

# Diversity and variability of two core taxa of the coastal marine microbiome

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## Introduction

### Cyanobacteria:

- ancient taxa of photosynthetic organisms present in most inland water
- critical role as the base of the food web and driver of biogeochemical cycles



### SAR11:

- group of small, carbon-oxidizing bacteria that have complex biochemical interactions with other plankton
- The most abundant taxa in marine systems



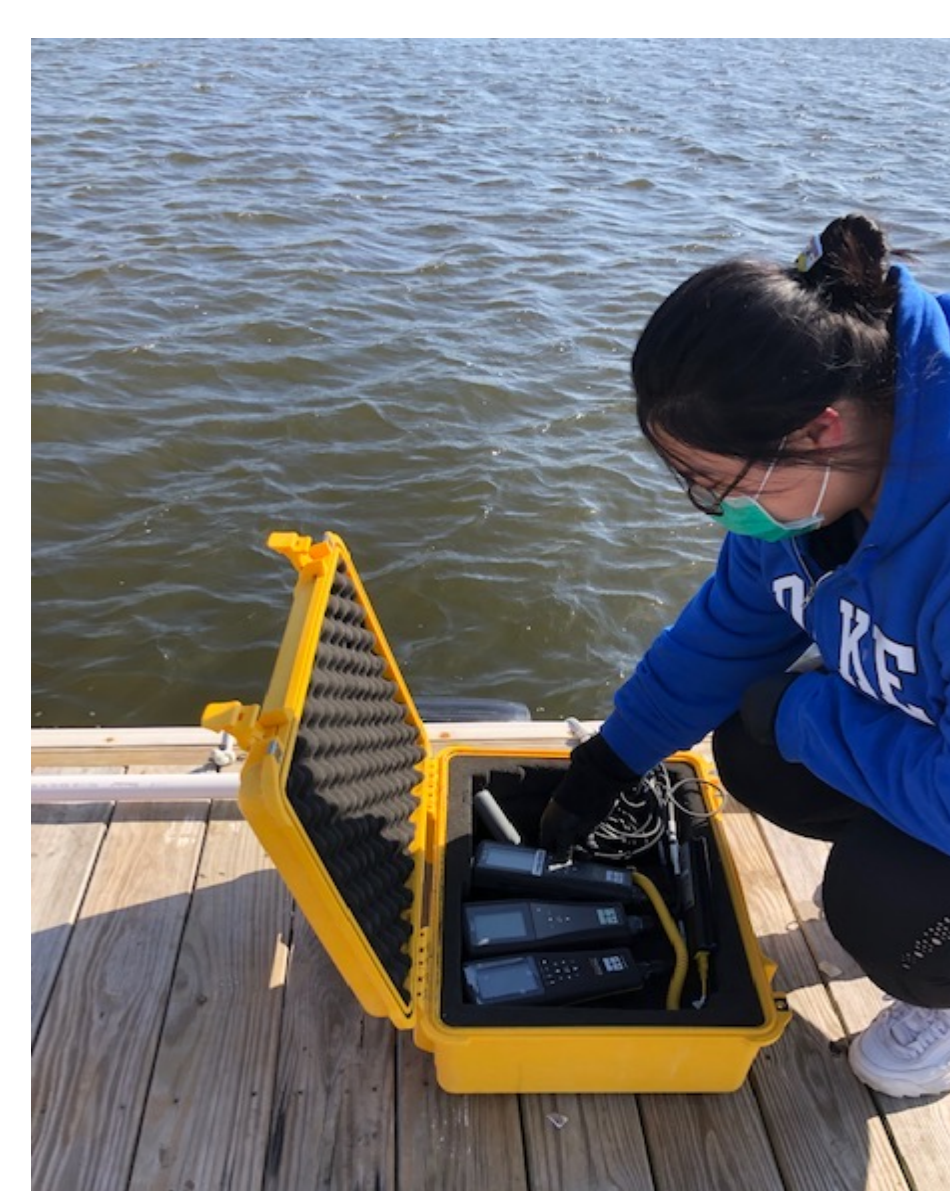
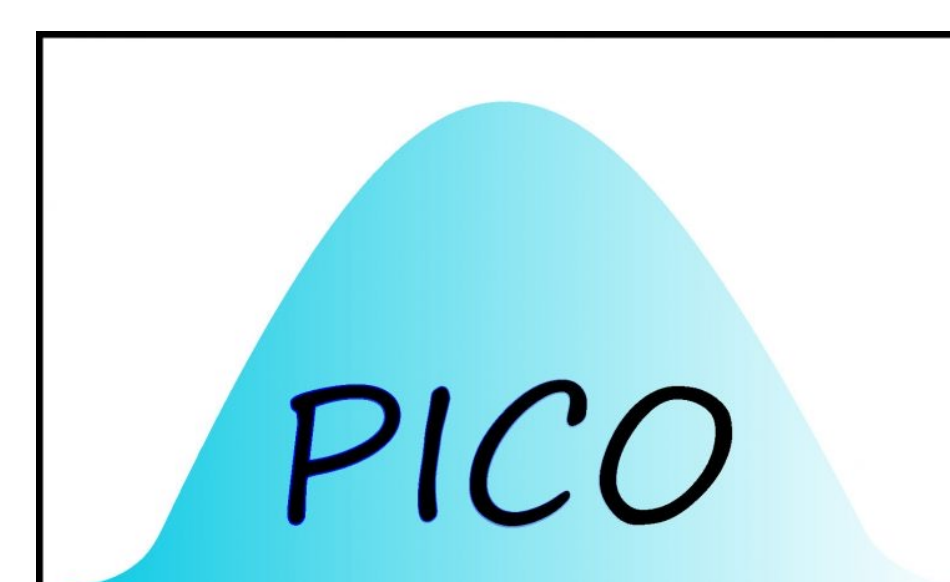
## Objectives

