

R/V Atlantic Explorer 1910 “Zooplankton Diel Rhythms”
Cruise Report

May 20-23rd, 2019

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“Collaborative Research: Diel physiological and vertical migratory rhythms in a tropical oceanic copepod”

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2. Background

The diel vertical migration (DVM) of zooplankton and fish across hundreds of meters between shallow and deep waters is a predominant pattern in pelagic ecosystems. DVM has consequences for biogeochemical cycling as it moves a substantial portion of surface fixed carbon and nitrogen directly to depth (e.g., 15 to 40 % of the total global organic carbon export). Estimates and predictive understanding of these fluxes are, however, poorly constrained at present. New observations have shown that one source of uncertainty is due to the assumption that metabolic rates and processes do not vary over the course of the day, except based on changes in temperature and oxygen availability. Rates are, however, driven also by differences in feeding, swimming behavior, and underlying circadian cycles. The proposed research will characterize the metabolic consequences of daily physiological rhythms and DVM for a model zooplankton species, the abundant subtropical copepod *Pleuromamma xiphias*. Flux processes (oxygen consumption, production of ammonium and fecal pellet production) will be interrogated using directed experiments testing the effects of temperature, feeding and circadian cycle. Circadian cycling will further be examined using transcriptomic and proteomic profiling. These experiments will be related to field samples taken at 6-h intervals over the course of the diel migration using an integrated suite of molecular and organismal metrics. Combined, these analyses will provide an understanding of which metabolic pathways and associated flux products vary in relation to particular environmental variables (food, light cycle, temperature). The metabolic data will then be integrated into abundance estimates from archived depth-stratified tows to achieve improved calculations of particulate organic carbon, nitrogen and respiratory active flux.

3. Cruise Objectives

The focus of this cruise was to characterize the daily changes in metabolism of the DVM species *P. xiphias* using both field and experimental approaches. Specifically, we wanted to characterize the contribution of circadian patterns and migration to variations in metabolism using integrated organismal, enzymatic, transcriptomic and proteomic approaches.

We planned two major experimental types:

- 1) A time series experiment in which we collected individuals from their natural location (deep during the day and from the surface during the night) over a daily cycle. Individuals were measured for organismal (oxygen consumption, fecal pellet production and ammonium excretion) as well as transcriptomic and proteomic physiological markers.

- 2) A circadian experiment in which individuals were collected at one time point, then measured or harvested over a two day period to observe underlying rhythmicity in organismal level physiology (oxygen consumption as well as urea, ammonium, DOC and DOM excretion) as well as transcriptomic and proteomic signatures.

PI Noyes, who is responsible for the outreach component of the project, focused on building images and experiences that will be part of the learning module and engaging social media. She also mentored a high school teacher who is developing a course on oceanography and a local high school student with interests in oceanography aboard the cruise.

The cruise leveraged ongoing collaborations with the BIOSSCOPE program (funded by Simons Foundation International) to characterize water column ecology and chemistry. The specific project objective of this collaboration was to measure the hydrographic concentrations of urea, ammonium, DOC and compound specific high resolution DOM via CTD during the day and night.

The cruise was also augmented by the participation of Susanne Neuer's group who is interested in zooplankton contributions to aggregation of marine picoplankton (tangential to OCE-1658527). Their project associated objective was to characterize the diel cycle in fecal pellets and their composition.

4. Cruise narrative

Amy Maas

MONDAY May 20: HYDRO

0930: Pre-departure, we discovered a problem with the Seabird/MOC unit. It was eventually found that the seabird system was left on overnight, resulting in a short in the Seabird 9 that was connected to the MOC. We hooked the MOC to the spare Seabird 9 and reset the calibrations, resulting in a functional MOC system.

1240: Arrive on station: Test CTD cast (C001). Susanne sampled for DNA and chl-a. Brittany ran a set of BIOSSCOPE and ammonium samples to get a sense of how the protocol works.

1400: MOC Test (MOC_001): Electronics and mechanical components worked! Not enough volume was filtering through the nets; we found we needed to not pull in the winch at all for a while so that the vertical velocity stayed slow. Unfortunately, sample capture failed due to tangled nets. Fortunately, we happened to collect an *Arietellus* for an ancillary project. A photo was taken on Neuer's microscope, and the individual was flash frozen in BIOS dry shipper.

