Microbial Ecology and Biogeography

OF THE

Southern Ocean

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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[1] 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, $\sim$ 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) instument operated by an unrelated oceanographic project. Seawater samples were prefiltered through a 20 μm plankton net, then filtrate was captured on sequential 3.0 μm, 0.8 μm and 0.1 μm polyethersulfone membrane filters (Supor membrane disc filter; Pall Life Sciences), and immediately stored at -20 °C (Rusch *et al.*, 2007; Ng *et al.*, 2010).

[1]Sampling was performed by Jeffrey M. Hoffman and Jeffrey B. Mcquaid

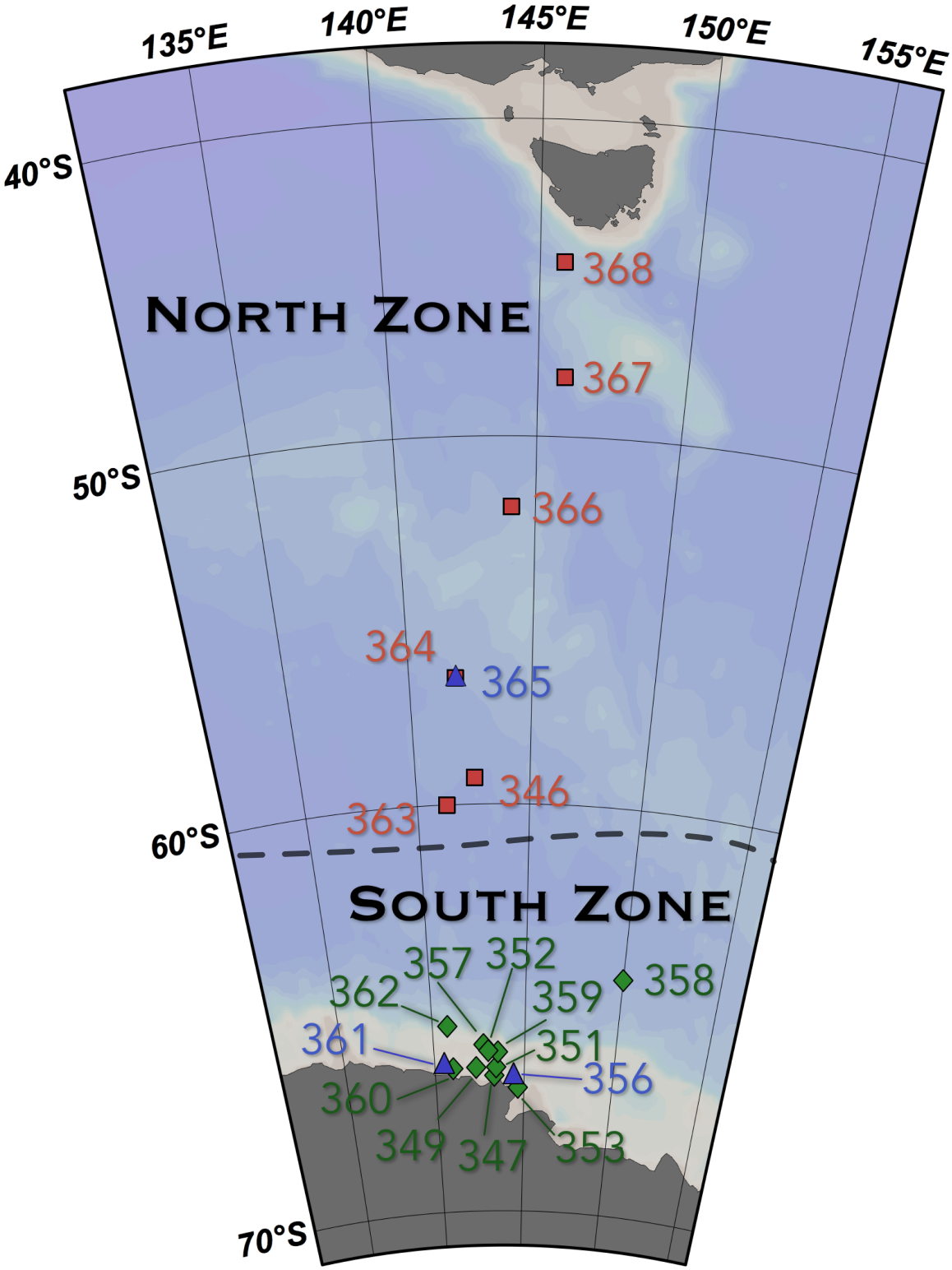

Figure 1: TODO caption here

Phylogenetic analysis of metagenomic data

Functional analysis of metagenomic data

Results

Metagenomic sequencing

Phylogenetic analysis of metagenomic data

Functional analysis of metagenomic data

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Meso-scale biogeographic drivers of planktonic diversity

Conclusions

References

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