- Determine the level of 'microdiversity' within two major taxa of marine microbes
- Describe the temporal variability of microdiversity over a 3 year period at a coastal ocean site near the Duke Marine Lab (Beaufort, NC); compare & contrast patterns for cyanobacteria and SAR11 taxa
- Investigate potential environmental drivers (e.g. temperature, salinity, etc.) of the observed seasonal and episodic changes

## Major Findings

- **Cyanobacteria oligotypes follow strong seasonal patterns**
- **SAR11 Oligotypes show abrupt changes in dominant type, but less seasonal trends**
- **Temperature and salinity are the major environmental variables contributing to variance in the microbial community for both OTUs and oligotypes.**

## Methods



Environmental variables measured in PICO Sampling include:

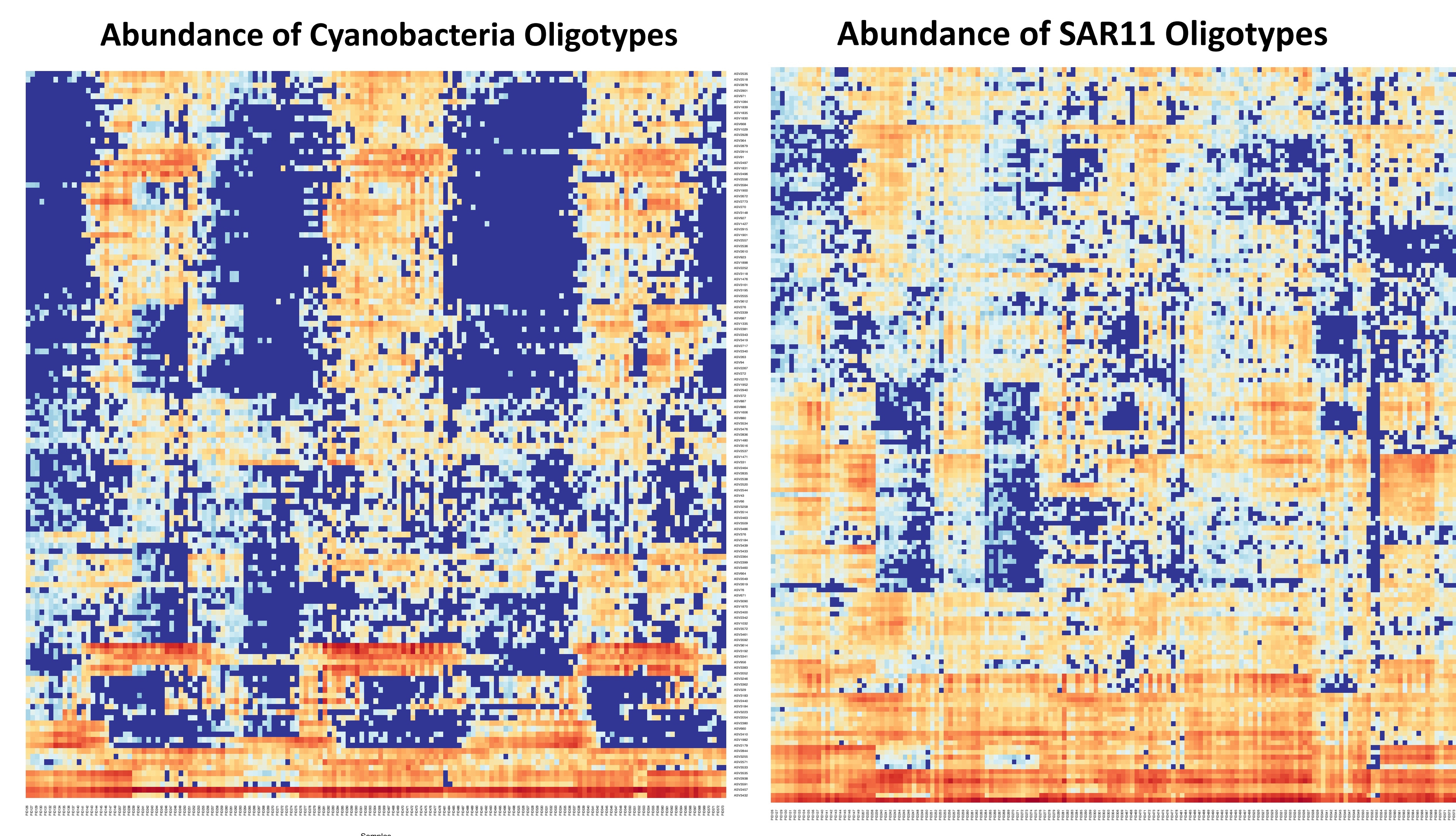
- Temperature; pH; oxygen; dissolved inorganic carbon; salinity, ammonium
- Chlorophyll; total Bacteria;
- Photosynthesis, photosynthetic Efficiency, respiration