1830: MOC Test (MOC_002): Removed all MOCNESS nets except 3 – one open, one with a closing cod end, and one open in an attempt to prevent tangles. Success. Organisms still came up in low numbers looking fairly damaged, but the tow was only to 150m, and it was not yet dark, so there is possibly not an issue.

2100: Reeve net (R_001): Moved the night cast later because it was not yet dark. Decided on using the Reeve which required finding extra shackles, lines and weights. All good. Got enough *P. xiphias* to sample for Proteomics (P), Transcriptomics (T), half of Enzymes (E) and Respiration (R) for TS1 from this tow. Started picking circadian organisms.

2200: Reeve (R_002): More *P. xiphias* for the circadian experiment (C1). Everyone started getting good at ID!

2300: Reeve (R_003): More circadian. Started putting animals into the Circadian experiment setup

2400: Reeve (R_004): Used this net (which came aboard at 0100) as the mid-night time point. Got organisms for P,T, E and R for TS2 from this tow.

TUESDAY May 21: HYDRO then NE

0140: Took down TS1. Only a few poops from these experiments.

0215: Set up TS2 using R_004 organisms

0400: BIOSCOPE CTD (C002) cast (1000 m)

0530: TS2 broken down. There were way more poops than TS1! (Interesting).

0600: Breakdown of Circadian Experiment C1_T1. The positive pressure filtering takes FOREVER. Organisms had to be removed and flash frozen first. To improve results next time, we should HCl the transfer pipette to limit contamination. Getting a decent protocol. Eventually (1030) the DOC was acidified by Brittany and we subsampled for DOM.

Deep MOC 0600 (MOC_003): Filtered 600-400m with ~400 flow counts (more than 1000 m³ per 100 m). The nets did not tangle, but organisms still came up looking pretty rough. Some actively swimming *P. xiphias*. Separated by gender and placed P,T, ½ of E and ½ R for TS3 from this tow. R set up at 8:50.

1000: Tropical Storm Andrea is headed directly towards HYDRO. We have chosen to relocate to the lee of Bermuda to avoid the worst of it. Moving now so that Brittany's daytime CTDs are in the same place for tonight and tomorrow.

1100: 200m CTD (C003) for filtered seawater. Shannon took large volume POC in the upper water column. The chl-a profile was very different: less pronounced, more vertically spread.

1200: Breakdown and sampling of C1_T2

1300: Deep MOC (MOC_004). Total success. Fully sampled TS4 and preserved a bunch of extra *P. xiphias* as backup. The remainder of the cod end was fixed in RNA later for Leo.

Comment from Brittany – the ammonium from C1_T1 was measurable. Yay!

Tropical Storm Andrea was named and is headed directly to HYDRO. Captain said that if we stay put we will not be able to sample tomorrow. Brittany needs BOTH her CTDs in the same place to make it worthwhile. So. **Steaming to new waystation to avoid the storm.** This delays our CTD but sets us up well for tomorrow. Did some extra tie down to be sure everyone is ready.

1700: Deep CTD (C004) cast (1000 m)

1810: Sampled C1_T3. One copepod had died; did NOT sample water from that vial.

1845: Broke down and sampled TS4. No poops.

2100: Two Reeves (R_005, R_006). Great yield for TS5. Preserved four fish from nets (R_005 and R_006) for Robbie Smith in ethanol.

0000 Break down and sampling of C1_T4

WEDNESDAY May 22, 2019: NE then S Bermuda

0100: Two Reeves (R_007, R_008). Great yield for TS6 from R_007. Misc. large migrators for Susanne's fecal pellet experiments were taken from both nets. Remainder of the cod ends from both tows were used for fecal pellet production experiments for Shannon.

0600: Break down and sampling of C1_T5

0730: Deep MOC (MOC_005) had a failure of electronics. Although the motor and net bar response were working, both the pressure and angle sensors failed to register. Chose to run the MOC blind of depth based on prior notes of MWO and flow counts. Successfully collected sample at depth. Discovered at the end of the tow that the difficulty was that the system was looking to the incorrect directory for its calibration file. This has been corrected for future tows. Collected sufficient animals for TS7. **Some of these samples may have accidentally been labeled as TS6; we think that they have the time stamp which will help us with disambiguation. The T&E samples went into cane 2***

1100: CTD to 790 (C005). Water for Susanne Neuer and bottles from the DCM for filtering. Water is being put into bottles for C2.

