	30
3.3.2.3 Fragment recruitment to verify Operational Taxonomic Unit (OTU) identification	31
3.3.2.4 Additional samples to test “polynya hypothesis”	31
3.3.3 Functional analysis of metagenomic data	31
3.3.3.1 BLAST comparison to KEGG database	31
3.3.3.2 Analysis of functional potential	32
3.3.3.3 Taxonomic decomposition	32
3.4 Results	33
3.4.1 Metagenomic sequencing	33
3.4.2 Phylogenetic analysis of metagenomic data	33
3.4.3 Fragment recruitment to verify OTU identification	39
3.4.4 Additional samples to test alternative “polynya hypothesis”	39
3.4.5 Functional analysis of metagenomic data	39
3.5 Discussion	43
3.5.1 Taxonomic groups differentiating the zones	43
3.5.1.1 GSO-EOSA-1	43
3.5.1.2 Ammonia-oxidizing Crenarchaeota	45
3.5.1.3 Cyanobacteria	45
3.5.1.4 SAR11 and SAR116 clades	46
3.5.1.5 Bacteroidetes	47
3.5.1.6 Rhodobacterales	47
3.5.1.7 Alteromonadales	48
3.5.1.8 Verrucomicrobia	48
3.5.2 Functional capacities differentiating the zones	48
3.5.2.1 Conclusions: Biogeographic role of the Polar Front	52
4 Deep water formation	55
4.1 Abstract	55
4.2 Introduction	55
4.3 Methods	56
4.4 Results and Discussion	56

5 The advection effect	59
5.1 Abstract	59
5.2 Introduction	59
5.2.1 Distance and environment effects in microbial biogeography	59
5.2.2 Water mass endemicity and advection of marine microorganisms	60
5.2.3 Aims and approach of this study	61
5.3 Methods	62
5.3.1 Sampling	62
5.3.2 DNA extraction	63
5.3.3 Sequencing	65
5.3.4 Taxonomic assignment	65
5.3.5 Physicochemical and spatial distances	65
5.3.6 Generation of advection distance matrix	66
5.3.7 Ordination of distance matrices and comparison to water masses	67
5.3.8 Testing of advection effect	67
5.3.9 Differential influence of advection on OTU subsets	68
5.4 Results	69
5.4.1 Sequencing and taxonomic assignment	69
5.4.2 Environment and distance effects	74
5.4.3 Testing the advection effect	76
5.4.4 Testing advection effect mechanisms	80
5.4.5 Differential effect of advection on OTU subsets	81
5.5 Discussion	81
5.5.1 Taxonomic resolution	82
5.5.2 Differential influence of advection on OTU subsets	83
5.5.3 Future work	83
6 General discussion	85
6.1 Contributions of this thesis	85
6.1.1 The Polar Front	85
6.1.1.1 Biogeographic role of the Polar Front	86
6.1.2 The advection effect	87
6.1.3 MINSPEC	88
6.2 Levels of description in microbial ecology and biogeography	89
References	90

List of Figures

1.1	Major fronts and water masses of the Southern Ocean	2
2.1	Results of MINSPEC validation	23
3.1	Map showing sites of seawater samples used in the Polar Front study	28
3.2	Rank-abundance curves for OTUs in each zone and size fraction	36
3.3	Contribution of OTUs to variance between the North and South zones	38
3.4	Read recruitment to reference genomes	40
3.5	Tree of GSO-EOSA-1 related 16S rRNA genes	44
3.6	Taxonomic decomposition of KEGG modules	49
4.1	Map showing sites of preliminary Antarctic Bottom Water (AABW) samples	57
4.2	Non-Metric Multidimensional Scaling (nMDS) of AABW, North Zone (NZ) and South Zone (SZ) samples	58
5.1	Map showing sites of samples used in the advection study	62
5.2	OTU assignments in the advection study	73
5.3	nMDS of advective distances between samples	74
5.4	nMDS of advective distances between samples	75
5.5	dbRDA ordination of relationship between environment and community	76
5.6	Encounter times for all samples in advection model	77
5.7	nMDS of advective distances between samples	79
5.8	Advection effect at different taxonomic resolutions	80
6.1	Biogeographic effect sizes	88

List of Tables

2.1	Examples of spurious OTU identifications	19
3.1	Details of samples used in Polar Front study	29
3.2	Additional samples used to test polynya hypothesis	31
3.3	Twenty most abundant OTUs	34
3.4	Highest-contributing OTUs to the difference between the North and South zones	37
3.5	Contributions of KEGG modules to variance between the North and South zones	41
3.6	Contributions of KEGG ortholog groups to variance between the North and South zones	42
4.1	AABW samples used in the preliminary analysis	56
4.2	Twenty most abundant OTUs in preliminary AABW samples	58
5.1	Full sample data for advection study	70
5.1	(cont.) Full sample data for advection study.	71
5.1	(cont.) Full sample data for advection study.	72
5.2	Correlations between dbRDA axes and physicochemical variables	75
5.3	Results of BVSTEP	82

List of Acronyms

GAAS Genome relative Abundance and Average Size.

AABW Antarctic Bottom Water.

AAD Australian Antarctic Division.

AAP Aerobic Anoxygenic Phototrophic.

ACC Antarctic Circumpolar Current.

ANOSIM Analysis of Similarities.

AOA Ammonia-Oxidizing Archaea.

AZ Antarctic Zone.

CASO Climate of Antarctica and the Southern Ocean.

CEAMARC Collaborative East Antarctic Marine Census.

DFAA Dissolved Free Amino Acids.

DMSP dimethylsulfoniopropionate.

DOC Dissolved Organic Carbon.

DOM Dissolved Organic Matter.

FISH Fluorescence *In Situ* Hybridization.

GOS Global Ocean Sampling expedition.

GSO-EOSA-1 Gammaproteobacterial Sulfur Oxidizer-EOSA-1.

HMW High Molecular Weight.

HNLC High Nutrient, Low Chlorophyll.

KEGG Kyoto Encyclopedia of Genes and Genomes.

MGI Marine Group I Crenarchaeota.

MMPA methylmercaptopropionate.

nMDS Non-Metric Multidimensional Scaling.

NZ North Zone.

OTU Operational Taxonomic Unit.

PF Polar Front.

PFZ Polar Frontal Zone.

POM Particulate Organic Matter.

SAF Subantarctic Front.

SAZ Subantarctic Zone.

SIMPER Similarity Percentages.

SO Southern Ocean.

STF Subtropical Front.

SZ South Zone.

Acknowledgements

Chapter 3

The Polar Front as a major biogeographic boundary in the Southern Ocean

Sections of this chapter have been previously published in Wilkins D., Lauro F. M., Williams T. J., DeMaere M. Z., Brown M. V., Hoffman J. M., Andrews-Pfannkoch C., McQuaid J. B., Riddle M. J., Rintoul S. R., and Cavicchioli R. (2012). Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. *Environmental Microbiology*.

3.1 Abstract

The Polar Front (PF) is a major oceanographic feature of the Southern Ocean (SO), dividing surface water masses with distinct physicochemical characteristics. To confirm and characterise the PF's role as a biogeographic barrier in the SO, sixteen metagenomic samples were collected on a latitudinal transect from waters near Hobart, Australia (44° S) to near the Mertz Glacier, Antarctica (67° S). The samples were shotgun sequenced, and the community composition and functional potential of the captured microorganisms were analysed. The SAR11 and SAR116 clades and the cyanobacterial genera *Prochlorococcus* and *Synechococcus* were strongly overrepresented north of the PF. Conversely, the Gammaproteobacterial Sulfur Oxidizer-EOSA-1 (GSO-EOSA-1) complex, the phyla Bacteroidetes and Verrucomicrobia and order Rhodobacterales were overrepresented in waters south of the PF. Functions enriched south of the PF included a range of transporters, sulphur reduction and histidine degradation to glutamate, while branched-chain amino acid transport, nucleic acid biosynthesis and methionine salvage were overrepresented north of the PF. The taxonomic and functional characteristics suggested a shift of primary production from cyanobacteria in the north to eukaryotic phytoplankton in the south, and reflected the different trophic states of the two regions. Overall, this study supported the PF as a defining biogeographic feature of the SO.

3.2 Introduction

The Southern Ocean (SO) consists of zones separated by circumpolar fronts, the locations of which vary with time and longitude (Whitworth, 1980; Orsi *et al.*, 1995; Sokolov and Rintoul, 2002). From north to south, the major fronts are the Subtropical Front (STF), the Subantarctic Front (SAF) and the Polar Front (PF) (Fig. 1.1). The SAF and PF are associated with the Antarctic Circumpolar Current (ACC), the world's largest ocean current and a defining oceanographic feature of the SO. Anthropogenic climate change may be driving the warming and freshening of the ACC (Böning *et al.*, 2008). It may also be shifting the ACC and associated fronts poleward; the mean path of the current has moved ~50 km south since the 1950s (Gille, 2002). If this migration continues, by 2100 it will have displaced a volume of water south of the ACC approximately equivalent to the Arctic Ocean (Fyfe and Saenko, 2005).

Climate change may also be affecting the zones separated by these fronts. The major zones of the SO are the Subantarctic Zone (SAZ), between the STF and SAF; the Polar Frontal Zone (PFZ), between the SAF and the PF; and the Antarctic Zone (AZ), between the PF and the Antarctic continent (Fig. 1.1). These zones have different physicochemical properties, such as density, salinity, temperature and nutrient concentrations (Sokolov and Rintoul, 2002), and the fronts represent stepwise transitions in these properties (Whitworth and Nowlin, 1987). However, as a consequence of climate change, waters on the poleward side of the ACC have become warmer and more saline, while those to the north cooler and fresher (Böning *et al.*, 2008).

The PF has been suggested to be a major biogeographic boundary in the distribution and abundance of both zooplankton (Chiba *et al.*, 2001; Hunt *et al.*, 2001; Esper and Zonneveld, 2002; Ward *et al.*, 2003) and bacterioplankton (Selje *et al.*, 2004; Abell and Bowman, 2005b; Giebel *et al.*, 2009; Weber and Deutsch, 2010). The effects of climate change on the physical oceanography of the SO may therefore have global ecological significance, particularly as the SO is a major site for sequestration of anthropogenic CO₂ (Sabine *et al.*, 2004; Mikaloff Fletcher *et al.*, 2006) through both physicochemical processes and the microbe-driven “biological pump” of CO₂ fixation (Thomalla *et al.*, 2011), potentially forming a feedback loop (Cox *et al.*, 2000). However, the microbial assemblages that inhabit the SO are generally poorly understood, and their diversity and functional capacity poorly characterised (reviewed in Murray and Grzymski, 2007). A community-level understanding is needed to predict the effects of a shifting ACC on the distribution, abundance and ecosystem functions of microorganisms.

