C-MORE

BLOOM Ecological **R**econnaisance (BLOOMER / KM0715)

Preliminary Cruise Report

Zehr Lab

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Personnel:

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We collected samples, performed experiments and participated in group experiments during the R/V Kilo Moana cruise. We also performed flow cytometry, and quantitative PCR on board. Samples were preserved from depth profiles for DNA and RNA, and samples were concentrated and preserved for flow cytometry.

Our objectives were to:

1. Determine the distribution of major groups of diazotrophs and nitrate utilizing cyanobacteria using molecular techniques
2. Attempt cultivation of major groups of diazotrophs, including heterotrophs and diatoms
3. Examine the the diel cycle of DNA compaction in unicellular diazotrophs
4. Collect metagenomic/metatranscriptomic samples for diazotrophic populations

Samples collected:

DNA samples were collected from stations 5, 9, 14, 18, 19, 10, 20, 21, 22, and 23.

RNA samples were collected from stations 5, 14, 19, and 24.

Samples for flow cytometry were collected and concentrated from stations 5, 9, 14, 18, 19, 20, 21, 22, 23, and 24.
Samples for analysis of diel cycle of DNA compaction in Crocosphaera were collected from stations 5 and 19.

Samples were sorted by FCM for Crocosphaera and for Prochlorococcus for genetic analyses. Samples were sorted for Group A unicellular cyanobacteria from Stations 5 and 9, for Prochlorococcus from Station 9, and for Crocosphaera from Station 14.

Concentrated samples were analyzed by quantitative PCR on board for Group A and B unicellular diazotrophic cyanobacteria from depth profiles at Stations 5, 9, 14, 18 and 19.

Experiments performed:

1. RNA diel experiments were performed with water from stations 5, 14, 19.
2. Cellular localization of N-15 uptake by unicellular and other diazotrophs, in conjunction with bulk N-15 experiment with Letelier/White group were performed at stations 5 and 19.
3. Effect of salinity gradient on growth of unicellular diazotrophs (preliminary experiment)
4. Participation in mixing experiment led by Letelier/White.

Summary of analyses performed and planned

We will analyze the DNA and RNA samples for abundance of the major groups of nitrogen fixing cyanobacteria. We also have results available for the depth profiles that were run on board for the Group A and B unicellular cyanobacteria from selected stations. For stations at which we ran diel nitrogenase gene expression assays, we will be able to identify which groups of unicellular cyanobacteria were likely to be active in nitrogen fixation.

Our cellular localization by nanoSIMS experiments, will be analyzed with Victoria Orphan. We hope to ascertain that the Group A unicellular cyanobacteria incorporate N from N_2, that they do it during the light, and that they fix CO_2.

We will also be analyzing our samples for cyanobacterial nitrate reductase to characterize the phylogenetic composition of the *Synechococcus* populations. This will be particularly interesting from the mixing experiments, and will be analyzed by Ryan Paerl.