MM14A-1409

# Distribution of bacterioplankton lineages within the dark ocean of the Sargasso Sea and their potential role in biogeochemical cycles


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## Overview

Marine bacterioplankton (bacteria and archaea) are recognized for their importance in global biogeochemical transformations. Studying their spatial and temporal distribution is necessary to understanding oceanic nutrient cycling.

***Table 1.*** *Selected bacterial and archaeal bacterioplankton lineages for this study and their metabolic potential.*

| | |
|---|---|
| SAR11 | Photoheterotrophy: proteorhodopsin[1,2] |
| SAR202 | Oxidation of recalcitrant organic compounds (FMNOs)[3] |
| SAR324 | Chemoautotrophy: carbon fixation (cbbL)[4] |
| Euryarchaeota | Methanogenesis (mcrA)[5], proteorhodopsin[6] |
| Thaumarchaeota | Chemoautotrophy: ammonia oxidation (amoA)[7] |

The Bermuda Atlantic Time-series site (BATS) offers an opportunity to study bacterioplankton communities with biogeochemical variables in the context of the oxygen minimum.

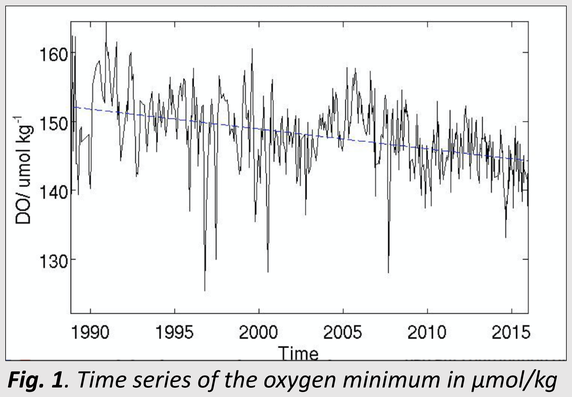



***Fig. 1****. Time series of the oxygen minimum in µmol/kg at BATS from 1989 to 2016.*

With cellular respiration by heterotrophic bacteria and archaea fueling the oxygen minimum (Fig. 2), studying the metabolic processes within this zone will contribute to our understanding of the ongoing decrease in dissolved oxygen concentrations (Fig. 1) and vertical expansion of the oxygen minimum zone at BATS.

## Methods

**1 Sampling**

CTD Rosette aboard the R/V *Atlantic Explorer*

**BATS site**
31˚40' N 64˚10"W
0-4500 m depth

July 2014 to December 2015

**2 Epifluorescent microscopy**

**DAPI stain**: total bacterioplankton

**FISH*:** SAR202

**CARD-FISH**:** SAR11, SAR324 & archaea

40 mL samples fixed with 10% formalin

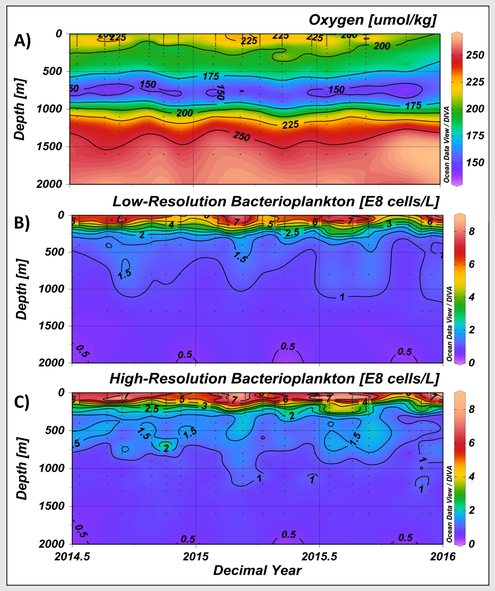
* Fluorescence *in situ* hybridization
** Catalyzed reporter deposition fluorescence *in situ* hybridization

**3 Gene analysis**

Phenol-chloroform DNA isolation method

***amoA*** & ***cbbL*** amplified by optimized PCR method

## Bacterioplankton contribute to the oxygen minimum




The distribution of total bacterioplankton was examined at high vertical resolution in the context of the low oxygen realm (Fig. 2A) revealing a subsurface maximum that negatively correlates with oxygen levels (Table 2).