Large scale metagenome surveys have not previously been performed in the SO. Compared to traditional environmental microbiological methods such as culture-based or DGGE surveys, metagenomic studies are able to offer both deeper (capture of sequence from rare taxa) and broader (larger sample sizes with greater statistical significance) data on the taxonomic makeup and functional capacities of marine microbial communities (e.g. Rusch *et al.*, 2007; Angly *et al.*, 2006; Dinsdale *et al.*, 2008). Metagenome sampling is also better suited to large-scale biogeographic studies, as it allows large numbers of samples to be taken across broad spatial and temporal scales with uniform sampling, storage and processing, compared to e.g. culture-based methods where technical replicability is more difficult.

This project is part of a metagenomic survey of the SO begun in the austral summer of 2006, based on the sampling design of the Global Ocean Sampling expedition (GOS) (Rusch *et al.*, 2007). The GOS sampling strategy involves size fractionation of plankton assemblages by passing seawater through a 20 µm prefilter then capturing planktonic biomass on sequential 3.0 µm, 0.8 µm and 0.1 µm filter membranes. As well as allowing deeper sequencing of metagenomes and thus better representation of low-abundance taxa (Rusch *et al.*, 2007), this approach allows comparison to other samples collected using the GOS methods (e.g. Brown *et al.*, 2012). This study will thus focus on the 0.1–20 µm fraction of the sampled microbial assemblages.

3.3 Methods

3.3.1 Sampling and metagenomic sequencing

Sampling¹ was conducted on board the RSV *Aurora Australis* during Australian Antarctic Division (AAD) cruise V3 Collaborative East Antarctic Marine Census (CEAMARC) / Climate of Antarctica and the Southern Ocean (CASO) from 13 December 2007–25 January 2008. This cruise occupied the SR3 latitudinal transect from Hobart, Australia (44° S) to the Mertz Glacier, Antarctica (67° S) within a longitudinal range of 140–150° E. Sixteen samples were obtained along almost the entire latitudinal range (Fig. 3.1).

A range of physicochemical data were recorded by integrated instruments on the RSV *Aurora Australis* including location, water column depth, water temperature, salinity, fluorescence and meteorological conditions (Table 3.1). These data were used to locate the PFZ based on a surface temperature gradient of ~1.35 °C across a distance of 45–65 km, placing the PF at approximately 59.70° S, consistent with previous descriptions (Moore *et al.*, 1999; Sokolov and Rintoul, 2002). Samples were accordingly grouped into “North” and “South” zones (Table 3.1). The North Zone (NZ) represents waters from the Subtropical, Subantarctic and PFZ regions, while the South Zone (SZ) represents the AZ.

¹Sampling was performed by Jeffrey M. Hoffman and Jeffrey B. McQuaid.

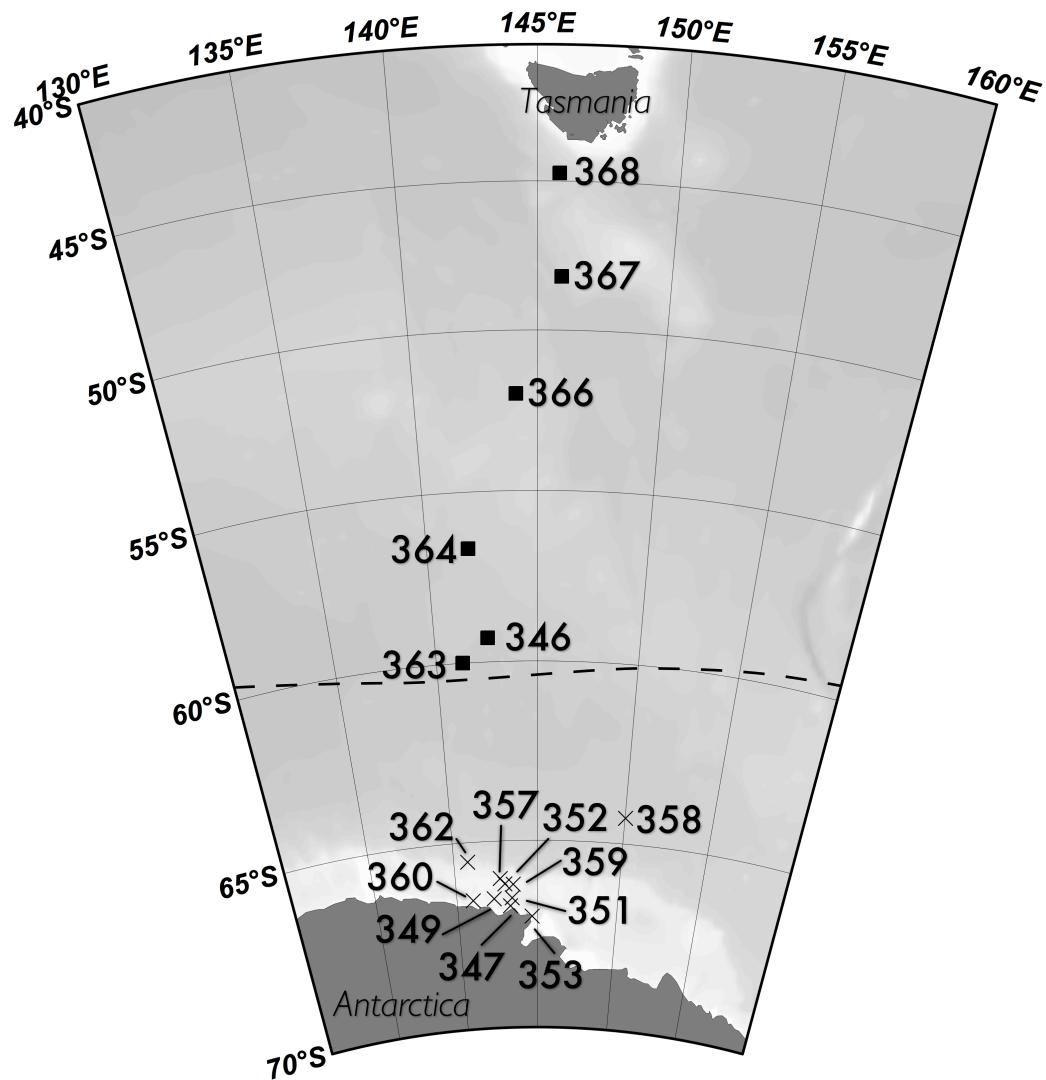


Figure 3.1: Sites of seawater samples used in this study. Squares indicate surface samples from the North Zone; crosses samples from the South Zone. The dashed line represents the Polar Front.

Table 3.1: Sampling time, location and physicochemical properties of samples used in this study. All data were retrieved from underway instruments aboard the RSV *Aurora Australis*.

Sample	Zone	Date	Latitude	Longitude	Water Column Depth (m)	Sample Depth (m)	Temperature (°C)	Salinity (PSU)	Fluorescence ($\mu\text{g L}^{-1}$)	Volume filtered (L)
346	North	20/12/2007	-59.31	142.59	4294	2	2.9	33.75	0.3	500
347	South	23/12/2007	-66.02	142.74	450	2	0.6	34.20	4.0	250
349	South	27/12/2007	-66.57	142.32	370	1.5	-1.3	34.40	2.3	250
351	South	28/12/2007	-66.56	143.43	823	1.5	-0.6	34.30	1.3	500
352	South	29/12/2007	-66.77	143.32	164	2.5	-0.8	34.30	3.1	500
353	South	30/12/2007	-67.05	144.68	180	2	-1.8	34.40	0.3	500
357	South	05/01/2008	-66.17	143.02	580	2	-0.4	34.15	2.5	500
358	South	09/01/2008	-64.30	150.03	3550	2	0	33.55	0.5	500
359	South	12/01/2008	-66.19	143.53	540	2	-0.2	34.21	2.5	500
360	South	13/01/2008	-66.58	141.02	316	2	-0.7	34.04	6.2	500
362	South	19/01/2008	-65.54	140.83	1064	2	0.7	32.20	0.5	500
363	North	22/01/2008	-60.00	141.31	4473	2	3.3	33.77	0.1	500
364	North	23/01/2008	-56.70	141.88	3693	2	4	33.70	0.5	500
366	North	24/01/2008	-52.02	144.14	3180	2	7.6	33.84	0.3	500
367	North	25/01/2008	-48.25	145.90	3490	2	11	34.43	0.2	500
368	North	26/01/2008	-44.72	145.78	3201	2	14.8	34.96	1.3	560

At each station, ~250–560 L of seawater was pumped from ~1.5–2.5 m below the sea surface into drums stored at ambient temperature on deck. Seawater samples were prefiltered through a 20 µm plankton net, then filtrand was captured on sequential 3.0 µm 0.8 µm and 0.1 µm 293 mm polyethersulfone membrane filters (Pall, Port Washington, USA), and immediately stored at –20 °C (Rusch *et al.*, 2007; Ng *et al.*, 2010).

DNA extraction² was performed at the J. Craig Venter Institute (Rockville, USA) as described in Rusch *et al.* (2007). Pyrosequencing was performed on a GS20 FLX Titanium instrument (Roche, Branford, USA) also at the J. Craig Venter Institute as described in Lauro *et al.* (2011). Duplicate reads and reads with many pyrosequencing errors were removed as described in Lauro *et al.* (2011).

3.3.2 Phylogenetic analysis of metagenomic data

3.3.2.1 BLAST comparison to RefSeq database

A subset of the RefSeq microbial (bacterial and archaeal) genome database (release 41, retrieved 31 May 2010 from <ftp://ftp.ncbi.nih.gov/refseq/release/>) was prepared by excluding sequences with the words “shotgun”, “contig”, “partial”, “end” or “part” in their headers (following Angly *et al.*, 2009). Because this database was not expected to contain representative genomes for every species present, Operational Taxonomic Units (OTUs) in this study are defined by the best species match to this database, and may for example represent congeners.

