Synopsis
SINC 11, October 5-7

Participants: R. Sterner, H. Carrick, S. Brovold, C. Small, B. Scott, B. Beall

General

New station this cruise, UWM (Upper Western Midlake), 47.5 N, 90.5 W.

First cruise for capturing digital images of sonar trace for more precise information on local topography and subsurface structure at multicore sites.

Environmental conditions

Sunny and warm for October. Waves in the calm-2' range for the entire cruise. Bumpiest on W AM. Surface temps 9.5 C at all stations. Distinct and relatively shallow DCM per the chl fluorescence and transmissometry.

Water chemistry

CD-1, mid-day Oct 5. Surface temperature = ~9.5C. Sampled depths (5, 10, 15, 20, 30, 80, 150, and 245m) for standard water chemistry parameters.

WM, mid-day Oct 6 Surface temperature = ~9.5C. Sampled modified in situ bottle array depths (2, 5, 10, 20, 30, 40, 60, 90, 120, 155m). High resolution depth sampling done for TP, NO3, NH4, TDP, NO3-isotope natural abundance, and chlorophyll by addition of depths (1, 3, 4, 7, 12, 15, 25, 35, 50, 70, 80, 100, and 110m).

CTD cast also done at UWM and STE-C.

^{14}C production, nitrification.

At site WM did standard, JGOFS based primary production in situ array with modified depths and bottle numbers. Began water collection at 12:21am and bottles were in the lake by 5:15am. Nitrification using Hicks method done at all depths. Contents of one bottle lost (155m dark Primary Production).

^{15}N nitrification measurements

Two bottles per depth in bottle array using same procedure as previous array experiments using 250uL of 40.38uM Ammonium 15N Chloride stock per bottle. We also added two light bottles with 15N-NH4 (in addition to the standard two dark bottles) in cages at depths 2, 5, 10, 20, 30, 40, 60 m to test for a decrease in nitrification rates when algae are competing for NH4.

On deck experiment done to examine nitrification response to NH4 concentration gradient for two depths; epi (5m) and hypolimnion (155m), and 8 concentrations of NH4 ranging from 0.013uM to 0.505uM.

Bottom sampling

Multicore used at CD-1, UWM, WM, and STE-C. Eight cores (2 per site) given to Katsev for oxygen profiling. Six other cores (less UWM) will be incubated for MIMS at St. Paul using core tops new last cruise.

Surficial sediments collected with Ponar at Grab #5, #6, #9, and #10.

Upon discussing with Jason Agnich, we determined that we could begin to save Print Screen image captures of the sonar information of Multicore sites. This provides high accuracy in location of core and potentially provides some information on whether cores are being taken in or out of donut rings on bottom.

Photographed all cores. Files archived on Netfiles under Photos.

Genetics
Samples from nucleic acid extraction were collected from near-surface and near-bottom depths at CD-1 (2×4 L filtered from 5m and 2×4 L from 245m) and WM (2×4 L filtered from 20m and 2×4 L from 155m). Samples were flash-frozen in liquid nitrogen before transport back to Bowling Green.

Flow cytometry
Triplicate samples from eight depths at CD-1 (5, 10, 15, 20, 30, 80, 150, 245 m) and ten depths at WM (2, 5, 10, 20, 30, 40, 60, 90, 120, 155 m) were preserved for flow cytometry (150 uL 10% formaldehyde added to 1350 uL water, incubated in dark 30 minutes) and flash-frozen in liquid nitrogen for transport and subsequent analysis at BGSU.

Fluorescence *in situ* hybridization
Samples for FISH analysis were prepared from four depths at CD-1(10, 20, 30, and 245m) and four depths at WM (5m, 20m, 60m, and 155m) as well as sediment overlying water from both sites. Whole water samples were fixed with formalin (1% v/v final concentration), then filtered through a 5.0µm membrane filter, then a 0.2 µm membrane filter. Both filter types were retained for subsequent FISH analysis back at BGSU.

Copper chelation experiments
Planned but not run due to lacking a regent.

Alternative phosphorus metabolism gene expression experiment
A short-term (~48h) incubation experiment was done to examine the phosphate-dependent expression of a suite of alternative phosphorus metabolism genes in picocyanobacteria. A 4L whole water sample was spiked with 20 µM PO_4 (final conc.),

with a parallel unamended control, and incubated in the flowing water incubator from 1250h on 5 Oct to 1200h on 7 Oct. Seston was collected on 0.2-µm pore-sized cartridge filters (Sterivex™) and flash-frozen in liquid nitrogen for RNA extraction and analysis at BGSU.

Microplankton enumeration

The abundance and biomass of microplankton was measured to evaluate the possible role abundance, growth and grazing may have on nutrient cycling in the water column of Lake Superior (Hunter Carrick). Samples were collected from the routine depth distribution profiles at both offshore sites in the lake (5, 15, 20, 30, 80, 150, and 245m depths at CD-1, and 5, 10. 20. 30. 40. 90, and 155m depths at WM). Subsamples were drawn from Niskin bottles and subsequently preserved with glutaraldehype (final conc 1%) for pico/nanoplankton and microplankton enumeration (both hetero- and autotrophs). These samples were immediately refrigerated, and microscope slides were prepared on shipboard within 24-hour of collection (Carrick and Schelske 1997).

Growth and Grazing Experiments

Whole water (4L each sample) was drawn from the surface mixed layer at both stations (15m at CDI and 20m at WM) and the hypolimnion (150 at CD1 and 155m at WM) in order to run growth-grazing experiments (Hunter Carrick). Duplicate bottles containing raw lake water were either spiked with the antibiotic ampicillin (i.e., arrest cytokinesis in most cyanobacteria and some bacterial populations) or left untouched (controls). Experiments were carried out on board at ambient light and temperature conditions for 24 hours. Subsamples were collected from all bottles, preserved (1% glutaraldehyde) and subsequently enumerated to estimate both growth and grazing loss rates on key prokaryotic populations.

NH4 Regeneration Experiment

Experiment run on water from 20m and 155m depths. Two replicates x light/dark x <2um, <20um, whole water, and whole water + zoops. (32 bottles). 550 mL samples were spiked with 750uL of 1495.2uM $^{15}NH_4Cl$, then split into 2 light and 2 dark replicates of 125mLs each. The 20m samples were incubated for 24 hours in the on-deck incubator w/1 layer of shade cloth for the light bottles and a black cloth bag for the dark bottles. The 155m samples were incubated in the fridge w/ dark bottles placed in a black cloth bag and the light bottles placed on the shelf. Samples were filter sterilized using 0.2um syringe filters rinsed with sample prior to collecting a sample.