1200: Break down and sampling of C1_T6

1300: Break down and sampling of TS7

1330: MOCNESS (MOC_006) The Seabird 11 was still connected to the CTD, and it took us a moment to realize. We figured it out then, had to re-cock the nets. Jillon labeled the motor with a note about which way to rotate. Tow a success. Set up TS8. Susanne used some of the deep bugs (*Euphausiids* and some *P. xiphias*).

1700: CTD to 1000m (C006)

1800: Break down and sampling of C1_T7

1910: Break down and sampling of TS8

2100: Reeve (R_009) in the water. Sea conditions deteriorated and there was a lot of heave. Captain said that we would not be able to deploy again, maybe for some time. **We made the decision to transit back to HYDRO where we think there will be better weather.** We had sufficient animals from the tow to fully populate TS9 with a few extra tubes. Female dominated. We decided that since we don't know what the sea state or the *P. xiphias* abundance will be at HYDRO, we will use this tow to populate the circadian (C2) experiment as well. Looks like we will have at least 5 females per time point per P or T. Put 14 extra females into cryo for Brook for testing.

2250: Set up respirations for TS9

0000: Broke down and sampled the final C1 time point (C1_T8)

0200: Reeve (R_010) Tow not at HYDRO; station chosen was south Bermuda

0300: CTD (C007) for aggregate experiment

0600: Break down and sampling of C2_T1

0700: MOC (MOC_007). Not hugely abundant, but sufficient for our purposes.

1100: CTD (C008) – POC for Shannon.

1200: Relocate to deeper water in support of the MOCNESS. Break down and sampling of C2_T2

1300: Deploy MOC (MOC_008). The instrument tripped oddly – once we fired a net the angle went to 15 degrees, and nothing we could do changed it. When we tripped the next net (400m) there was no net response. We then tripped everything to try and make sure we would not break any nets on the way up. The closing cod end had a small catch but it looked to be midwater organisms (krill, cyclothone and *P. xiphias*). We used the *P. xiphias* in our TS12 respirations and preserved some, but I don't feel certain of the depth from which they came (nominally 600-400 m).

1830: Pick up pilot

1900: AE docked at St. George's

5. Equipment configuration

Amy Maas & Leocadio Blanco-Bercial

5.1. Deck Configuration

Main instrumentation for the cruise was the CTD rosette (the standard for the RV Atlantic Explorer), Reeve net, and the MOCNESS equipped with the SIO electronics. Both the CTD and the CTD rosette operate a SeaBird 9, connected to the same 11 deck box. A tucker trawl (1 m) was also brought onboard, but not used.

The CTD/rosette was housed in the CTD garage and run from the D5 Winch off the Starboard side. It was on tracks and was pulled back into the CTD garage when conditions were too hot or sea state was poor; otherwise it was sampled directly off the deck.

The MOCNESS was positioned on the center of the aft deck. A block was placed hanging from the braided line, as the existing blocks were not suitable for conductive cable. There was a clean, metal van on the forward port side of the deck, but this did not limit mobility. A black crate was positioned under the crane holding back-up parts and tools for the MOCNESS. The Reeve net and its two cod ends were also stored here. Two blue barrels were placed on the port side of the deck to hold the cod ends when they were attached to the net but not being deployed in order to prevent them from rolling.

The MOCNESS was deployed on a 0.322 conducting cable off of a D7 winch. The unit was not being used in its typical configuration. It was fitted with newly engineered closing cod ends that tripped with a pull line when a net was fired. The objective of these was to collect organisms from depth and maintain them in their local conditions (dark and cold) until they came to the surface to be sampled for physiology. In support of this, the instrument was equipped with only three nets: an open net for the downcast, one net with the new specialized cod end, and a third open net for the upcast. A first test was run with six nets, with a configuration of 0 (no cod end), 1, 2, 3 (all with closing system), 4 (regular MOCNESS cod end) and 5 (no cod end). The tow resulted in a failure; all nets became tangled with the lines. We decided to remove all nets but 3 (configuration no cod end/closing/no cod end). It is likely that the six net configuration will function as intended by modifying line management on the closing cod ends, perhaps with either floaters or a hose. But, as time was limited, we preferred to play it safe and leave only one net with a closing cod end. As mentioned, the MOCNESS was outfitted with an SIO control unit, and a Seabird 9/11 connection. It did NOT have a temperature or salinity sensor, as we were trying to limit the things that could tangle with the new closing cod ends. Mid-cruise, we discovered that the SIO instrumentation relies on the T/S sensors to create its processed file where it calculates the volume filtered, so the profiles were blank. The data could still be recovered using the Seasave system, since it is just Seabird data now. As these datasets were only ancillary to the purpose of the cruise, we did not correct for this oversight. In retrospect, we believe that it would have been possible to deploy with the sensors without fouling the trip lines, and we will try that during the next deployment of this new configuration.