The metagenomic reads from each sample were compared against this database using TBLASTX, with default parameters except for: E-value threshold 1.0×10^{-3} , cost to open gap 11, cost to extend gap 1, masking of query sequence by SEG masking with lookup table only. The outputs of all TBLASTX searches against RefSeq were processed by MINSPEC, and hits not belonging to the minimal OTU sets were removed.

3.3.2.2 OTU abundances and variance between zones

The relative OTU abundances for each sample were determined using the PERL script Genome relative Abundance and Average Size (GAAS) (Angly *et al.*, 2009). Briefly, GAAS estimates the relative abundance of OTUs from the number and quality of BLAST matches (“hits”) to each OTU, taking into account differences in genome size. GAAS was run with the default settings. To normalise for reads which did not yield acceptable hits, the relative abundances for each sample were scaled by that sample’s effective BLAST hit rate. An OTU profile was generated for each sample by encoding the scaled relative abundance of each OTU from each size fraction as a separate variable.

To test the hypothesis that the oceanic zones harbour significantly different communities, Analysis of Similarities (ANOSIM) with 999 permutations was performed on a standardised, log-transformed Bray-Curtis resemblance matrix of OTU profiles. Similarity Percentages (SIMPER) analysis was performed to identify the contribution of individual OTUs to differences between the zones. All statistical procedures were performed in PRIMER 6 as described by Clarke and Warwick (2001).

²DNA extraction was performed by Cynthia Andrews-Pfannkoch and others at the J. Craig Venter Institute.

Table 3.2: Dates and locations of additional samples used to falsify the hypothesis that the Mertz Glacier polynya was responsible for the observed biogeographic partitioning.

Sample	Date	AAD Voyage Number	Latitude	Longitude
388	20/10/2008	V1 2008–09	−63.8090	115.1613
398	22/10/2008	V1 2008–09	−64.8018	112.3730
390	30/10/2008	V1 2008–09	−64.8152	80.7204
392	13/12/2008	V2 2008–09	−64.1826	76.4537
393	15/12/2008	V2 2008–09	−55.2573	74.2531

3.3.2.3 Fragment recruitment to verify OTU identification

To confirm that identified OTUs were truly present, and not resulting from hits to small regions of genomic identity, plots of read recruitment and coverage to reference genomes were generated using R and PERL. Six samples, three from the SZ and three from the NZ, were randomly selected and their 0.1 μm fractions used as sources of recruited reads. As shotgun sequencing of a metagenome should be essentially random, it was predicted that these plots would show fairly even coverage of the reference genomes. Genomes where all recruited reads were concentrated in a few small regions would be likely candidates for OTUs which were not present, but shared a small genomic region with an OTU which was present.

3.3.2.4 Additional samples to test “polynya hypothesis”

Because many samples from the SZ were taken in the region of the Mertz Glacier polynya, an alternative hypothesis for any difference observed between the SZ and NZ would be that the difference represented the effect of the polynya, rather than the PF. A set of samples collected³ from waters south of the PF on different voyages and in a different longitudinal range were used to test this hypothesis. Sampling, DNA extraction and sequencing were performed as described above, although only the 0.1–0.8 μm size fraction was processed. The resulting metagenomic reads were compared to RefSeq and weighted relative abundances calculated with GAAS as described above.

Two ANOSIM tests were performed on the standardised and log-transformed Bray-Curtis resemblance matrices of the samples’ OTU abundance profiles and similarly prepared matrices representing only the 0.1 μm fractions of the SZ and NZ samples. In the first ANOSIM test (“polynya hypothesis”), all samples from the Mertz Glacier polynya region (i.e. all SZ samples apart from 358) were grouped together, while the samples from the open ocean were placed in a separate group. In the second test (“PF hypothesis”), the additional samples were grouped with all the SZ samples.

3.3.3 Functional analysis of metagenomic data

3.3.3.1 BLAST comparison to KEGG database

In order to identify functional differences between the zones, the set of metagenomic reads from each sample was compared against the Kyoto Encyclopedia of Genes and Genomes

³Collection was performed by Ricardo Cavicchioli, Federico M. Lauro and Mark V. Brown. TODO who else was on these voyages?

(KEGG) GENES database (retrieved 2 July 2010 from `ftp://ftp.genome.jp/pub/kegg/genes/fasta/genes.pep`) with BLASTX, with default parameters except for: maximum number of database sequence alignments 10; E-value threshold 1.0×10^{-3} ; gap opening penalty 11; gap extension penalty 1; masking of query sequence by SEG masking for lookup table only.

3.3.3.2 Analysis of functional potential

Genes identified by BLASTX were aggregated to KEGG ortholog groups according to the KEGG Orthology schema (`ftp://ftp.genome.jp/pub/kegg/genes/ko`, retrieved Mar 29 2011), and ortholog group abundances calculated for each sample. Following Coleman and Chisholm (2010), a read was considered a hit to a given ortholog group if the top three hits for that read (or all hits if fewer than three total hits) were to genes from the same ortholog group, and had bit scores > 40 . If the bit score difference between any two top hits was greater than 30, only the hits above this difference were considered.

Ortholog group counts were then used to calculate the abundance of KEGG modules. Because many ortholog groups are members of more than one module, the abundance a_m of each module m was calculated as

$$a_m = \sum_{K=1}^n \frac{C_K}{M_K}$$

where n is the number of ortholog groups K belonging to module m , C_K is the number of hits to ortholog group K , and M_K is the total number of modules to which K belongs. To account for differences in sequencing depth between samples, module abundances were scaled to 500,000 reads per sample. To test the hypothesis that the NZ and SZ harbour significantly different functional potential, one-way ANOSIM with 999 permutations was performed as above on a standardised, log-transformed Bray-Curtis distance resemblance matrix of the module and ortholog group profiles. A functional profile was generated for each sample by summing the scaled abundances of each module from all size fractions, and SIMPER performed as above to identify modules which contributed highly to the variation in functional potential between the two zones.

3.3.3.3 Taxonomic decomposition

To link modules with a high contribution to variance or otherwise of interest to specific OTUs (“taxonomic decomposition”), a script was written which decomposed each module to its constituent ortholog groups, then each ortholog group to each representative gene sequence in the KEGG database. Because each KEGG sequence is associated with a particular organism, this allowed the abundance of each module to be decomposed into the relative contribution from each of these organisms. This allowed functional contributions to be putatively assigned to genera which were not identified in our taxonomic analysis, as the database included gene sequences for organisms for which a full genome was not available. To aid interpretation of these results, the taxonomic decompositions for some modules were aggregated to higher taxonomic ranks, such as class or family.

3.4 Results

3.4.1 Metagenomic sequencing

6.6 Gbp of 454 sequence data representing microorganisms in the size range 0.1–3.0 μm was obtained from 16 samples. After removal of low-quality reads, 454 sequencing yielded 157,507–597,689 reads per sample (mean 354,399) of lengths ranging from 100 to 606 bp (mean 378).

3.4.2 Phylogenetic analysis of metagenomic data

The proportion of reads in each sample which yielded hits to RefSeq ranged from 25–85% (mean 62%). The most abundant OTUs in each sample are given in Table 3.3 and a full list of OTU abundances in the supplementary material (PF-all-OTUs.csv). All samples and size fractions exhibited very low OTU evenness (Fig. 3.2).

Table 3.3: Relative abundances (as percentages) of the twenty most abundant OTUs identified in this study, in each zone and size fraction.

OTU	North			South		
	0.1 µm	0.8 µm	3.0 µm	0.1 µm	0.8 µm	3.0 µm
" <i>Candidatus Pelagibacter ubique</i> " HTCC1062	61.76	25.00	23.87	58.85	22.40	17.61
<i>Nitrosopumilus maritimus</i> SCM1	0.01996	0.01438	0.009508	1.076	1.309	1.210
" <i>Candidatus Ruthia magnifica</i> " str. Cm (<i>Calyptogena magnifica</i>)	0.6699	0.6458	0.5484	2.987	2.616	1.025
<i>Roseobacter</i> sp. OCh 114	0.3125	2.932	1.588	0.4477	3.994	2.657
<i>Synechococcus</i> sp. CC9902	0.1081	9.837	4.973	0.0007484	0.004156	0.09733
<i>Silicibacter pomeroyi</i> DSS-3	0.2578	2.286	1.154	0.3070	2.505	1.576
<i>Gramella forsetii</i> strain KT0803	0.2412	1.210	1.755	0.4993	2.347	1.890
" <i>Candidatus Vesicomyosocius okutanii</i> " strain HA	0.4634	0.4642	0.2078	1.970	1.807	0.2174
<i>Robiginitalea biformata</i> strain HTCC2501	0.2751	1.099	1.297	0.4722	1.878	1.405
<i>Flavobacterium psychrophilum</i> strain JIP02/86	0.1718	0.8409	1.224	0.4316	1.960	1.598
<i>Synechococcus</i> sp. CC9311	0.03014	4.624	4.409	0.0007221	0.002778	0.02764
" <i>Candidatus Puniceispirillum marinum</i> " IMCC1322	0.6444	2.077	1.267	0.3586	1.377	0.7109
<i>Silicibacter</i> sp. TM1040	0.2274	1.652	0.8738	0.2709	1.803	1.233
<i>Jannaschia</i> sp. DFL-12	0.1776	1.378	0.7350	0.2443	1.692	0.8009
<i>Zunongwangia profunda</i> strain SM-A87	0.1522	0.7487	1.059	0.2968	1.410	1.204
<i>Colwellia</i> sp. 34H	0.02345	0.3636	2.736	0.05207	0.5140	1.041
<i>Coraliomargarita akajimensis</i> strain DSM 45221	0.03698	0.07573	0.1197	0.1154	1.543	1.680
<i>Jannaschia</i> sp. CCS1	0.1173	0.9344	0.4784	0.1711	1.230	0.8239
<i>Pseudoalteromonas atlantica</i> strain T6c	0.01251	0.4772	1.993	0.02270	0.4089	1.132
<i>Saccharophagus degradans</i> 2-40	0.06532	0.4325	0.5429	0.1289	1.072	0.8663
<i>Flavobacterium johnsoniae</i> strain UW101	0.08822	0.4220	0.6141	0.2034	0.9389	0.8578
<i>Capnocytophaga ochracea</i> strain DSM 7271	0.1143	0.4830	0.5399	0.2314	0.8815	0.6814
<i>Marinomonas</i> sp. MWYL1	0.03777	0.2529	0.3026	0.1514	1.300	0.7006
<i>Cellvibrio japonicus</i> strain Ueda107	0.05884	0.3080	0.3231	0.1155	0.9917	0.4713
<i>Marinobacter hydrocarbonoclasticus</i> VT8	0.04093	0.2889	0.3883	0.08418	0.7195	0.3848
<i>Pseudoalteromonas haloplanktis</i> strain TAC125	0.01389	0.2505	0.8896	0.03427	0.3561	0.6530
<i>Teredinibacter turnerae</i> strain T7901	0.05665	0.3051	0.3081	0.1138	0.9174	0.5127
<i>Acinetobacter baumannii</i> strain SDF	0.004886	0.007187	0.4073	0.006260	0.04218	1.459

ANOSIM analysis showed that the zones harbor significantly different microbial communities ($R = 0.451$, $p = 0.004$). SIMPER was performed in order to identify the contribution of individual OTUs to the difference between the NZ and SZ. The results for the highest contributors are provided in Table 3.4, and are graphically summarised for all OTUs in Fig. 3.3.

