

Microbial Ecology and Biogeography  
OF THE  
Southern Ocean

David Wilkins

September 22, 2012

# Contents

<b>List of Figures</b>	<b>iii</b>
<b>List of Tables</b>	<b>v</b>
<b>Acknowledgements</b>	<b>vii</b>
<b>Abstract</b>	<b>ix</b>
<b>Introduction</b>	<b>1</b>
Some test text to preview layout <i>etc.</i> . . . . .	1
Microbial ecology of the Southern Ocean . . . . .	1
Oceanography of the Southern Ocean . . . . .	1
Water masses and fronts . . . . .	1
Effect of climate change . . . . .	1
Role of the Polar Front in biogeography . . . . .	1
Project questions and hypotheses . . . . .	1
<b>The Polar Front as a major biogeographic boundary in the Southern Ocean</b>	<b>3</b>
Summary . . . . .	3
Introduction . . . . .	3
Methods . . . . .	3
Sampling and metagenomic sequencing . . . . .	3
Phylogenetic analysis of metagenomic data . . . . .	5
Functional analysis of metagenomic data . . . . .	5
Results . . . . .	5
Metagenomic sequencing . . . . .	5
Phylogenetic analysis of metagenomic data . . . . .	5
Functional analysis of metagenomic data . . . . .	5
Discussion . . . . .	5
Conclusions . . . . .	5
<b>Meso-scale biogeographic drivers of planktonic diversity</b>	<b>7</b>
<b>Conclusions</b>	<b>9</b>



# List of Figures

- 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. 4



# List of Tables



# Acknowledgements





# Abstract

# Introduction

## **Some test text to preview layout *etc.***

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).