***Table 2.*** *Correlation between oxygen levels and total bacterioplankton counts.*

| Depth | 0-400 m | 400-2000 m |
|---|---|---|
| r | 0.6823 | -0.6848 |
| p | <0.001 | <0.001 |
| n | 153 | 122 |

***Fig. 2****. A) Oxygen levels, B) bacterioplankton abundance at low-resolution sampling and C) bacterioplankton abundance at high-resolution sampling from Jul. 2014 to Dec. 2015.*

## Spatial and temporal distribution of select lineages

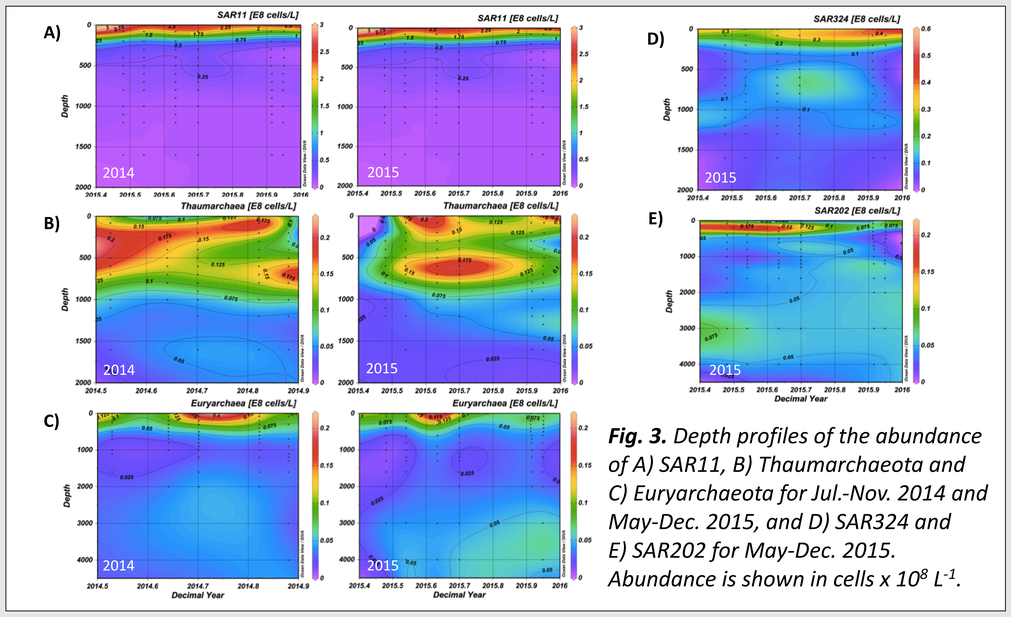



***Fig. 3.*** *Depth profiles of the abundance of A) SAR11, B) Thaumarchaeota and C) Euryarchaeota for Jul.-Nov. 2014 and May-Dec. 2015, and D) SAR324 and E) SAR202 for May-Dec. 2015. Abundance is shown in cells x $10^8$ $L^{-1}$.*