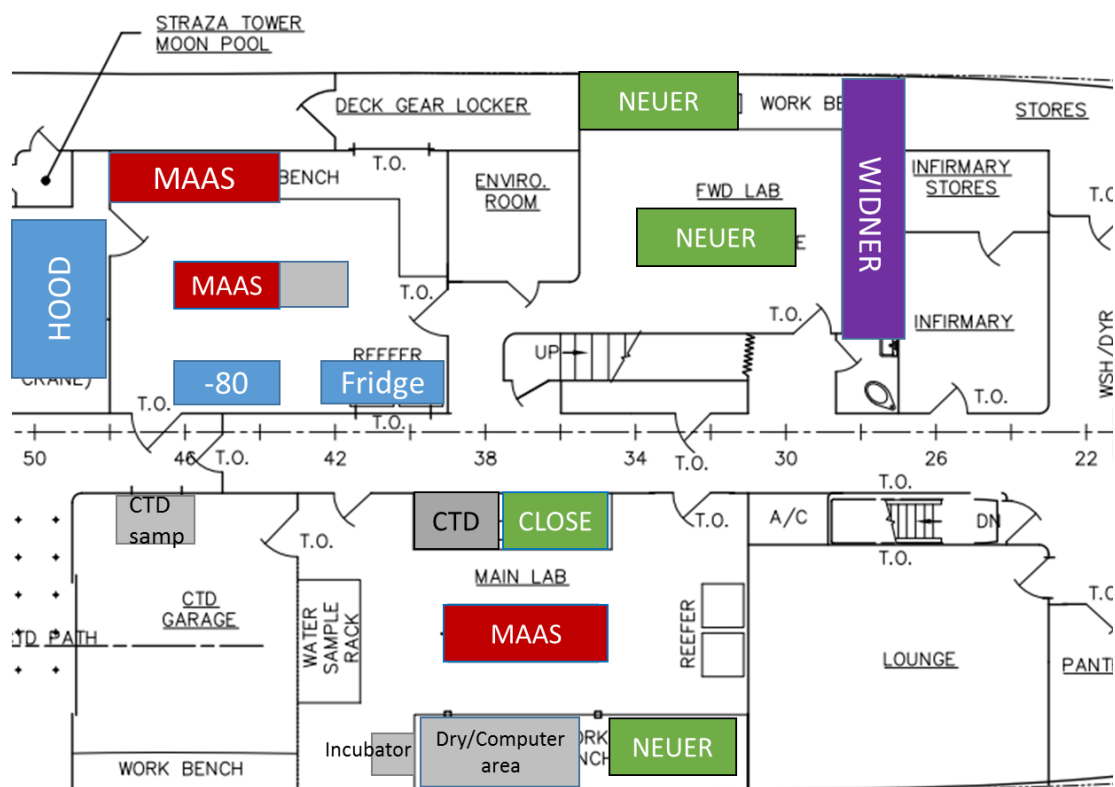
The Reeve net (our specialized 1 m net with 20 L cod end) was deployed off the aft deck from ¼ inch wire (not conductive) using the D4 winch. The net was attached via a pear ring and swivel. Also attached to this ring was a down line with a weight to keep the net flying straight.

5.2. Lab Configuration

The lab maintained its usual configuration for the cruise (Figure 1). The only variations were the inclusion of one stand up incubator in the main lab, the presence of two dry shippers, and a water-bath in the aft lab. The incubator had to be taken apart (door taken off as well as bottom plate on the front) to get through the door to the main lab. The shelf in the CTD garage was also removed for this procedure. BATS kindly loaned their POC filtration rig for CTD sampling. Samples were stored in the aft lab -80, fridges, and freezers. Some lights were covered with red cellophane to reduce light exposure of the copepods, but the protocol of using them was modified when we discovered that it made organismal capture practically impossible. Weighing the advantages of fast capture over light exposure, we resorted to full lighting. All hazardous sampling (formalin, paraformaldehyde, HCl spiking, and cleaning baths) occurred in the hood in the aft lab.

CTD and MOCNESS operations were run by scientists from the aft port of the bridge.

