Variability in North Atlantic marine microbial communities in relation to patterns of nutrient availability, nitrogen fixation, and net community production

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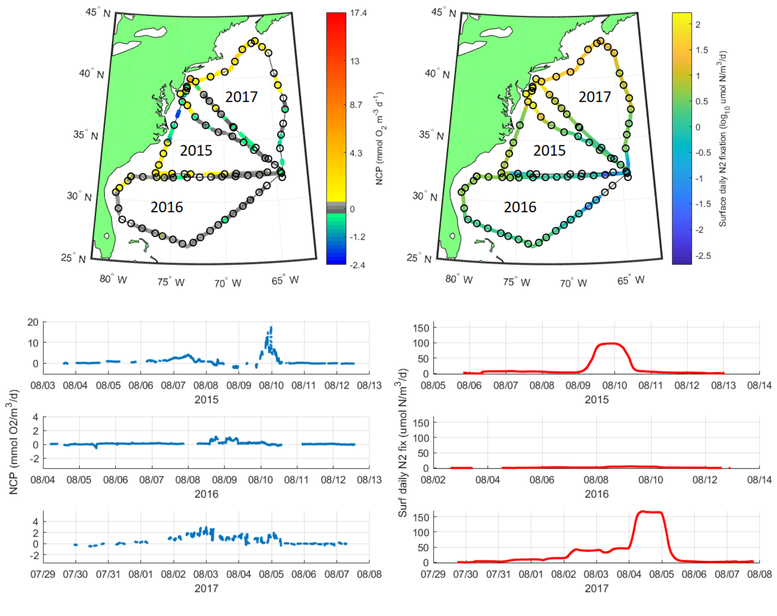
Abstract

Nutrient availability to marine microorganisms moderates the productivity of ocean ecosystems. Assessing the response of microplankton communities across diverse marine biomes to different nutrient inputs will improve our understanding of microbially-driven cycling of carbon and nutrients in the surface oceans. From samples collected in August 2015, 2016, and 2017 across the Western North Atlantic, we determined quantitative abundances of eukaryotic and prokaryotic microplankton using an internal standard rRNA amplicon sequencing approach. We examine relationships between microplankton community structure and nutrient concentrations, daily nitrogen fixation rates, net community production (NCP) rates, and measured respiration. We find that eukaryotic diversity is negatively related to NCP, N_2 fixation, phosphate, and community respiration. Productive coastal samples with high observed nitrogen fixation rates (>100 umol N/m^3/d) are dominated by Chrysophytes, *Gonyaulacales*, and *Aureococcus Anophagefferens.* High nitrogen fixation rates were also strongly associated with the abundance of Cryptophytes. These preliminary findings provide intriguing insights into how marine microbial communities, productivity, and nutrient cycling may be linked in this region.

Methods

- Expeditions in August 2015, 2016, and 2017 in W. North Atlantic.
- NCP calculated from continuous O_2/Ar measurements via EIMS method (Cassar et al., 2009) (Figure 1). Data represent preliminary NCP rates, not yet corrected for vertical O_2/Ar fluxes.
- Concurrent measurements of nitrogen fixation rates via flowthrough incubation acetylene reduction (FARACAS) (Cassar et al., 2018).
- Quantitative 16S/18S rRNA amplicon sequencing (Satinsky et al., 2013; Lin et al., in review) to determine phytoplankton community structure.
- Community and particle-associated (<3um) respiration assays (oxygen bottle incubations).
- Discrete macronutrients/trace metal sampling in 2016, 2017.
- Associations between quantitative prokaryotic/eukaryotic abundances and NCP, N_2 fixation, and macronutrients examined using partial-least-squares (PLS) regression analysis.

Figure 1



Preliminary results

- Elevated NCP, N_2 fixation rates, and Chlorophyll-a observed in the Mid-Atlantic Bight, off coastal New England, Nova Scotia (Figure 1).
- More diverse microbial communities observed in less-productive, low-phosphate waters with low N_2 fixation and respiration rates.
- Coastal stations with peak productivity dominated by *Aureococcus anophagefferens* (*Pelagomonadales*), Chrysophytes, *Gonyaulacales*, and *Planctomycetes* (Figure 2).
- Higher abundances of Dinoflagellates, Syndiniales, SAR11, *Prochlorococcus*, SAR86, and *Rhodospirillales* in open-ocean samples (Figure 2).
- Eukaryotic Shannon's H diversity inversely related to NCP (Pearson: -0.64, p<0.001; Spearman: -0.21, p<0.03) and N_2 fixation (Pearson: -0.73, p<0.001; Spearman: -0.22, p<0.05) (Figure 3).
- PLS regression reveals nitrogen fixation and NCP strongly associated with Chrysophytes, *Aureococcus,* and several Cryptophyte clades.

