

Microbial Ecology and Biogeography  
OF THE  
Southern Ocean

David Wilkins

September 21, 2012

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# Acknowledgements





# Abstract

# Introduction

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The Roseobacter clade is an abundant and ecologically significant group of marine bacteria, found at high (> 15%) abundance in most marine surface environments (Ano (2005) and references therein). Unlike some other major proteobacterial groups which are strongly associated with a particular ecological niche (e.g. the SAR11 clade), roseobacters have diverse metabolic abilities, with members capable (for example) of aerobic anoxygenic phototrophy (Biebl, 2005; ?), degradation of dimethylsulfoniopropionate (DMSP) by at least two pathways (Moran *et al.*, 2007; Miller and Belas, 2004), carbon monoxide oxidation (King, 2003) and heterotrophic utilisation of a broad range of substrates (reviewed in (Brinkhoff *et al.*, 2008)). Roseobacters are found in the planktonic fraction as well as in commensal association with phytoplankton and metazoans (reviewed in Ano (2005)).

## **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 (TODO: cite PF manuscript)*

## 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).

At each station, ~ 500 L of seawater was pumped from ~ 2 m below the sea surface into drums stored at ambient temperature on deck. In the case of deep samples, ~ 10–50 L of seawater was collected opportunistically from Niskin bottles attached to a CTD (Conductivity, Temperature and Depth) instrument operated by an unrelated oceanographic project. Seawater 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), and immediately stored at  $-20^{\circ}\text{C}$  (Rusch *et al.*, 2007; Ng *et al.*, 2010).

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

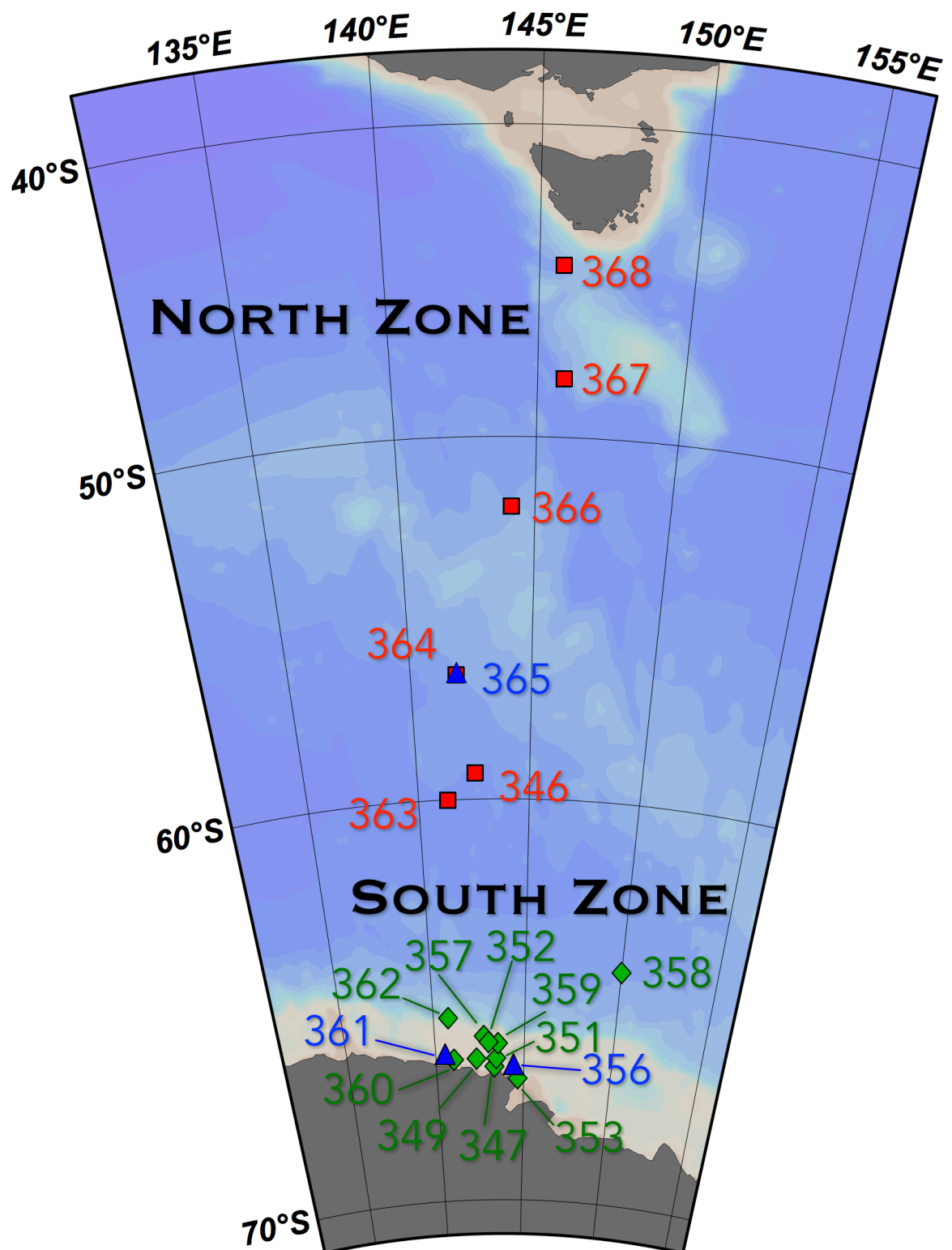


Figure 1: TODO caption here

**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**





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



# Conclusions



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