Figure 1: Lab configuration for AE1910



6. Time Series

6.1. Objective

To determine in situ patterns in respiration and ammonium production and how these link to gene expression/protein abundance, animals will be collected every ~ 6 hours from their natural location. Sunrise during this cruise was ~600 and sunset was ~2200. We found that we needed to

wait a full hour after these time points to collect organisms from their appropriate depths as it apparently takes a little while to swim!

6.2. Methods

Every day during the cruise we conducted 4 experiments- after dawn, midday, dusk and midnight- to look at field patterns in physiology. Animals were collected by special closing cod end on the MOCNESS during the day and the Reeve net during the night. Upon retrieval we selected for *P. xiphias* and confirmed ID and gender under the microscope. The preference was to use females. The first 4 were flash frozen (transcriptome), then 6 went into respiration experiments (see below), then 4 were flash frozen (protein), and the final 10 were flash frozen (enzyme). Often we sampled more just in case.

Table 1: Time Series schedule

Date (local)	20-May	21-May	22-May	23-May
0000-0100		stop/clean	stop/clean	stop/clean
0100-0200		TS_2	TS_6	TS_10
0200-0300		Shallow Reeve	Shallow Reeve	Shallow Reeve
0300-0400		start	start	start
0400-0500				
0500-0600		stop/clean	stop/clean	stop/clean
0600-0700		TS_3	TS_7	TS_11
0700-0800		deep MOC	deep MOC	deep MOC
0800-0900				pteropods for
0900-1000		start*	start*	start
1000-1100				
1100-1200		stop/clean	stop/clean	stop/clean
1200-1300	CTD FSW m	CTD FSW m	CTD FSW m	CTD FSW m
1300-1400		TS_4	TS_8	TS_12
1400-1500	deep MOC (testing)	deep MOC	deep MOC	deep MOC
1500-1600				
1600-1700	start	start*	start*	start
1700-1800				
1800-1900	stop/clean	stop/clean	stop/clean	stop/clean
1900-2000				
2000-2100	TS_1	TS_5	TS_9	
2100-2200	Shallow	Shallow Reeve	Shallow Reeve	
2200-2300	start	start	start	
2300-2400				

Lines=Night shift

Prior to the mid-day cast we did a CTD to collect filtered seawater for our daily experiments from the DCM (~120 m). This water was filtered through a 0.2 GFF using a Georig. Water for incubations was maintained in glass 1-L jars and was brought to temperature in the stand-up incubator prior to experiments.

During time series respiration experiments, we put 6 individuals into respiration setups – 50 mL glass respiration syringes (set to 30 mL) with O₂ sensors. There were two controls per experiment. These were set upright in stands with 0.2 micron filtered water at temp with glass

beads (we forgot to dark wrap the syringes). They were kept at 20°C in the incubator. At the end of 3 h the water was expelled at an upward 30° angle (to prevent squishing of fecal pellets) into 15 mL falcon tubes (10 mL sample). These were kept in the fridge until they were measured daily at sea. The copepod and any fecal pellets were then rinsed into a petri dish. The copepod was rinsed once in DI water and put in a cryovial, then frozen at -80 for wet/dry weight (after the boat). The fecal pellets were enumerated and photographed for dimensions then frozen for microbial community analysis (S.Neuer). After breakdown, syringes and other materials were rapidly cleaned so that we could quickly set up the next TS experiment.

6.3. Initial Results

After some initial difficulties in sampling (we needed to wait longer for organisms to migrate) we were highly successful in collecting organisms from all depths. It was noticed on the last day that a few cryovials had fallen out of the dry shipper (?) making them useless for analysis. These were TST3TM, TS2T#2, and TS1T.