---

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

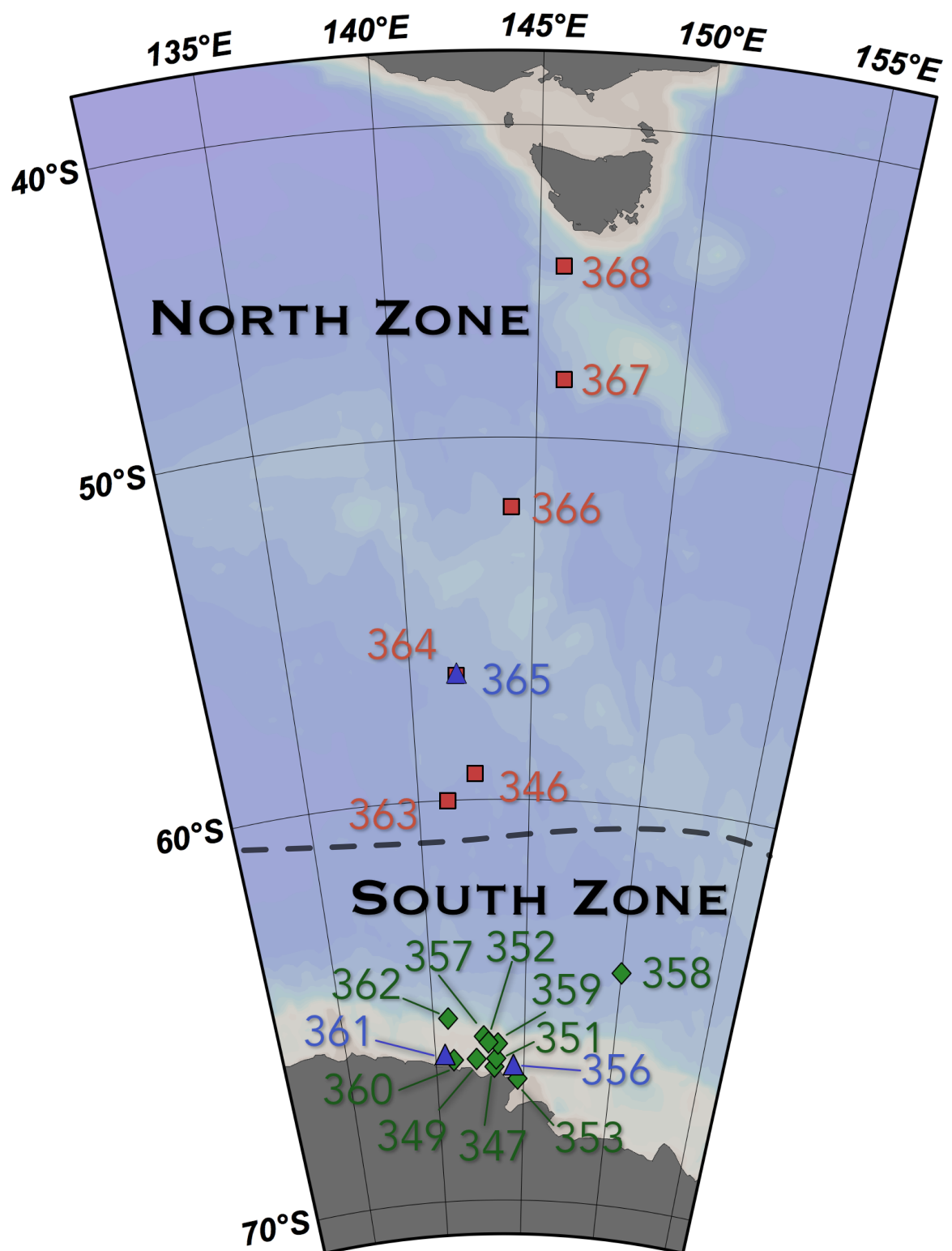


Figure 1: Sites of seawater samples used in this study. Red squares indicate surface samples from the North Zone; green diamonds samples from the South Zone; and blue triangles indicate deep samples. The dashed line gives the approximate location of the Polar Front.

**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



# References

- Buchan, Moran - 2005 - Overview of the Marine Roseobacter Lineage. pages 1–13, 2005.
- Biebl H. *Dinoroseobacter shibae* gen. nov., sp. nov., a new aerobic phototrophic bacterium isolated from dinoflagellates. *INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY*, 55(3):1089–1096, 2005.
- Brinkhoff T., Giebel H.-A., and Simon M. Diversity, ecology, and genomics of the Roseobacter clade: a short overview. *Archives of Microbiology*, 189(6):531–539, 2008.
- King G. M. Molecular and culture-based analyses of aerobic carbon monoxide oxidizer diversity. *Applied and Environmental Microbiology*, 69(12):7257–7265, 2003.
- Miller T. R. and Belas R. Dimethylsulfoniopropionate Metabolism by *Pfiesteria*-Associated Roseobacter spp. *Applied and Environmental Microbiology*, 70(6):3383–3391, 2004.
- Moran M. A., Belas R., Schell M. A., González J. M., Sun F., Sun S., Binder B. J., Edmonds J., Ye W., Orcutt B., Howard E. C., Meile C., Palefsky W., Goesmann A., Ren Q., Paulsen I., Ulrich L. E., Thompson L. S., Saunders E., and Buchan A. Ecological Genomics of Marine Roseobacters. *Applied and Environmental Microbiology*, 73(14):4559–4569, 2007.
- Ng C., Demaree M. Z., Williams T. J., Lauro F. M., Raftery M., Gibson J. A., Andrews-Pfannkoch C., Lewis M., Hoffman J. M., Thomas T., and Cavicchioli R. Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. *The ISME journal*, 4(8):1002–1019, 2010.
- Rusch D. B., Halpern A. L., Sutton G., Heidelberg K. B., Williamson S., Yooseph S., Wu D., Eisen J. A., Hoffman J. M., Remington K., Beeson K., Tran B., Smith H., Baden-Tillson H., Stewart C., Thorpe J., Freeman J., Andrews-Pfannkoch C., Venter J. E., Li K., Kravitz S., Heidelberg J. F., Utterback T., Rogers Y.-H., Falcón L. I., Souza V., Bonilla-Rosso G., Eguiarte L. E., Karl D. M., Sathyendranath S., Platt T., Bermingham E., Gallardo V., Tamayo-Castillo G., Ferrari M. R., Strausberg R. L., Nealson K., Friedman R., Frazier M., and Venter J. C. The Sorcerer II Global Ocean Sampling expedition: northwest Atlantic through eastern tropical Pacific. *PLoS Biology*, 5(3):e77–e77, 2007.