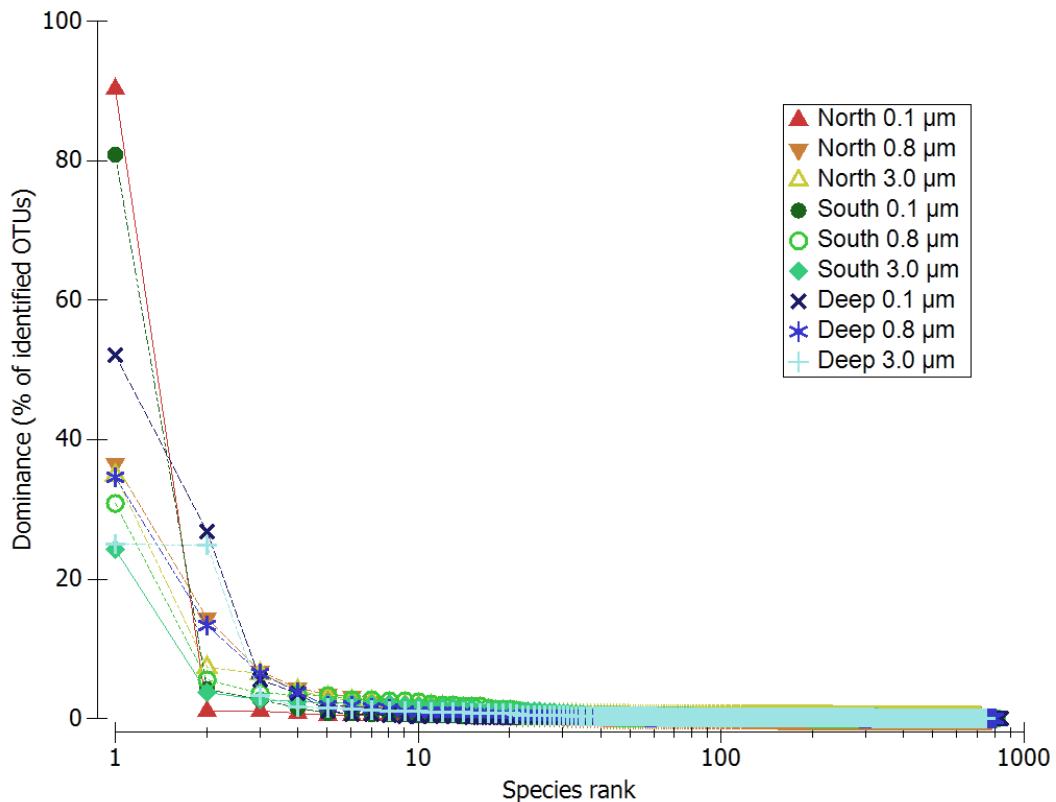


Figure 3.2: Rank-abundance curves for OTUs identified in each zone and size fraction. The dominance of a given OTU is its relative abundance as a percentage of all identified OTUs. The x-axis is scaled logarithmically. Generated using PRIMER 6.

Table 3.4: The thirty OTUs with the highest contributions to the difference between the NZ and SZ. Abundances are zonal averages and have been standardised and log-transformed. As each OTU on each size fraction was encoded as a separate variable in the SIMPER analysis, the size fraction is given after each OTU name.

OTU	Abundance South	Abundance North	Contribution to variance (%)
<i>Synechococcus</i> sp. CC9311 0.8 µm	0.00	1.08	2.88
<i>Synechococcus</i> sp. CC9902 0.8 µm	0.00	1.04	2.81
<i>Synechococcus</i> sp. CC9311 3.0 µm	0.01	0.98	2.59
<i>Synechococcus</i> sp. CC9902 3.0 µm	0.04	0.76	2.03
" <i>Candidatus Pelagibacter ubique</i> " HTCC1062 3.0 µm	1.97	2.40	1.97
" <i>Candidatus Ruthia magnifica</i> " str. Cm (<i>Calyptogena magnifica</i>) 0.1 µm	0.82	0.25	1.57
<i>Colwellia</i> sp. 34H 3.0 µm	0.34	0.66	1.32
" <i>Candidatus Ruthia magnifica</i> " str. Cm (<i>Calyptogena magnifica</i>) 0.8 µm	0.74	0.25	1.32
" <i>Candidatus Pelagibacter ubique</i> " HTCC1062 0.8 µm	2.32	2.48	1.32
" <i>Candidatus Vesicomyosocius okutanii</i> " strain HA 0.1 µm	0.62	0.18	1.20
<i>Coraliomargarita akajimensis</i> strain DSM 45221 0.8 µm	0.48	0.04	1.13
<i>Coraliomargarita akajimensis</i> strain DSM 45221 3.0 µm	0.49	0.06	1.10
<i>Roseobacter</i> sp. OCh 114 0.8 µm	1.01	0.81	1.08
<i>Pseudoalteromonas atlantica</i> strain T6c 3.0 µm	0.38	0.54	1.08
" <i>Candidatus Vesicomyosocius okutanii</i> " strain HA 0.8 µm	0.57	0.19	1.04
<i>Acinetobacter baumannii</i> strain SDF 3.0 µm	0.45	0.18	0.95
<i>Gramella forsetii</i> strain KT0803 0.8 µm	0.72	0.43	0.94
<i>Marinomonas</i> sp. MWYL1 0.8 µm	0.46	0.11	0.92
<i>Roseobacter</i> sp. OCh 114 3.0 µm	0.76	0.54	0.91
<i>Flavobacterium psychrophilum</i> strain JIP02/86 0.8 µm	0.63	0.32	0.89
<i>Silicibacter pomeroyi</i> DSS-3 0.8 µm	0.75	0.69	0.86
<i>Brachyspira hyodysenteriae</i> strain WA1 3.0 µm	0.47	0.19	0.84
" <i>Candidatus Ruthia magnifica</i> " str. Cm (<i>Calyptogena magnifica</i>) 3.0 µm	0.34	0.21	0.82
<i>Pseudoalteromonas haloplanktis</i> strain TAC125 3.0 µm	0.22	0.33	0.77
<i>Robiginitalea bifomata</i> strain HTCC2501 0.8 µm	0.61	0.40	0.74
<i>Nitrosopumilus maritimus</i> SCM1 0.1 µm	0.27	0.01	0.72
<i>Gramella forsetii</i> strain KT0803 3.0 µm	0.59	0.59	0.71
<i>Lysinibacillus sphaericus</i> strain C3-41 3.0 µm	0.29	0.02	0.71
<i>Nitrosopumilus maritimus</i> SCM1 0.8 µm	0.25	0.01	0.70
<i>Silicibacter</i> sp. TM1040 0.8 µm	0.59	0.55	0.69

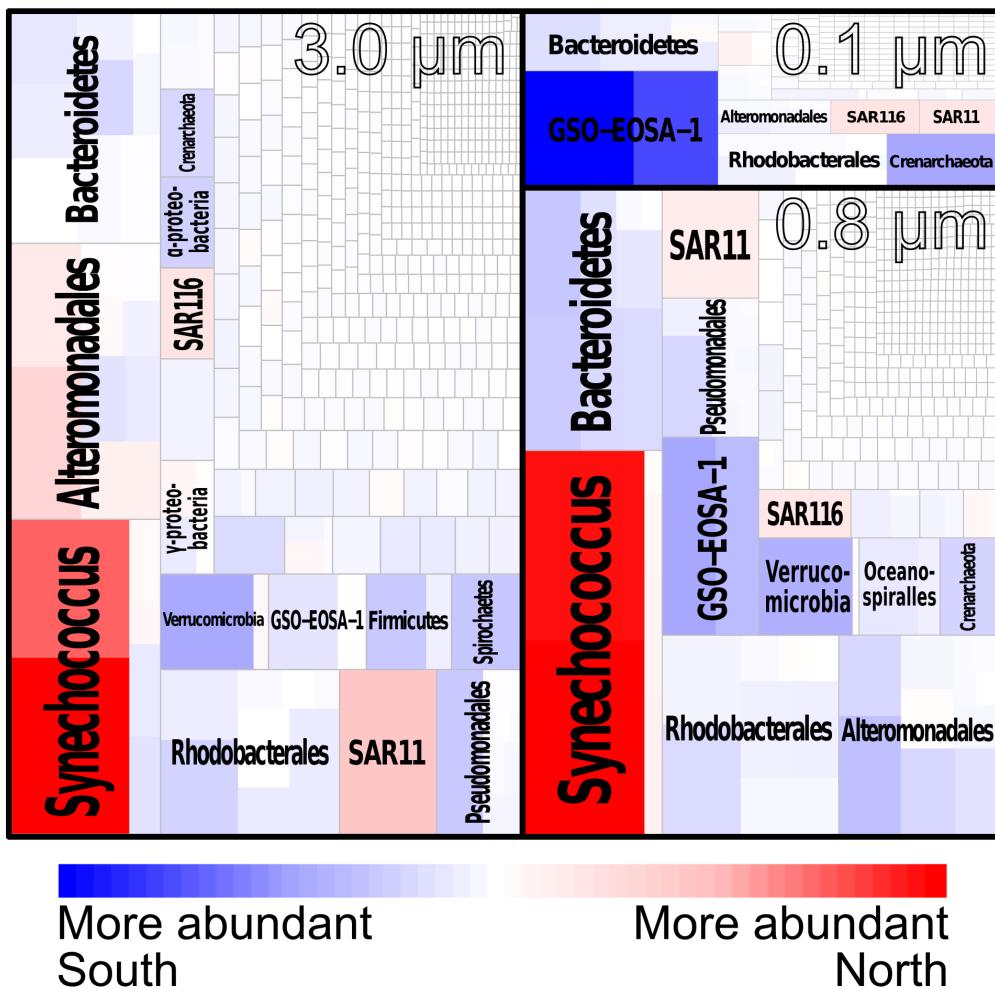


Figure 3.3: Contribution of OTUs to variance between the North and South zones, and differential abundance of OTUs from each size fraction between the two zones. Each coloured (red or blue) rectangle represents an OTU identified through analysis of BLAST matches between SO metagenome data and the RefSeq database. The area of each rectangle as a proportion of the total plot area corresponds to that OTU's contribution to the total variance between the two zones. The colour of each rectangle corresponds to difference in relative abundance of that OTU between the zones, with blue indicating a higher relative abundance south of the PF, and red a higher abundance north of the PF. OTUs from clades or taxonomic ranks of interest have been grouped, with labels in bold and groups separated by gray lines. Groups and OTUs with a low contribution to variance which were not grouped are unlabeled. OTUs from each size fraction have also been grouped, with labels in black outline and size fractions separated by thick black lines. The data used to generate this figure are given in the supplementary material (PF-OTUs-SIMPER.csv).