site	TS	Date/Time	T	P	E	R Time	R	F	NH ₄
H	1	5/20, 2230	4F [#]	5F	5	2240	5	0,0,0,0,2	5
H	2	5/21, 0130	4, 4F [#]	4F, 2M	5M, 5, 5M	0230	6	1,0,3,2,1,2	6
H	3	5/21, 0820	1F, 2M [#]	2F	2M*/1F*	0850	2	0,0	2
H	4	5/21, 1300	4F,4F	4F,4F, 4M	5,5,>5,>5,>5	1545	6	0,0,0,0,0,0	6
NE	5	5/21, 2200	4F,4F,4F	4F,4F,4F,5F,5F,10	5F,5F,5F	2300	4*	0,0,0,0,1*	4
NE	6	5/22, 0200	4F, 5F	4F,F7,5M	5M, 5F, 6	0310	6	0,1,0,1,3,1	6
NE	7	5/22, 0900	4F,4F	5F, 4F, 4M	5, 10, 5	0945	5 [#]	0,0,0,0,1	5 [#]
NE	8	5/22, 1450	4F,4F,4M	4F, 4F, 4M	5	1610	6	0,0,0,0,0,0	6
NE	9	5/22, 2230	4F,4F,4F,M	4F,4F,M, 15	5F,5F, 5	2250	6	0,1,0,0,0,1	6
S	10	5/23, 0300	4F, 4F	4F,4F	5F,5,8,5F,10M	0400	6	3,1,1,0,L,0	6
S	11	5/23, 0900	4F, 4F	4F,5F,4M,3M	5M, 5	0945	5 [#]	0,2,2,1,1,0	6
S	12	5/23, 1430	4F	3F, 2F	5	1505	6	0,0,0,0,0,0	6

* sample from a dead individual

organism los

7. Circadian Experiments

7.1. Objectives

To determine circadian patterns in respiration, ammonium, urea, DOC, and DOM production and how these link to gene expression/protein abundance. This gives us circadian patterns in respiration rate and whether ammonium, urea, and DOC pulse excrete and are influenced by starvation/captivity.

Table 3: Schedule for the Circadian Experiment

	Mon.	Tues.	Wed.	Thurs.	Fri.	Sat.
Date (local)	20-May	21-May	22-May	23-May	24-May	25-May
0000-0100		setup	sample	END	sample	END
0100-0200				setup		
0200-0300						
0300-0400						
0400-0500				MOC		
0500-0600					sample	
0600-0700		sample*	sample	sample*		
0700-0800						
0800-0900						
0900-1000						
1000-1100	TRANSIT					
1100-1200					sample	
1200-1300	Water	sample *	sample	sample*		
1300-1400						
1400-1500						
1500-1600						
1600-1700						
1700-1800				TRANSIT		
1800-1900		sample *	sample	sample*	sample	
1900-2000						
2000-2100						
2100-2200						
2200-2300	Reeve		Reeve			
2300-2400						

Grey = day shift Lines=Night shift

7.2. Methods

During the cruise, two long-duration (~48 h) circadian experiments were conducted (Table 3). Water for the experiment was collected during standard mid-day CTD casts from the DCM (~120 m). This water was filtered through a 0.2 GFF using a Georig and stored in glass jars in the stand-up incubator to come to temperature.

Net capture was from evening tows. During the first experiment individuals were collected from repeated Reeve tows from 2100-2400 and were mixed male and female individuals. During the second experiment individuals were collected from a single Reeve tow at 2100 and were all female. During both experiments 6 individuals were placed into respiration setups – 60 mL glass respiration jars maintained at 20°C in the closed (dark) water bath. These were maintained with

two controls for 48 h. At the end of the respiration individuals were flash frozen for later dry and wet weight.

The remaining individuals were placed individually into the pre-filled ~115 mL glass jars. We set up 10 individuals for each time point and we set up one control (jar with no individual but the same FSW) for time point 1-3. Jars for water analysis had been DOC cleaned in the muffle furnace prior to the cruise. These were always handled with gloves. Jars were placed in cardboard boxes (two per time point) and placed randomly in the incubator. Every six hours 5 individuals were removed from jars with a plastic transfer pipette and 10 were flash frozen, 5 each for transcriptomic and proteomic analysis. Water from the 5 occupied jars and the control was sampled using a positive pressure system past a 0.2 micron teflon filter. For ammonium, 10 mL was stored in a pre-treated 15 mL falcon tube and measured daily. For urea, 30 mL was stored in a 50 mL falcon tube and frozen for analysis on land. For DOC analysis, 35 mL was stored in EPA vials that had been cleaned previously in a muffle furnace. These were acidified within 24 h. Prior to acidification, Brittany Widner took an aliquot of the DOC water for her DOM analysis.

7.3. Preliminary Results

Originally we intended to filter the water prior to removing the organisms. Filtering was so slow, however, that we needed to remove the animal with a transfer pipette prior to water sampling. Another operational difficulty was that jars were not uniformly filled but held between 110-120 mL of water. These methods need improvement for next time. This should not affect the proteomics/transcriptomics but will influence our calculation of excreta products which are measured in moles/L. Generally we agree that the setup of the second (C2) experiment was better although time point 7 was measured 1 h late. It was noticed on the last day that a few cryovials had fallen out of the dry shipper, making them useless for analysis. For this experiment the only affected vial was C1T8M.

