Microbial Ecology and Biogeography

OF THE

Southern Ocean

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Acronyms

UFO Unidentified Flying Object.



Acknowledgements



Abstract

Introduction

This is a test of the acronyms: I saw a Unidentified Flying Object (UFO). It was not the first UFO I'd ever seen. In fact, I've seen 100 UFOs.

Here is some greek: µg.

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.

Summary

Introduction

Methods

Sampling and metagenomic sequencing

Sampling¹ 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 meterological data (TODO provide table). These data were used to locate the (TODO abbreviations package? PFZ) based on a surface temperature gradient of ~ 1.35 °C across a distance of 45–65 km, placing the (TODO abbreviations? PF) at approximately -59.70° of latitude, consistant with previous descriptions TODO EDITING HERE NEED SOKOLOV AND RINTOUL REF

At each station, \sim 250–560 L of seawater was pumped from \sim 1.5–2.5 m below the sea surface into drums stored at ambient temperature on deck. In the case of deep samples, \sim 225–230 L of seawater was collected opportunistically from Niskin bottles attached to a CTD (Conductivity, Temperature and Depth TODO give infor on CTD - SeaBird?) instument operated by an unrelated oceanographic project. Seawater samples were prefiltered through a 20 μm plankton net, then filtrate was captured

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

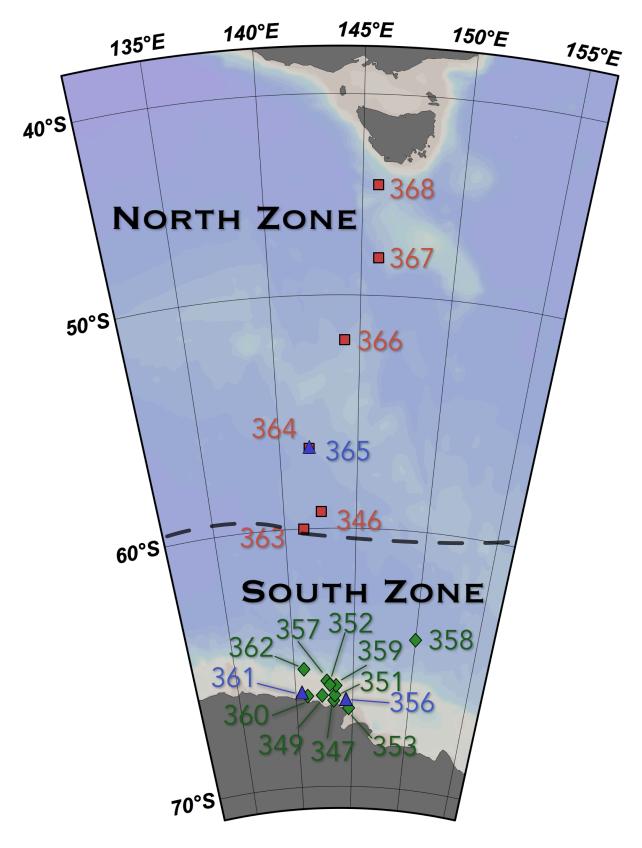


Figure 1: Sites of seawater samples used in this study. Red squares indicate surface samples from the North Zone; green diamonds samples from the South Zone; and blue triangles indicate deep samples. The dashed line gives the approximate location of the Polar Front.

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	Table 1: An important table								
Sample	Local Time	Latitude	Longitude	Water Column Depth (m)	Sample Depth (m)	Water Temperature (°C)	Salinity (PSU)	Fluorescence (µg/l)	Volume seawater filtered (L)
346	20/12/07	-59.312	142.5949	4294	2	2.9	33.75	0.25	500
347	23/12/07	-66.0213	142.738	450	2	0.6	34.2	4	250
349	27/12/07	-66.5662	142.3169	370	1.5	-1.3	34.4	2.3	250
351	28/12/07	-66.5587	143.4303	823	1.5	-0.55	34.3	1.3	500
352	29/12/07	-66.765	143.324	164	2.5	-0.75	34.3	3.1	500
353	30/12/07	-67.0521	144.6786	180	2	-1.8	34.4	0.3	500
356	03/01/08	-66.7617	144.4138	920	920	-1.89	34.69	0.1	230
357	05/01/08	-66.1719	143.0193	580	2	-0.4	34.15	2.5	500
358	09/01/08	-64.3001	150.0306	3550	2	0	33.55	0.45	500
359	12/01/08	-66.1903	143.5292	540	2	-0.24	34.21	2.5	500
360	13/01/08	-66.5817	141.0211	316	2	-0.65	34.04	6.19	500
361	14/01/08	-66.4727	140.5572	1203	1170	-1.77	34.56	0.1	225
362	19/01/08	-65.5367	140.8287	1064	2	0.7	32.2	0.5	500
363	22/01/08	-60.0001	141.3094	4473	2	3.3	33.77	0.1	500
364	23/01/08	-56.6953	141.878	3693	2	4	33.7	0.5	500
365	23/01/08	-56.6967	141.9125	3693	3693	0.48	34.69	0.1	230
366	24/01/08	-52.0233	144.1362	3180	2	7.6	33.84	0.25	500
367	25/01/08	-48.2487	145.9025	3490	2	11	34.43	0.2	500
368	26/01/08	-44.718	145.7775	3201	2	14.75	34.96	1.25	560

on sequential 3.0 μ m, 0.8 μ m and 0.1 μ m polyethersulfone membrane filters (Supor membrane disc filter; Pall Life Sciences TODO location), 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).

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

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

Meso-scale biogeographic drivers of planktonic diversity

Conclusions

References

- Lauro F. M., Demaere M. Z., Yau S., Brown M. V., Ng C., Wilkins D., Raftery M. J., Gibson J. A., Andrews-Pfannkoch C., Lewis M., Hoffman J. M., Thomas T., and Cavicchioli R. An integrative study of a meromictic lake ecosystem in Antarctica. *The ISME journal*, 5(5):879–895, 2011.
- Ng C., Demaere 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.
- 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.