## Future Work

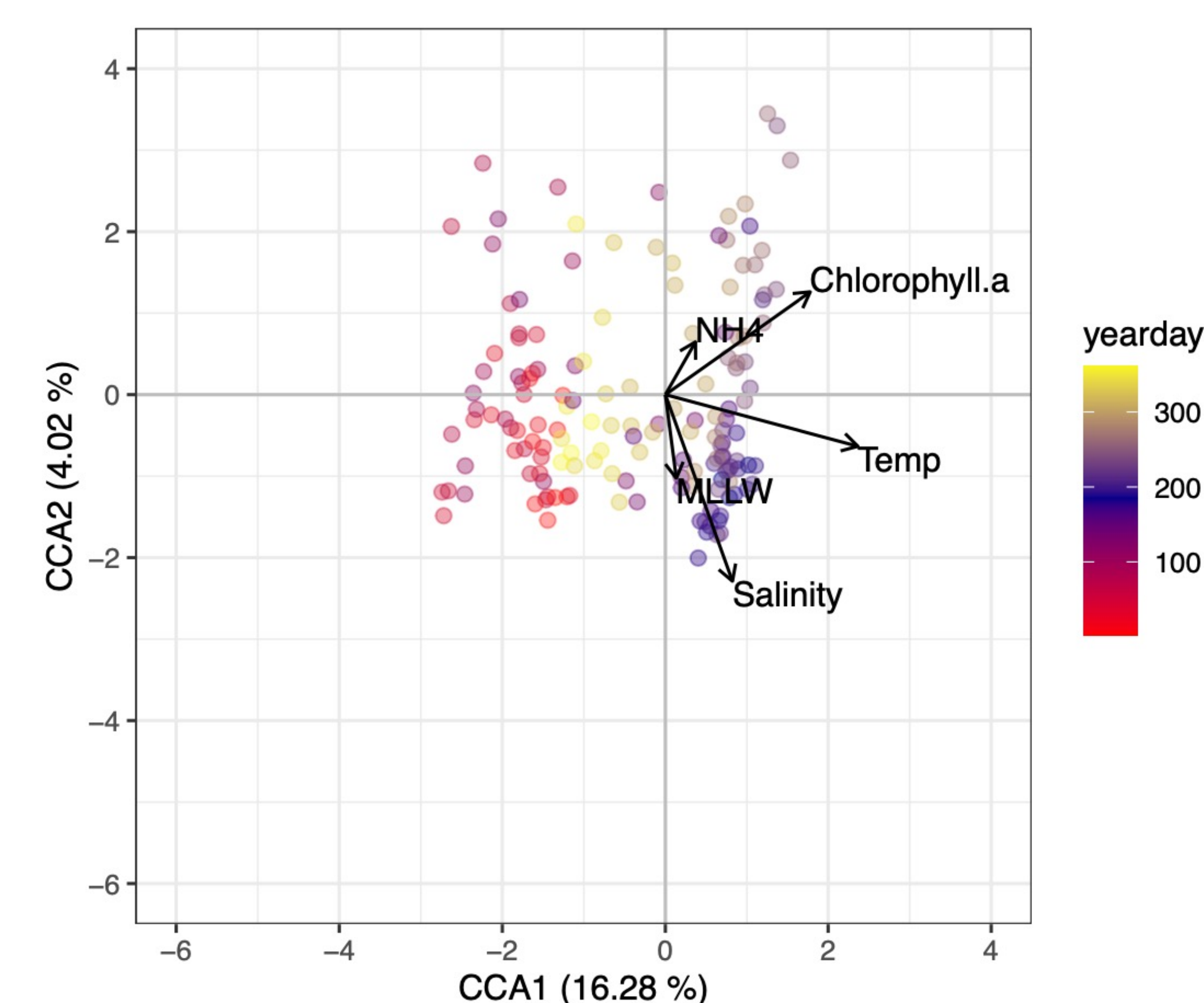
Isolation (domestication) of dominant *Synechococcus* (Cyanobacteria) taxa; genomes (and metagenomes from environmental sampling) will be used to determine relationships between environment and taxa success

## Results

Patterns over 3-year period (2011-2013)



**Figure 1.** (Left) Heatmap of the  $\log_2(\text{absolute abundance}+1)$  for the top 130 Cyanobacteria oligotypes with the highest mean absolute abundance from 2011-2013. (Right) Heatmap of the  $\log_2(\text{absolute abundance}+1)$  for the top 154 SAR11 oligotypes with the highest mean absolute abundance from 2011-2013.



**Figure 2.** Canonical correspondence analysis (CCA) biplot for cyanobacterial OTUs. CCA relates community composition to environmental variables for each sample. The percent of variation in the microbial community explained by each axis is indicated in parentheses after the axis label. Environmental variables are represented by vectors, including temperature, salinity, chlorophyll a, and ammonium ( $\text{NH}_4$ ). Each circle represents the microbial community composition at a specific time point, and the color gradient indicates the year day.