Table 4: Sample log for the Circadian Experiments

xpt	T	date, time	T	P	R	note
1	1	5/21, 630	3M, 2F	2M, 2F		Why 9 animals?
1	2	5/21, 1215	2M, 2F	2M, 2F		Extra non-px not in excreta, 1 dead
1	3	5/21, 1810	2M, 1F	2M, 2F		
1	4	5/22, 0100	2M, 2F	3M, 2F		
1	5	5/22, 0600	1M, 3F	2M, 2F		
1	6	5/22, 1204	1M, 3F	2M, 2F		
1	7	5/22, 1800	1M, 3F	2M, 2F		
1	8	5/23, 0025	2M*, 3F	3M, 2F	1F, 3M, 1DM	
2	1	5/23, 0600	5F	5F		
2	2	5/23, 1200	5F	5F		
2	3	5/23, 1800	5F	5F		
2	4	5/24, 0000	lost	5F		
2	5	5/24, 0600	4F	5F		
2	6	5/24, 1200	5F	5F		
2	7	5/24, 1900	5F	5F		
2	8	5/25, 0000	lost	5F	3F, 2M	

8. Widner

Brittany Widner, Woods Hole Oceanographic Institution

8.1. CTD Sampling

Brittany Widner and Dan Lowenstein attended from WHOI. They handled most CTD sampling (Appendix 3). They collected samples from the CTD rosette for ammonium, urea, and cyanate concentrations (4 casts, 12 depths each cast). They also collected dissolved and particulate metabolite samples from 3 CTDs (6 depths each) using the protocols of the Kujawinski lab (1, 2) as well as a novel low volume protocol that they are developing. They also collected samples from the CTD rosette for nutrients, DNA, particulate organic carbon (POC), dissolved organic carbon (DOC), and bacterial cell counts following the BIOSSCOPE protocols. These samples were collected from 4 CTDs from 9 depths (first CTD) and 12 depths (other three CTDs). These are being initially processed (DNA/cell counts) and stored (all) at BIOS until the July BIOSSCOPE cruise where they will be collected by the Carlson lab for analysis at UCSB or sent to Oregon for sequencing.

8.2. Chemistry for Experiments

Samples were collected for ammonium from the zooplankton time series experiments and for ammonium, urea, cyanate, and dissolved metabolite concentrations from the zooplankton circadian rhythm experiments. Ammonium samples were processed onboard using the nanomolar OPA method (3) and the remaining samples will be analyzed in the lab following the cruise.

References

1. W. M. Johnson, M. C. Kido Soule, E. B. Kujawinski, Extraction efficiency and quantification of dissolved metabolites in targeted marine metabolomics. *Limnology and Oceanography: Methods* **15**, 417-428 (2017).
2. M. C. Kido Soule, L. K., J. W.M., E. B. Kujawinski, Environmental metabolomics: Analytical strategies. *Mar. Chem.* **177**, 374-387 (2015).
3. R. M. Holmes, A. Aminot, R. Kerouel, B. A. Hooker, B. J. Peterson, A simple and precise method for measuring ammonium in marine and freshwater ecosystems. *Canadian Journal of Fisheries and Aquatic Sciences* **56**, 1801-1808 (1999).

9. Neuer

Susanne Neuer, Arizona State University

9.1. Roller Tank Experiments

On May 23, 2019 we collected water from the C007 cast (0300 local time) from the deep chlorophyll maximum (DCM, 150m depth) at Hydrostation to set up 15 1-L roller tank (RT) incubations. These incubations were carried out with the objective to test the role of zooplankton (fecal pellets, molts) in the formation of visible aggregates. We set up the experiment using animals (various pteropods and crustaceans) collected during the preceding night time net cast on May 23 and added the animals to the tanks (Table 4). Animals were incubated in the stationary tanks for approximately 12 hours and were then removed from the tanks. The tanks were topped off with the same DCM water and then set up on a rolling platform at about 3 rpm by about 2100

on May 23. The incubations were transferred to an environmental chamber upon arrival at BIOS in the afternoon (around 1400) of May 24 and incubated at 20 C until take-down on May 27, 2019 at 9AM. If aggregates were present, they were recorded and harvested for imaging and mounted on a slide for later on microscopic analysis. Preliminary data showed that visible aggregates formed in some of the treatments that had contained animals, most of them of fecal pellet or potential prey origin. Pteropods were identified by Amy Maas, crustaceans by Leocadio Blanco Bercial

Table 4. Animal and control treatments of the AE 1910 roller tank experiment and preliminary results on formation of aggregates after 3.5 days of incubation.

