Molecular and microscopic characterization of sinking particles at the Bermuda-Atlantic Time Series Study station (BATS)

Bianca N. Cruz1, Samantha Brozak2, and Susanne Neuer1

1 School of Life Sciences, Arizona State University, Tempe, AZ
2 School of Mathematical and Statistical Sciences, Arizona State University

Background

The biological carbon pump is mediated mainly by large (>0.5mm) particles, called "marine snow" that sink out of the euphotic zone to the deep ocean (Fowler and Krause 1986). Marine snow can be comprised of aggregates of phytoplankton cells, detritus, and/or fecal matter. At BATS, while the size of sinking particles (Burkholder et al. 2015) and the plankton communities associated with bulk particle organic carbon (POC flux (Amacher et al. 2015)) have been described, the characteristics of these sinking particles is yet to be known.

The use of DNA-based methods complemented with microscopy allow for the study of the relative contribution of plankton taxa to different particle types and help elucidate their predominant methods of transport to depth, such as through direct formation of aggregates, or by grazing and formation of sinking fecal pellets.

Objectives

- Determine the different particle types that contribute to flux at different depths.
- Characterize sinking particles using microscopy.
- Describe the community associated with different sinking particle types.

Methods

Sampling

Bermuda

BATS

• "Dead" (non-fixed) and "Live" (2% formalin-fixed) polyacrylamide gels were deployed within particle interceptor trap tubes at 150 m, 200 m, and 300 m depths at the Bermuda-Atlantic Time Series Study station (BATS) (Figs. 1, 2) during cruises 2F9/H/BATS3139 and 2F11/H/BATS3319 in September 2013 and March 2014, respectively.

• Live Gel Traps (white circles) were deployed for 100 hours. The tube was then retrieved for 20 hours, and the gel was stained with DAPI and visualized using a Stereomicroscope (Zeiss Stemi 2000-C).

• Live pellets were then stained with DAPI and visualized using a Stereomicroscope (Zeiss Stemi 2000-C) to determine if the aggregated material had nucleated.

Particle flux image analyses

- The entire surface area of all gels were imaged upon trap recovery and 10 nonoverlapping images picked for subsequent determination of particle area and ellipsoids using ImageJ software.

- Particles were categorized and their organic carbon content was determined from volumes using conversion factors from Alldredge 1998 and Gonzalez and Smetacek 1994.

Microscopy

- "Dead" particles were stained with DAPI and polyacrylamide-specific stain concanavalina a then mounted onto microscope slides for visualization using epifluorescence and confocal microscopy.

DNA-based community analyses

- Bacterial taxa from individually-picked particles were determined by Illumina MiSeq of the V4 region of the 16S rRNA gene, respectively.

Contribution of different particle types to flux

- Phytoplankton aggregates dominated particle and flux volume at all depths (>80%, all fluxes).
- Fecal pellet-nucleated aggregates contributed the least (<15%) relative to phytoplankton aggregates and fecal pellets (>75%) to fluxes at all depths.
- Relative contribution of fecal pellets to flux decreased with depth.
- Live traps showed higher fluxes of all particle types compared to dead traps.

Results

Microscopic characterization of sinking aggregates

Phytodetrital aggregates

- Relatively transparent aggregates composed predominantly of Phaeocystis, Prochlorococcus, Synechococcus, and coccolithophores.
- Phytoplankton and heterotrophic bacterial aggregates are nucleated and able to sink rapidly.

Fecal pellet-nucleated aggregates

- More dense aggregates with nucleated fecal pellets that are less likely to sink rapidly.

Conclusion & Future Work

- Phytoplankton aggregates dominated particle fluxes.
- These phytoplankton aggregates are composed of a matrix of transparent, polysaccharide substances, likely transparent exopolymeric particles (TEP).
- Relative composition of particle-associated and free-living bacterial taxa differ.
- Future work will include the analysis of eukaryotic taxa within the different particle types.
- This work is part of a larger effort to study picophytoplankton-bacteria interactions and their role in aggregation.

References