Figure 2

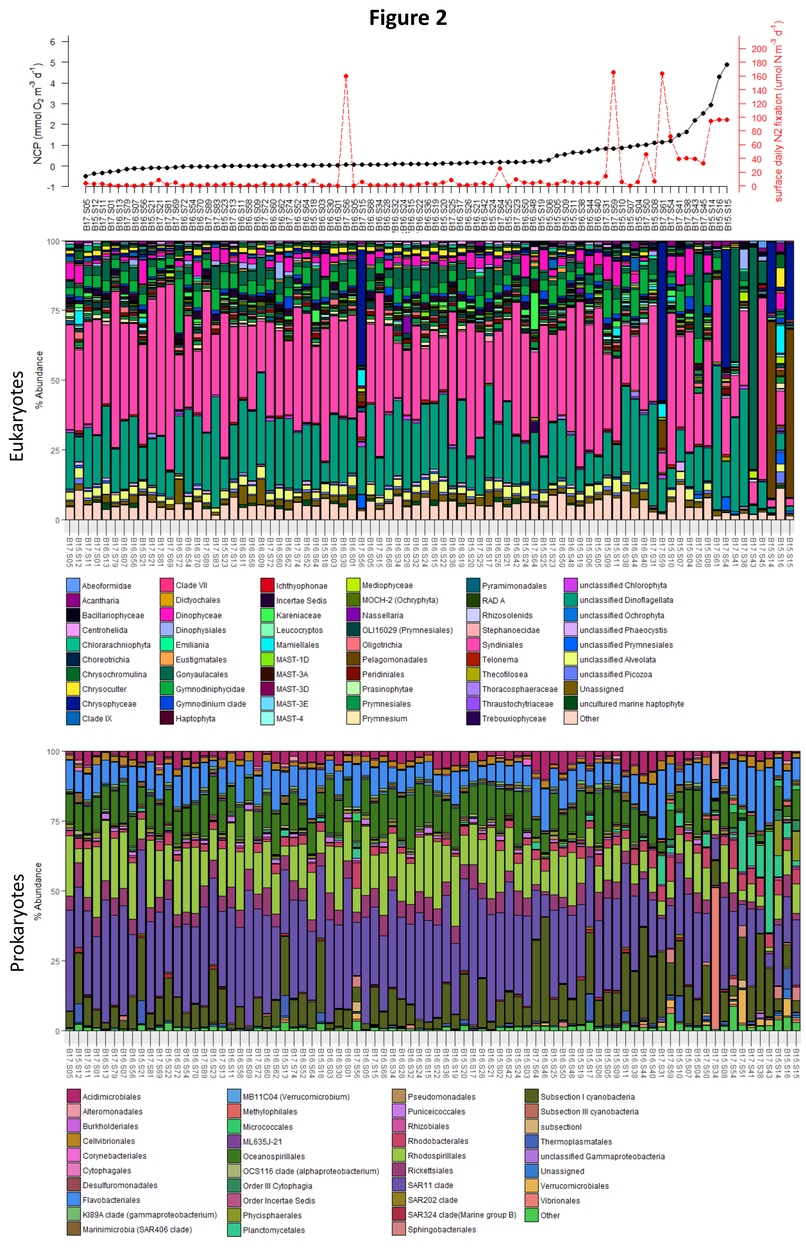
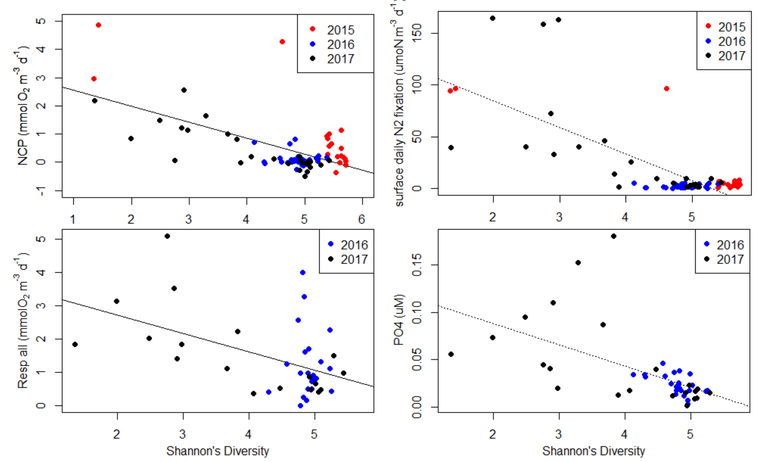


Figure 3



Conclusions

- Markedly different community structure at stations with low versus high measured NCP.
- Stations with high productivity and Chl-a often show low eukaryotic diversity, are dominated by brown-tide-forming algae: Chrysophytes and *Aureococcus anophagefferens*.
- Stations with high eukaryotic diversity consistently exhibit low NCP and N_2 fixation rates.
- Such productivity-diversity patterns suggest competitive exclusion processes may be important to driving eukaryotic community structure in this region.
- Nitrogen fixation rates associated with abundances of some Cryptophyte clades. This may indicate a response of these taxa to diazotrophic N inputs, or reflect ecological interactions between these algal clades and N-fixers.

Future Directions

- Examination of relationships between specific prokaryotic/eukaryotic taxa and nutrient concentrations using partial-least-squares (PLS) regression analysis.
- Expansion of analyses to identify relationships between sampled surface trace metal concentrations and microplankton community structure.
- Network analyses to identify clusters of co-occurring prokaryotic/eukaryotic microplankton taxa across the studied region.

References

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