The SIMPER analysis found that no single OTU contributed more than 2.9% of variance and 74% of variance was contributed by OTUs with a contribution less than 1%. There was also a large difference in the contribution to variance of the three size fractions, with approximately 52% of all variance contributed by OTUs from the 3.0 μm fraction, 37% by the 0.8 μm fraction, and 9% by the 0.1 μm fraction. Notably, OTUs within several taxonomic groups that had high contribution to variance covaried in their relative representation in the NZ and SZ. For example, Bacteroidetes and GSO-EOSA-1 representatives were on average more abundant in the SZ; while *Prochlorococcus* and *Synechococcus*

species, SAR11 and SAR116 were on average more abundant in the NZ (Fig. 3.3). Some groups, such as the Alteromonadales, had variable relative representation depending on size fraction.

3.4.3 Fragment recruitment to verify OTU identification

As predicted, read recruitment to reference genomes produced fairly even coverage, especially in the high-abundance OTUs. This indicates that OTU identification was accurate and unlikely to be confounded by small regions of genomic identity. Fig. 3.4 gives examples of read recruitment plots to three high-abundance and three low-abundance OTUs.

3.4.4 Additional samples to test alternative “polynya hypothesis”

The ANOSIM analysis strongly supported the “PF hypothesis” ($R = 0.435, p = 0.002$), i.e. that the PF was primarily responsible for the difference observed between the NZ and SZ, over the “polynya hypothesis” ($R = 0.29, p = 0.005$) that the influence of the Mertz Glacier polynya was responsible. This also provides evidence that the PF effect is robust over a longitudinal range and over time.

3.4.5 Functional analysis of metagenomic data

ANOSIM analysis of the samples’ KEGG ortholog group and module profiles revealed that the zones had significantly different functional potential (ortholog group: $R = 0.642, p = 0.001$; module: $R = 0.871, p = 0.001$). SIMPER was performed on the profiles in order to identify the specific functional differences between the zones. The highest-contributing modules are given in Table 3.5, and a complete list in the supplementary material (PF-modules-SIMPER.csv). The highest-contributing ortholog groups are given in Table 3.6, and a complete list in the supplementary material (PF-ortholog-groups-SIMPER.csv). No single ortholog group or module contributed more than 2.2% of the variance, indicating a complex and diverse pattern of functional differences. There was a strong trend for ortholog groups and modules with higher contributions to variance to be overrepresented in the NZ in the 3.0 μm fraction but the SZ in the smaller fractions, indicating that the functional diversity of each zone was strongly segregated by size fraction.

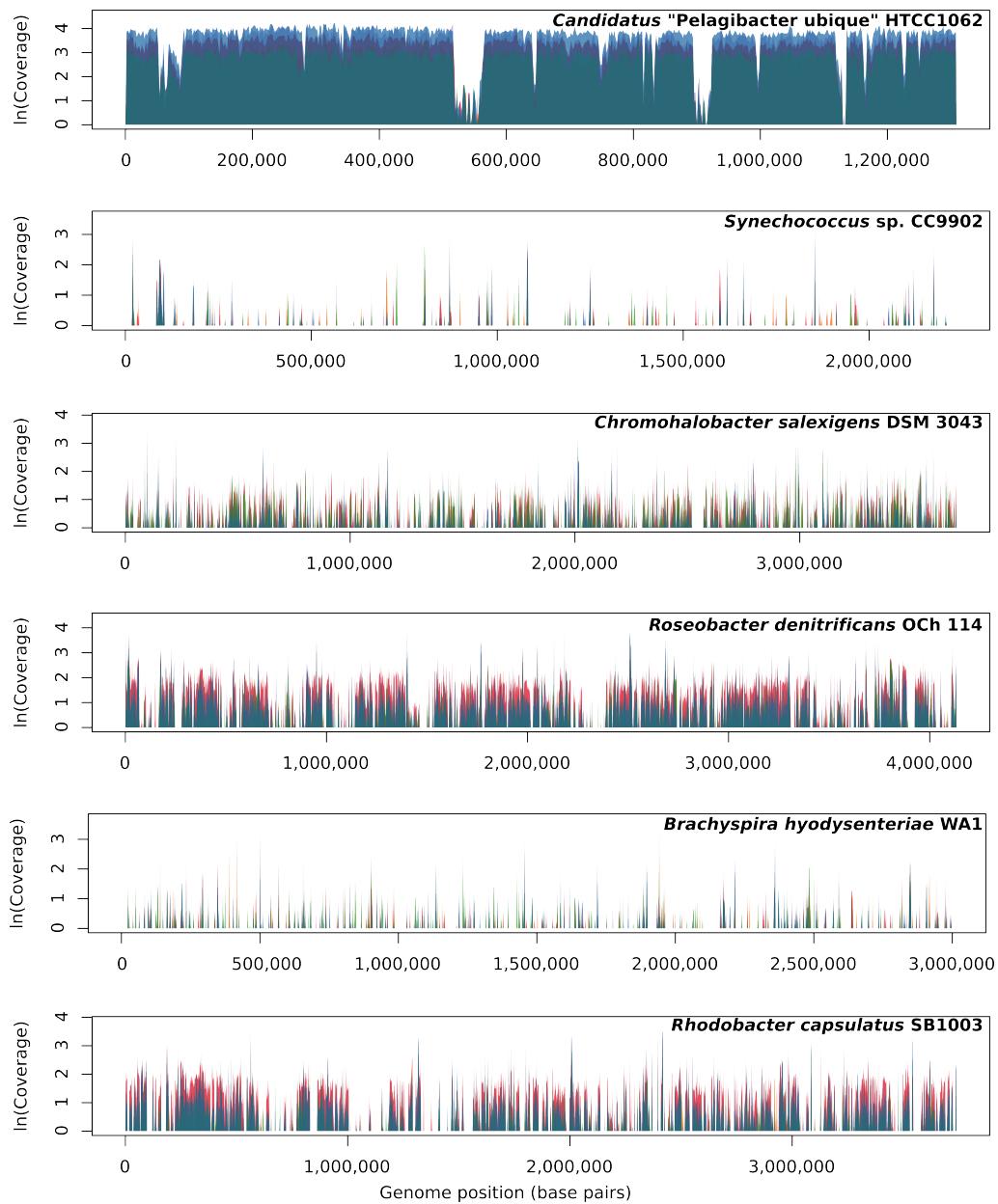


Figure 3.4: Examples of read recruitment (fragment recruitment) plots of metagenomic reads to reference genomes. Coloured regions indicate coverage for each of six example samples: pink sample 346; orange 347; red 358; green 361; blue 362. The even distribution of recruitment sites across the genome suggests that OTUs identifications are relatively accurate; an OTU identification resulting from a small region of genomic identity would generate a plot with read recruitment concentrated in small islands.

Table 3.5: The thirty KEGG modules with the highest contributions to the difference between the NZ and SZ. Abundances are zonal averages and have been standardised and log-transformed.

KEGG module	Abundance South	Abundance North	Contribution to variance (%)
Photosystem II	0.42	0.57	2.21
Complex I (NADH dehydrogenase), NADH dehydrogenase I/diaphorase subunit of the bidirectional hydroge-nase	0.01	0.24	1.80
Photosystem I	0.43	0.34	1.70
Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP → dCDP/dCTP,dTDP/dTTP	0.51	0.66	1.16
Histidine degradation, histidine → N-formiminoglutamate → glutamate	0.42	0.31	1.14
Methionine salvage pathway	0.29	0.43	1.14
sn-Glycerol 3-phosphate transport system	0.29	0.16	1.11
Complex I (NADH dehydrogenase), NADH dehydrogenase I	1.08	1.05	1.06
Branched-chain amino acid transport system	0.79	0.83	0.96
Dipeptide transport system	0.14	0.02	0.95
Adenine nucleotide biosynthesis, IMP → ADP/dADP,ATP/dATP	0.62	0.74	0.95
Glycine betaine/proline transport system	0.66	0.56	0.94
Sulfur reduction, sulfate → H ₂ S	0.54	0.44	0.91
Simple sugar transport system	0.46	0.39	0.90
Peptides/nickel transport system	0.99	0.98	0.89
Ribosome, eukaryotes	0.26	0.27	0.89
Multiple sugar transport system	0.55	0.55	0.86
Type II general secretion system	0.21	0.21	0.82
Sulfonate/nitrate/taurine transport system	0.45	0.37	0.82
Guanine nucleotide biosynthesis, IMP → GDP/dGDP,GTP/dGTP	0.72	0.82	0.81
RNA polymerase II, eukaryotes	0.11	0.20	0.76
Histidine biosynthesis, PRPP → histidine	0.94	0.86	0.76
Putrescine transport system	0.18	0.09	0.72
Leucine biosynthesis, pyruvate → 2-oxoisovalerate → leucine	1.29	1.37	0.71
C5 isoprenoid biosynthesis, non-mevalonate pathway	0.70	0.77	0.71
Leucine degradation, leucine → acetoacetate + acetyl-CoA	0.64	0.59	0.71
Thiamine transport system	0.13	0.05	0.69
Spliceosome, 35S U5-snRNP	0.18	0.20	0.68
Cytochrome b6f complex	0.14	0.12	0.67
Menaquinone biosynthesis, chorismate → menaquinone	0.25	0.27	0.66

Table 3.6: The thirty KEGG ortholog groups with the highest contribution to the difference between the NZ and SZ. Abundances are zonal averages and have been standardised and log-transformed. As each ortholog group on each size fraction was encoded as a separate variable in the SIMPER analysis, the size fraction is given after each ortholog group name.

