

Microbial Ecology and Biogeography  
OF THE  
Southern Ocean

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# Acknowledgements





# Abstract

# **Introduction**

**Microbial ecology of the Southern Ocean**

**Oceanography of the Southern Ocean**

**Water masses and fronts**

**Effect of climate change**

**Role of the Polar Front in biogeography**

**Project questions and hypotheses**



# 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. Biogeographic partitioning of Southern Ocean picoplankton revealed by metagenomics. Molecular Ecology, 2012.*

And another try: (Wilkins *et al.*, 2012).

## Summary

## Introduction

## Methods

### Sampling and metagenomic sequencing

Sampling<sup>1</sup> was conducted on board the RSV *Aurora Australis* during cruise V3 CEAMARC/CASO (Collaborative East Antarctic Marine Census / Climate of Southern Ocean) from 13 December 2007 – 26 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. Nineteen samples (16 surface, 3 deep) were obtained along almost the entire latitudinal range (Figure 1).

A range of data were recorded by integrated instruments on the RSV *Aurora Australis* including location, water column depth, water temperature, salinity, fluorescence and meteorological data (TODO provide table). These data were used to locate the (TODO abbreviations package? PFZ) based on a surface temperature gradient of  $\sim 1.35$  °C across a distance of 45–65 km, placing the (TODO abbreviations? PF) at approximately  $-59.70^\circ$  of latitude, consistent with previous descriptions TODO EDITING HERE NEED SOKOLOV AND RINTOUL REF

At each station,  $\sim 500$  L of seawater was pumped from  $\sim 2$  m below the sea surface into drums stored at ambient temperature on deck. In the case of deep samples,  $\sim 10$ –50 L of seawater was collected opportunistically from Niskin bottles attached to a CTD (Conductivity, Temperature and Depth

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<sup>1</sup>Sampling was performed by Jeffrey M. Hoffman and Jeffrey B. McQuaid

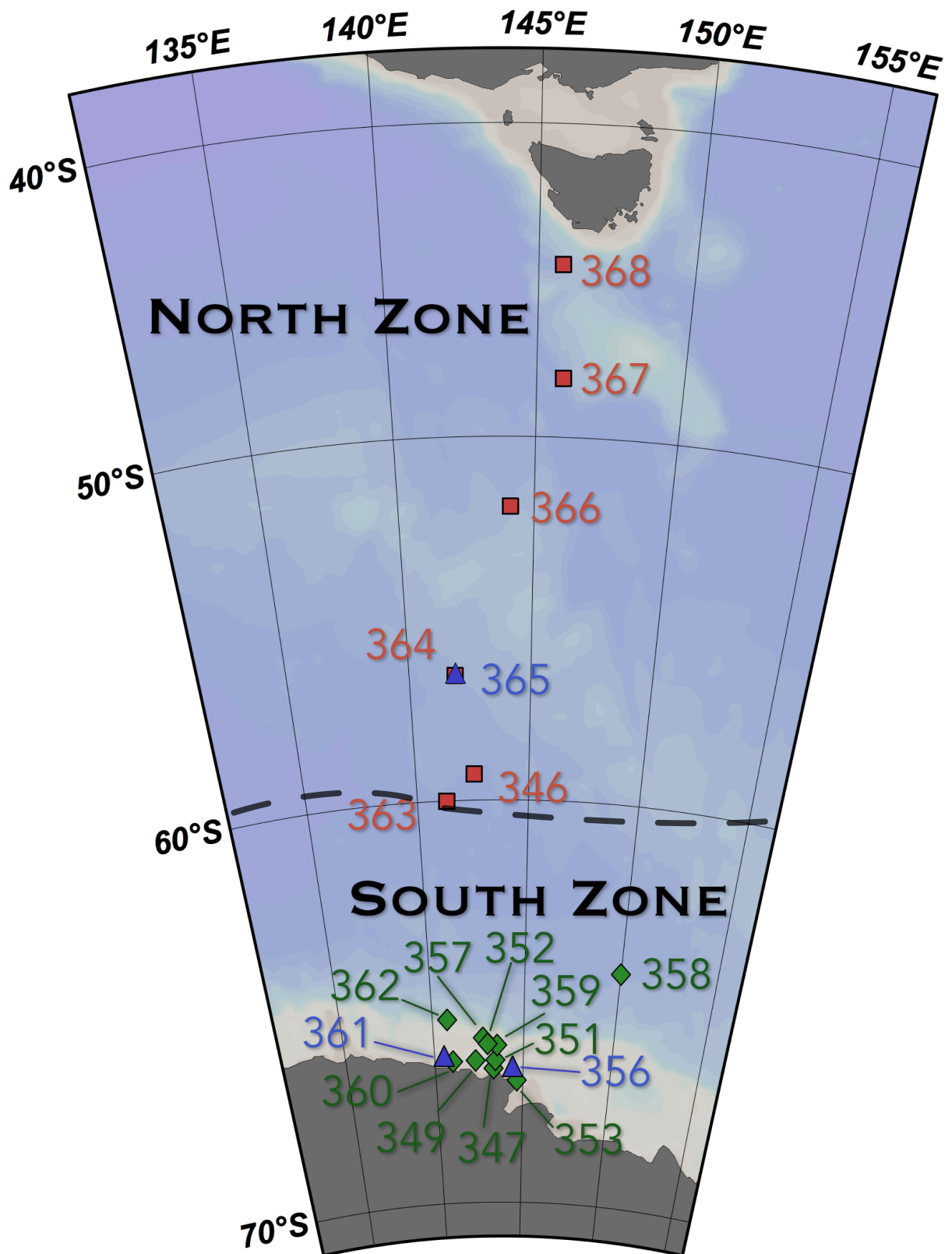


Figure 1: Sites of seawater samples used in this study. Red squares indicate surface samples from the North Zone; green diamonds samples from the South Zone; and blue triangles indicate deep samples. The dashed line gives the approximate location of the Polar Front.

TODO give infor on CTD - SeaBird?) instument operated by an unrelated oceanographic project. Sea-water samples were prefiltered through a 20  $\mu\text{m}$  plankton net, then filtrate was captured on sequential 3.0  $\mu\text{m}$ , 0.8  $\mu\text{m}$  and 0.1  $\mu\text{m}$  polyethersulfone membrane filters (Supor membrane disc filter; Pall Life Sciences TODO location), and immediately stored at  $-20\text{ }^{\circ}\text{C}$  (Rusch *et al.*, 2007; Ng *et al.*, 2010).

DNA extraction<sup>2</sup> 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).

## **Phylogenetic analysis of metagenomic data**

## **Functional analysis of metagenomic data**

## **Results**

### **Metagenomic sequencing**

### **Phylogenetic analysis of metagenomic data**

### **Functional analysis of metagenomic data**

## **Discussion**

## **Conclusions**

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





# **Meso-scale biogeographic drivers of planktonic diversity**



# Conclusions



# References

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