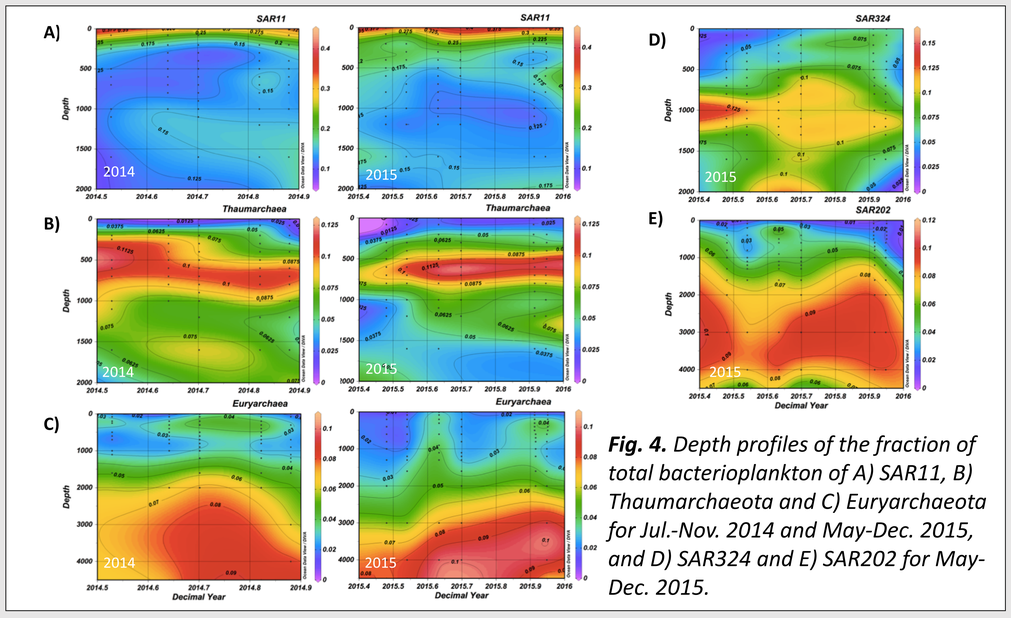



***Fig. 4.*** *Depth profiles of the fraction of total bacterioplankton of A) SAR11, B) Thaumarchaeota and C) Euryarchaeota for Jul.-Nov. 2014 and May-Dec. 2015, and D) SAR324 and E) SAR202 for May-Dec. 2015.*

## Nitrification and carbon fixation

Genes for archaeal ammonia oxidation (*amoA*: ammonia monooxygenase) and carbon fixation (*cbbL*: form I RubisCO) associated with *Thaumarchaeota* and SAR324, respectively, were investigated throughout the water column[7,8].

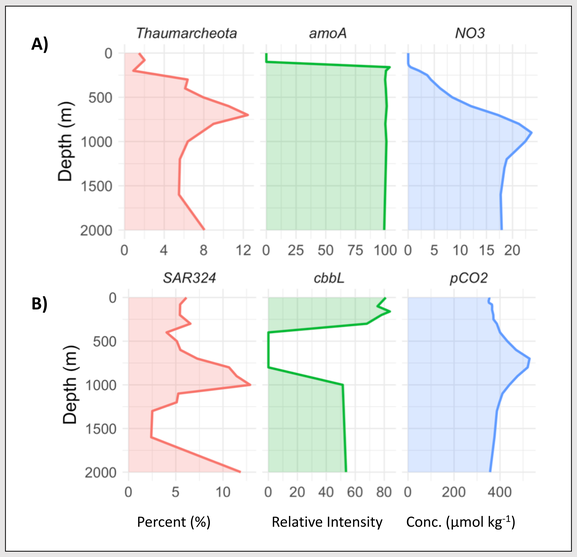



***Fig. 5****. A) Thaumarchaeota percent contribution, amoA gene intensity and nitrate concentrations and B) SAR324 percent contribution, cbbL gene intensity and pCO2 levels for Nov. 2014.*

## Conclusion

**Bacterioplankton** respiration contributes to the oxygen minimum.

**SAR11** abundance and percent contribution are highest in surface and mesophotic waters (~0-400 m).

***Thaumarchaeota*** abundance and percent contribution are highest in the upper oxycline (~400-800 m) and show a relationship with **archaeal ammonia oxidation**.

**SAR324** contributes the most to the lower oxycline (~800-1200 m) bacterioplankton community and show correlation with **carbon fixation**.

***Euryarchaeota* & SAR202** contribute the most to the deep ocean (>2000 m) bacterioplankton community.

## Future Directions

- Further *amoA* and *cbbL* depth profile analysis through qPCR.
- Illumina sequencing of 16S rRNA gene amplicons.
- Lineage abundance and diversity data will be put into the context of the biogeochemical data provided at BATS.

## Acknowledgments


We would like to acknowledge Simons Foundation International for their support through the BIOS-SCOPE award to Craig Carlson and the National Science Foundation for their support of the BATS Program at BIOS through award OCE-1258622 to Rodney Johnson. We thank REU interns Gabriel Schuler and Sarah Amiri for their help with initial data collections, and the Canadian Associates of BIOS for their support of Katelyn McLeod and Miguel Desmarais. We wish to thank the crew of the R/V Atlantic Explorer and the technicians in the BATS Program for sample collection.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