KEGG ortholog group	Abundance South	Abundance North	Contribution to variance (%)
Hypothetical protein 3.0 µm	0.11	0.24	0.26
Hypothetical protein 0.8 µm	0.68	0.57	0.24
Ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] 0.8 µm	0.17	0.24	0.15
DNA polymerase III subunit alpha [EC:2.7.7.7] 0.8 µm	0.25	0.19	0.14
Hypothetical protein 0.1 µm	0.26	0.24	0.12
Proline dehydrogenase / delta 1-pyrroline-5-carboxylate 0.8 µm	0.10	0.04	0.12
Aminomethyltransferase [EC:2.1.2.10] 0.8 µm	0.25	0.19	0.12
Ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] 3.0 µm	0.02	0.08	0.12
Sarcosine oxidase, subunit alpha [EC:1.5.3.1] 0.8 µm	0.22	0.17	0.12
Integrator complex subunit 6 3.0 µm	0.07	0.05	0.11
Multicomponent Na ⁺ :H ⁺ antiporter subunit D 0.8 µm	0.11	0.05	0.11
Glutamine synthetase [EC:6.3.1.2] 0.8 µm	0.24	0.19	0.11
Pyruvate dehydrogenase E1 component [EC:1.2.4.1] 0.8 µm	0.15	0.10	0.11
Cobaltochelatase CobN [EC:6.6.1.2] 0.8 µm	0.11	0.06	0.11
Formate dehydrogenase, alpha subunit [EC:1.2.1.2] 0.8 µm	0.15	0.10	0.11
DNA-directed RNA polymerase subunit beta [EC:2.7.7.6] 3.0 µm	0.03	0.08	0.11
Glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14] 0.8 µm	0.25	0.22	0.11
Dimethylglycine dehydrogenase [EC:1.5.99.2] 0.8 µm	0.17	0.14	0.11
Flagellin 0.8 µm	0.06	0.10	0.10
DNA-directed RNA polymerase subunit beta [EC:2.7.7.6] 3.0 µm ⁴	0.03	0.08	0.10
Photosystem II PsbA protein 0.8 µm	0.01	0.06	0.09
Aldehyde dehydrogenase (NAD+) [EC:1.2.1.3] 0.8 µm	0.17	0.13	0.09
Glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14] 3.0 µm	0.02	0.07	0.09
Thymidylate synthase (FAD) [EC:2.1.1.148] 0.8 µm	0.02	0.06	0.09
Topoisomerase IV subunit A [EC:5.99.1.-] 0.8 µm	0.11	0.07	0.09
DNA mismatch repair protein MutS 0.8 µm	0.13	0.08	0.09
Glutamate dehydrogenase [EC:1.4.1.2] 0.8 µm	0.07	0.03	0.09
DNA polymerase I [EC:2.7.7.7] 0.1 µm	0.12	0.11	0.09
GTP-binding protein 0.8 µm	0.26	0.21	0.09
GTP-binding protein 3.0 µm	0.03	0.07	0.09

3.5 Discussion

3.5.1 Taxonomic groups differentiating the zones

3.5.1.1 GSO-EOSA-1

The Gammaproteobacterial Sulfur Oxidizer-EOSA-1 (GSO-EOSA-1) cluster, represented in RefSeq by the OTUs “*Candidatus Vesicomyosocius okutanii*” strain HA and “*Candidatus Ruthia magnifica*” strain Cm. (*Calyptogena magnifica*) (Walsh *et al.*, 2009), made a large contribution to variance between the NZ and SZ, with higher abundance in the SZ: relative abundances of GSO-EOSA-1 in the SZ were 5.2%, 3.4% and 0.25% in the 0.1, 0.8 and 3.0 μm size fractions respectively, compared to 1.1%, 0.84% and 0.30% in the NZ (Table 3.3). The contribution to variance of this group was highest in the 0.1 μm size fraction, followed by 0.8 μm and 3.0 μm (Table 3.4). This pattern most likely represents a small cell size and lack of association with particulate matter.

“*Ca. R. magnifica*” and “*Ca. V. okutanii*” are chemoautotrophic endosymbionts of deep-sea bivalves (Kuwahara *et al.*, 2007; Newton *et al.*, 2007) and are thus unlikely to be present in open ocean surface waters. However, GSO-EOSA-1 representative ARCTIC96BD-19 has recently been reported at high abundance in Antarctic coastal waters (Ghiglione and Murray, 2011; Grzymski *et al.*, 2012). The majority of 16S rRNA genes from this metagenome with best BLASTN hits to “*Ca. R. magnifica*” and “*Ca. V. okutanii*” clustered with ARTIC96BD-19 in a neighbour-joining phylogenetic tree (Fig. 3.5), indicating this is the dominant GSO-EOSA-1 representative.



Figure 3.5: Neighbour-joining tree of GSO-EOSA-1-like 16S rRNA gene sequences from the metagenomes in this study. Sequences labeled in black text are reads from the metagenomes. Red labels are 16S rRNA gene sequences from Gammaproteobacterial Sulfur Oxidizers (GSO) and other Gammaproteobacteria. The tree was constructed using ARB (Ludwig *et al.*, 2004).

Single-cell genomic analysis of ARCTIC96BD-19 from global mesopelagic waters indicates the lineage is probably mixotrophic, able to couple carbon fixation to oxidation of reduced sulphur compounds as well as assimilate organic carbon (Swan *et al.*, 2011). GSO-EOSA-1 cytochrome C oxidase (CoxII) has been identified in a winter metaproteome of Antarctic Peninsula coastal waters, suggesting the capacity for aerobic respiration (Williams *et al.*, 2012a). Taken together, this evidence suggests the GSO-EOSA-1 representative in Antarctic coastal waters is a versatile chemolithoautotroph capable of aerobic respiration.

It has been proposed that during the winter months, chemolithoautotrophy is dominant over photoautotrophy as the major carbon fixation process in AZ waters due to the lack of available light, both from seasonal darkness and ice shading (Grzymski *et al.*, 2012). The high relative abundance of GSO-EOSA-1 in SZ compared to NZ waters may therefore represent the remnants of an annual winter increase in population in the marginal ice zone which does not occur in the open ocean.

3.5.1.2 Ammonia-oxidizing Crenarchaeota

Nitrosopumilus maritimus SCM1 and *Cenarchaeum symbiosum* are chemolithoautotrophic, nitrifying members of the Marine Group I Crenarchaeota (MGI) (Preston *et al.*, 1996; Walker *et al.*, 2010) and are the only representatives in the reference database of the Ammonia-Oxidizing Archaea (AOA). The contribution of OTUs of *C. symbiosum* to the AOA signature was low. As *C. symbiosum* is a sponge symbiont (Preston *et al.*, 1996) and given the poor representation of AOA in RefSeq, it is likely this OTU has attracted sequences originating from planktonic AOA and *C. symbiosum* itself is not present. AOA were moderate contributors to variance between the NZ and SZ, and were overrepresented in the SZ in all size fractions (Fig. 3.3). As with the GSO-EOSA-1 cluster, MGI have been proposed to be abundant chemolithoautotrophs and therefore major drivers of winter carbon fixation in Antarctic coastal waters (Grzymski *et al.*, 2012; Williams *et al.*, 2012a).

Sample 353 had a particularly high relative abundance of *N. maritimus* OTUs (7.5% of the 0.1 μm fraction; 0.8 μm : 11%; 3.0 μm : 12%). This sample was taken closer to the Antarctic continent (3.7 km) than any other, in relatively shallow (180 m) waters 17.6 km from the Mertz Glacier. The high abundance of ammonia oxidizers may reflect an input of ammonia from terrestrial sources (e.g. penguin guano), or resuspension of benthic sediments in which MGI are abundant (Bowman and McCuaig, 2003) by near-shore turbulence and iceberg scouring. Breakdown of water column stratification has been previously suggested as a cause of increased AOA abundance in Antarctic coastal surface waters (Kalanetra *et al.*, 2009).

3.5.1.3 Cyanobacteria

OTUs of the cyanobacterial genera *Prochlorococcus* and *Synechococcus* were overrepresented in the NZ in all size fractions (Fig. 3.3). The mean relative abundance of cyanobacteria in samples 367 and 368, the two northernmost samples, was strikingly higher than the mean abundance across all other samples in the NZ. *Synechococcus* sp. CC9902 alone composed greater than 22% of the 0.8 μm fraction in these samples, consistent with *Synechococcus* species' average cell diameter of approximately 0.9 μm . The high abundance of both

cyanobacterial genera on the 3.0 μm fraction has previously been reported (Lauro *et al.*, 2011) and may be attributable to aggregation (Lomas and Moran, 2011).

Samples 367 and 368 were separated from the other samples north of the PF by the STF. While the STF was not a significant boundary on the assemblage level, it may mark a significant biogeographic boundary for these cyanobacteria. *Synechococcus* and *Prochlorococcus* together represent a large proportion of both phytoplankton abundance and carbon fixation in temperate and tropical waters, in many regions contributing more than half of total primary production (Liu *et al.*, 1997, 1998; André *et al.*, 1999). The role of the STF in determining the latitudinal range of *Synechococcus* and *Prochlorococcus* is therefore important, as it will affect models of ocean productivity under changing climactic conditions, and warrants further investigation. Despite the high abundance of cyanobacteria north of the STF, they were also a significant feature of the SAZ; for example, *Synechococcus* sp. CC9902 composed 3–5% of the 0.8 μm fraction in SAZ samples.

These results extend the latitudinal distribution of both *Prochlorococcus* and *Synechococcus* to include presence at very low abundance as far south as the Antarctic coast. *Prochlorococcus* have been reported to be restricted to tropical and subtropical waters within 40° of latitude (Partensky *et al.*, 1999), and to be a negligible (Ghiglione and Murray, 2011) or undetectable (Grzymski *et al.*, 2012) component of marine microorganisms in Antarctic waters. However, these findings are consistent with findings of a logarithmic relationship of cyanobacterial numbers with temperature, where cyanobacteria were found at concentrations of 103–104 cells per litre even in the coldest waters, approximately four orders of magnitude less than in waters around Tasmania (Marchant *et al.*, 1987). Cyanophage proteins have also been detected in a metaproteomic analysis of Antarctic Peninsula coastal surface waters (Williams *et al.*, 2012a).

3.5.1.4 SAR11 and SAR116 clades

“*Candidatus Pelagibacter ubique*” HTCC1062 is a good representative of total SAR11 abundance in this study, as it is a member of the SAR11 phylotype which is most abundant in SO waters (Brown *et al.*, 2012). “*Ca. P. ubique*” HTCC1062 was the most abundant OTU across all samples and fractions (NZ average: 62%, 25% and 24% of the 0.1 μm , 0.8 μm and 3.0 μm fractions respectively; SZ: 59%, 22% and 18%) and one of the most significant contributors to variance between the NZ and SZ. The high abundance of SAR11 in the 0.1 μm fraction is consistent with the small size of SAR11 cells (Rappé *et al.*, 2002). The higher representation in the NZ may reflect the competitiveness of SAR11 members in regions with low Dissolved Organic Carbon (DOC) concentrations due to low primary productivity (Giovannoni *et al.*, 2005; Alonso and Pernthaler, 2006), such as the High Nutrient, Low Chlorophyll (HNLC) SAZ. Overall, these findings are consistent with reports that SAR11 is ubiquitous in the world’s oceans (Mary *et al.*, 2006; Carlson *et al.*, 2009) and more abundant north of the ACC (Giebel *et al.*, 2009).

OTUs of “*Candidatus Puniceispirillum marinum*” from the SAR116 clade were a moderate contributor to variance between the NZ and SZ with higher abundance in the NZ (Fig. 3.3). A genomic analysis reported “*Ca. P. marinum*” IMCC1322 to be a metabolic generalist with genes for aerobic CO fixation, C1 metabolism and a “*Ca. P. ubique*”-like dimethylsulfoniopropionate (DMSP) demethylase, suggesting SAR116 and SAR11 occupy

similar ecological niches (Oh *et al.*, 2010). In the Scotia Sea, SAR116 abundance (determined using Fluorescence *In Situ* Hybridization (FISH)) was reported to be higher in more productive waters where SAR11 numbers were lower (Topping *et al.*, 2006). However, this analysis across an extended latitudinal transect indicates that overall SAR11 and SAR116 have similar biogeographic distributions.

3.5.1.5 Bacteroidetes

OTUs of the phylum Bacteroidetes, in particular members of the class Flavobacteria, were found to be abundant (NZ average: 1.2%, 5.0% and 6.9% of the 0.1 µm, 0.8 µm and 3.0 µm fractions respectively; SZ: 2.3%, 9.8% and 9.1%) and significant contributors to variance between the NZ and SZ (Fig. 3.3). Flavobacteria have been previously reported to compose the majority of both Bacteroidetes (Murray and Grzynski, 2007) and total planktonic biomass (Abell and Bowman, 2005b) in the SO, as well as being abundant in sea ice (Brown and Bowman, 2001). As heterotrophic degraders of High Molecular Weight (HMW) compounds in the form of both Dissolved Organic Matter (DOM) and Particulate Organic Matter (POM) (Kirchman, 2002), marine Flavobacteria are major components of marine aggregates (Rath *et al.*, 1998; Crump *et al.*, 1999; Zhang *et al.*, 2007). The higher abundance of Flavobacteria OTUs on the 0.8 µm and 3.0 µm fractions indicates their association with particulate matter. Similar size partitioning of SO Flavobacteria has previously been reported (Abell and Bowman, 2005b).

The higher abundance of OTUs of Flavobacteria in the SZ may reflect an input of cells from melting sea ice (Brown and Bowman, 2001), the higher rates of primary productivity in the south, and the role of the Flavobacteria as degraders of HMW DOM. Because deposition of marine snow is a major route for sequestration of fixed carbon in the ocean (e.g. Hessen *et al.*, 2004), the Flavobacteria that associate with this particulate matter represent a remineralising shunt, which would decrease carbon sequestration by this route.

3.5.1.6 Rhodobacterales

Members of the order Rhodobacterales were abundant (NZ average: 1.2%, 10% and 5.5% of the 0.1 µm, 0.8 µm and 3.0 µm fractions respectively; SZ: 1.6%, 13% and 7.9%) and high contributors to variance, overrepresented in the SZ on all size fractions. As several members of the Roseobacter clade have been shown to have symbiotic relationships with marine eukaryotic algae (Buchan *et al.*, 2005; Wagner-Döbler and Biebl, 2006), and their abundance in the SO has previously been linked to phytoplankton blooms (West *et al.*, 2008; Obernosterer *et al.*, 2011), it is likely that their overrepresentation in the SZ is related to the higher density of phytoplankton in the AZ.

OTUs of *Roseobacter denitrificans* Och114 and *Silicibacter pomeroyi* DSS-3 were consistently the most abundant Roseobacter clade representatives. *R. denitrificans* and *S. pomeroyi* fall within a subclade of Aerobic Anoxygenic Phototrophic (AAP) members of the Roseobacter clade (Swingley *et al.*, 2007). These species have diverse mixotrophic metabolisms, with genomic and experimental evidence of photoheterotrophic respiration of organic carbon, fixation of CO₂, oxidation of CO, oxidation of reduced sulfur compounds, and utilization of the abundant marine osmolyte DMSP (King, 2003; Moran *et al.*, 2004; Wagner-Döbler and Biebl, 2006; Swingley *et al.*, 2007; Brinkhoff *et al.*, 2008; Howard

et al., 2008). This metabolic diversity suggests a complex ecological role, particularly with respect to the capture and release of climatically active gases (CO_2 , CO, dimethylsulfide) involved in carbon and sulfur cycling.

3.5.1.7 Alteromonadales

Members of the gammaproteobacterial order Alteromonadales were large contributors to variance. Most OTUs were overrepresented in the SZ but some were overrepresented in the NZ on the 3.0 μm fraction (Fig. 3.3). *Colwellia psychrerythraea* 34H was one of the most abundant OTUs in the Alteromonadales that exhibited this distribution (NZ average: 0.14%, 2.2% and 16% of the 0.1 μm , 0.8 μm and 3.0 μm fractions respectively; SZ: 0.52%, 5.1% and 10%). *C. psychrerythraea* 34H was isolated from Arctic sediment, grows well at low temperatures and secretes extracellular polysaccharides (Huston *et al.*, 2000; Junge *et al.*, 2003; Methé *et al.*, 2005). Similar to other *Colwellia* species grown under laboratory conditions, cells have widths of 0.4–0.8 μm and lengths of 1.5–4.5 μm (Jung *et al.*, 2006). Growth temperature can have a major impact on cell morphology, enzyme secretion and global gene expression in psychrophiles (e.g. Feller and Gerdar, 2003; Junge *et al.*, 2003; Williams *et al.*, 2011; Cavicchioli, 2006; Campanaro *et al.*, 2011). Moreover, marine bacteria can alter their cell dimensions in response to nutrient flux (e.g. Kjelleberg *et al.*, 1987). It is therefore possible that the populations of Alteromonadales captured on the 3.0 μm filters (overrepresented in the NZ) had different physiological properties to those on the 0.1 and 0.8 μm filters (overrepresented in the SZ).

3.5.1.8 Verrucomicrobia

Two representatives of the phylum Verrucomicrobia, *Coraliomargarita akajimensis* and *Akkermansia* sp. Muc-30, were moderate contributors to variance and overrepresented in the SZ (Fig. 3.3). Surprisingly given the small cell size of *C. akajimensis* (Yoon *et al.*, 2007), its contribution to variance increased with size fraction. A global survey reported a similar fractionation pattern, and suggested marine Verrucomicrobia may be predominantly particle attached (Freitas *et al.*, 2012). However, little else is known about the distribution and ecological roles of marine Verrucomicrobia (Freitas *et al.*, 2012).

3.5.2 Functional capacities differentiating the zones

A number of modules with transport functions (sn-glycerol 3-phosphate transport system, dipeptide transport system, peptides/nickel transport system, simple sugar transport system, sulfonate/nitrate/taurine transport system) were overrepresented in the SZ (Table 3.5). As the genomes of copiotrophic bacteria have evolved to have a higher number of narrow-specificity transporters relative to oligotrophic genomes (Lauro *et al.*, 2009), these differences may reflect the higher nutrient availability and thus a dominance of copiotrophs in the SZ. The taxonomic contributors to these modules were varied, although members of the Rhodobacterales were prominent (Fig. 3.6).

The glycine betaine/proline transport module was also overrepresented in the SZ, though this probably reflects glycine betaine's role as an osmo- and cryoprotectant in the

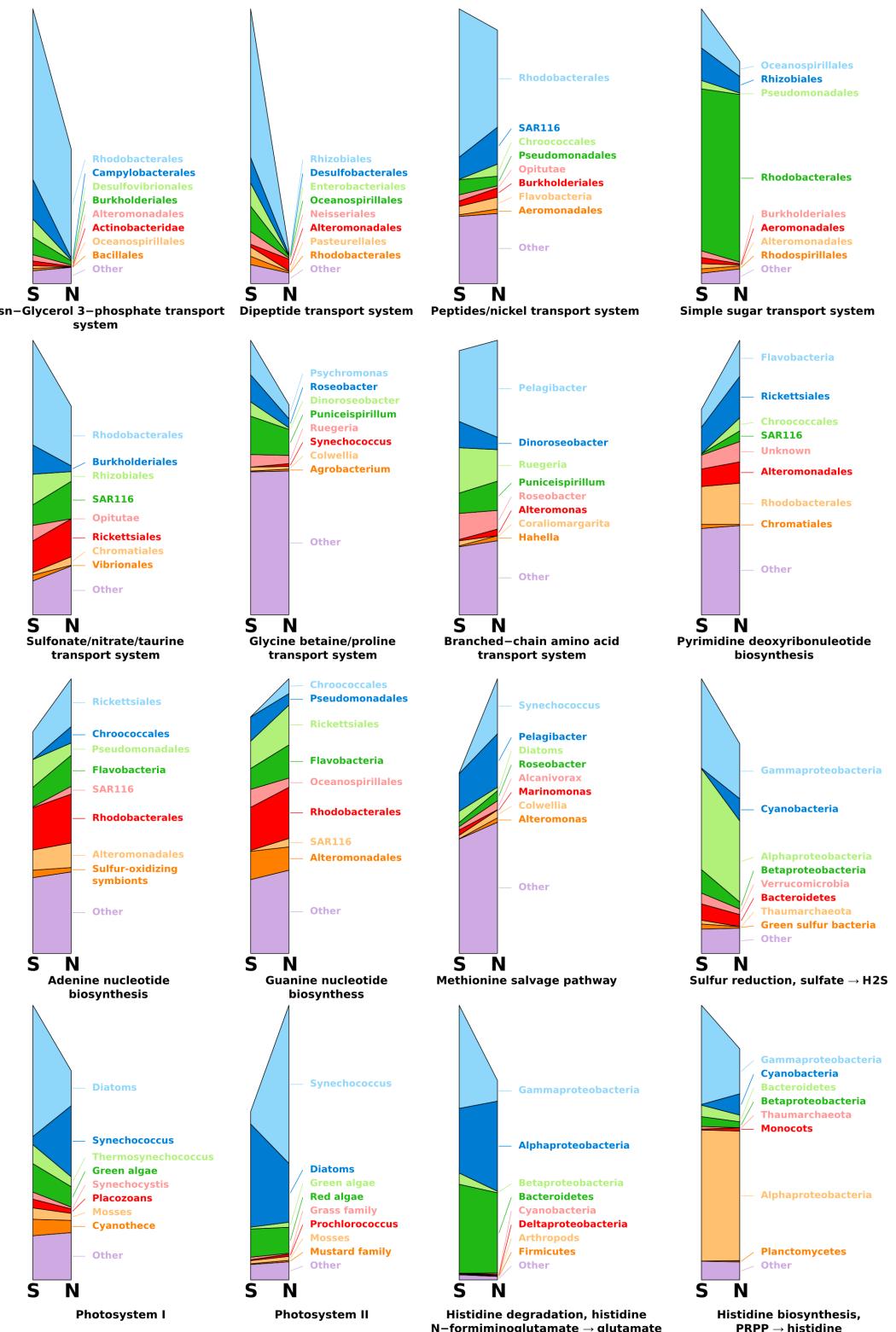


Figure 3.6: Decomposition of KEGG modules of interest to contributing classes, orders or genera. The left side of each stack (S) indicates the proportion of the module abundance contributed by each class, order or genus in the South Zone, while the right side (N) represents the North Zone. As the contributions are relative and represent unitless module abundances, no axis is given and proportions are not comparable between modules. Contributing classes, orders or genera are arranged in descending order of the difference in the relative contributions between the zones. Only the eight highest contributors for each module are shown, with the remainder collapsed into the “Other” group. The taxonomic ranks to which each module was decomposed are as follows: sn-glycerol 3-phosphate transport, peptide-nickel transport, simple sugar transport and sulfonate/nitrate/taurine transport were decomposed to order; glycine betaine/proline transport and branched-chain amino acid transport to genus; pyrimidine deoxyribonucleotide biosynthesis, adenine nucleotide biosynthesis and guanine nucleotide biosynthesis to order; methionine salvage to genus; sulphur reduction to class; photosystem I and photosystem II to genus; histidine degradation to glutamate and histidine biosynthesis to class.

colder SZ waters. This is supported by the major taxonomic contributor to this module, genus *Psychromonas*, which includes several psychrophilic species.

One exception to this pattern was the branched-chain amino acid transport system module, overrepresented in the NZ. The genera *Pelagibacter* and *Puniceispirillum* were major contributors to this module’s overabundance in the NZ (Fig. 3.6). As both SAR11 (Giovannoni *et al.*, 2005) and SAR116 (Grote *et al.*, 2011) representatives encode branched-chain amino acid transporters, the abundance of this module is likely to represent taxonomic differences between the zones.

Biosynthesis pathways for all major nucleic acids (pyrimidine deoxyribonucleotide biosynthesis, adenine nucleotide biosynthesis, guanine nucleotide biosynthesis) were consistently high contributors to variance and overabundant in the NZ. This pattern seems inconsistent with the more oligotrophic nature of the NZ, as oligotrophic cells generally have smaller genomes (Lauro *et al.*, 2009) and slower growth rates than copiotrophs, and would therefore be expected to require a lower rate of de novo nucleotide biosynthesis. A possible explanation for this is that SZ cells have higher availability of extracellular DNA as a byproduct of decaying phytoplankton (Lomas and Moran, 2011), which can be imported and salvaged for nucleic acids (Paul *et al.*, 1988) thus reducing the requirement for de novo synthesis. No single taxonomic group contributed a large fraction of the difference in this module (Fig. 3.6), suggesting this is a widespread adaptation.

The methionine salvage pathway module had a large contribution to variance between the zones and was overrepresented north of the PF. This may reflect the higher availability of DMSP in the SZ as a byproduct of blooming eukaryotic algae. DMSP is a major carbon and sulfur source for marine microorganisms, and is commonly assimilated by bacteria through demethylation to methylmercaptopropionate (MMPA), followed by further catabolism to the climatically important compounds dimethylsulfide or methanethiol (review in Curson *et al.*, 2011). However, when DMSP is scarce, MMPA may be derived from methionine through the alternative methionine salvage pathway (Reisch *et al.*, 2011). The genus *Synechococcus*, a noted contributor to marine DMSP uptake and assimilation (Vila-Costa *et al.*, 2006), was a very high contributor to the abundance of this module in the NZ (Fig. 3.6), suggesting *Synechococcus* species may use this route when DMSP is unavailable.

The sulfur reduction module was overrepresented in the SZ, and it is likely that this result is strongly driven by taxonomic differences. While the taxonomic breakdown indi-

cated a large number of genera contributed to the difference, the Gammaproteobacteria were the highest-contributing class (Fig. 3.6). This module also includes the assimilatory sulfate reduction pathway, which is widespread in marine bacteria, but is absent from SAR11, with known representatives reported to lack genes for assimilatory sulfate reduction (*cysDNCHIJ*) (Tripp *et al.*, 2008). The higher relative abundance of SAR11 in the NZ may therefore contribute to the lower abundance of genes for assimilatory sulfate reduction in that zone.

The sulfur reduction module also included adenylylsulfate reductase (APS reductase, encoded by *aprAB*), an enzyme implicated in sulfite detoxification during heterotrophic growth on organosulfonates (Meyer and Kuever, 2007) (N.B. in recent KEGG releases, *aprA* is no longer included in this module). As the GSO-EOSA-1 representative SUP05 has been found to encode APS reductase, the overabundance of this module may reflect sulfur oxidation through the reverse dissimilatory sulfate reduction pathway (Walsh *et al.*, 2009). Also, Roseobacter clade bacteria are involved in the decomposition of abundant organic sulfur compounds (e.g. DMSP, organosulfonates), and hence have been accorded an important role in marine sulfur cycling (Moran *et al.*, 2007).

The photosystem II module was overrepresented in the NZ. Given the underrepresentation of cyanobacterial OTUs in the SZ, this may reflect a dominance of primary production by eukaryotic algae south of the PF and cyanobacteria to the north. Decomposition of the taxonomic affiliations of ortholog groups contributing to this module found OTUs of *Synechococcus* and *Prochlorococcus* to be major contributors to the difference (Fig. 3.6). Variation in the photosystem I module, which was marginally overrepresented in the SZ, could largely be attributed to diatoms and other eukaryotic phytoplankton (Fig. 3.6), again supporting a dominance of eukaryotic phytoplankton in SZ primary production. Diatoms have previously been reported at higher abundance south of the PF, and their distribution is likely to be linked to the higher concentration of dissolved silica in that region (Trull *et al.*, 2001). As both eukaryotic phytoplankton and cyanobacteria would be expected to encode both complete photosystems, the differences in module abundance probably reflect the degree of similarity between the photosystem I and II genes in the KEGG database and those found in the sampled environments.

The histidine degradation to glutamate module, which comprises four ortholog groups mediating the degradation of histidine to glutamate via N-formiminoglutamate, was overrepresented in the SZ. The histidine biosynthesis module was also overrepresented in the SZ. While the concentration of dissolved histidine in the SO is generally low (Kawahata and Ishizuka, 2000), blooming eukaryotic phytoplankton (which are more prevalent in the SZ) may deplete nitrate while releasing Dissolved Free Amino Acids (DFAA). As DFAA become available, they are used by bacteria to sense the decaying bloom. Histidine may therefore act as a proxy for DFAA to regulate the expression of bacterial aminopeptidases, which are involved in lysing diatoms (Bidle and Azam, 2001). The class Bacteroidetes, while a small contributor to the histidine biosynthesis module in the SZ, was a large contributor to histidine degradation (Fig. 3.6), supporting an association between Bacteroidetes and phytoplanktonic bloom products. It is also possible that uptake and degradation of histidine to glutamate (which generates ammonia as a by-product) may function as a limited nitrogen source.

3.5.2.1 Conclusions: Biogeographic role of the Polar Front

These results show that there are major taxonomic and functional differences across the PF. The differences in functional potential between the NZ and SZ reflect both their taxonomic profiles and fundamental trophic and ecological differences. In particular, they provide genomic support that the NZ is more oligotrophic than the SZ (Pollard *et al.*, 2002; Giovannoni *et al.*, 2005; Alonso and Pernthaler, 2006; Lauro *et al.*, 2009), and are consistent with the observation that primary production is higher south of the PF (Strutton *et al.*, 2000; Williams *et al.*, 2010). Our findings extend previous work in defining the PF as a strong biogeographic boundary which shapes not only the composition, but also the functional capacity of microbial communities in the SO.

These results do not exclude the possibility that other major SO fronts, particularly the STF and SAF, are also significant biogeographic boundaries, as has been reported in some previous reports for specific taxonomic groups (e.g. Abell and Bowman, 2005b). While the sampling resolution in this study was not sufficient to resolve the effects of other fronts, there are some indications in the data of further structure within the zones. The two samples north of the STF had significantly larger cyanobacterial populations than the remaining NZ samples (see discussion of *Prochlorococcus* and *Synechococcus*, above). Future sampling across these fronts at higher resolution will provide the data necessary to investigate finer biogeographic patterns.

The nature and function of microbial communities in the SO are of global significance. Knowledge of these communities and their biogeographic drivers has relevance for understanding and predicting the long-term effects of climate change. These findings provide a basis for predicting how climate change-driven shifts in the SO may affect microbial communities; in particular, the effects of changes in the nature and location of the ACC on the ecosystem functions of SO microorganisms.

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