Tank #	Treatment (one animal each tank unless otherwise noted)	Aggregate # /type
1	<i>Cuvierina atlantica</i>	one small
2	<i>Cuvierina atlantica</i>	none
3	<i>Clio pyramidata</i>	none
4	<i>Clio pyramidata</i>	two, possibly of prey origin
5	Gastropod	one of fecal pellet origin
6	<i>Clio pyramidata</i>	one, string like, possibly with piece of shell
7	Eucarida (Decapoda)	two of fecal pellet origin
8	<i>Euphausia brevis</i> and <i>hemigibba</i> (one each)	none
9	<i>Euphausia hemigibba</i> (one large and one small)	one of fecal pellet origin
10	<i>Thyssanopoda aequalis</i>	none
11	<i>Thyssanopoda aequalis</i>	five of fecal pellet origin
12	<i>Cuvierina atlantica</i>	1 small
13	control	1 small
14	control	none
15	3 fecal pellets of <i>Pleuromamma xiphias</i>	one particle after 36hr, then disappeared

9.2. Species Specific Fecal Pellets

During two occasions (evening of the 22nd and 23rd) individual migratory organisms were collected from the Reeve net and placed into fecal pellet production beaker towers containing 0.2 micron filtered water. These towers consisted of two nested beakers with the top one having a 1 micron mesh filter rather than a solid bottom. Organisms were allowed to excrete waste for 12 h prior to fecal pellet collection.

10. Doherty

Shannon Doherty, University of Miami

10.1. CTD Sampling

Particulate organic matter (POM) profiles were taken to interpret the results of community fecal pellet experiments. POM will be analyzed for carbon and nitrogen concentrations, bulk carbon and nitrogen stable isotope ratios, and compound-specific stable isotope ratios. On May 21, 2019

and May 23, 2019 water was collected and filtered (Atlantic Explorer filtration rig, 47 mm GF/F, 8-20 L) from CTD casts 3 and 8 respectively. Filters were collected for POM, stored at -80 °C and transported on ice to the University of Miami. Water from cast 3 was collected at 7 depths from 25-200 meters to generate a detailed stable isotope profile of the photic zone, and water from Cast 8 was collected at 7 depths from 25-500 meters to generate a profile of the photic zone and upper mesopelagic.

10.2. Community Fecal Pellets

A mixed community of zooplankton were collected from after the 02:00 Reeve net tows on May 22nd and 23rd 2019. These organisms were collected to isolate size fractions of the zooplankton community and then were incubated to capture the fecal pellets generated by the various size fractions of the community. The fecal pellets and zooplankton will be analyzed in the same manner as the POM discussed above with the goal of tracing the interaction between POM, zooplankton, and their fecal pellets in the water column.

After organisms for the Time Series, Circadian, and Species Specific Fecal Pellet experiments had been removed, the remaining community was filtered out of the cod end using 2.5 mm, 1 mm, and 0.25 mm meshes. On May 22 four size classes for selected for incubation: >2.5 mm, >1 mm, 1-2.5 mm, and 0.25-1 mm. On May 23 only the 1-2.5 mm and 0.25-1 mm size classes were selected. Each size class was incubated in a mesh-bottom container filled with ~500 mL 0.2 micron filtered sea water (from the daily 1250 CTDs) and incubated for 12 hours. The zooplankton remained above the mesh bottom while the fecal pellets fell below the mesh and collected in the bottom on an exterior container. After 12 hours, the zooplankton were removed, rinsed off the mesh, and filtered down onto 47 mm, 100 micron nylon filters. The fecal pellets collected at the bottom of the container were filtered onto 47 mm, 6 micron nylon filters. Zooplankton and fecal pellet filters were stored at -80 °C and transported on ice to the University of Miami.

11. Opportunistic Sampling

One deep sea copepod was sampled from the first MOCNESS (MOC_001). It was collected from the closing cod ends (600-400 m), photographed and flash frozen for Dr. Leocadio Blanco Bercial.

After sampling the *P. xiphias*, the entire remaining contents of one of the deep tows (MOC_006, 5/22 16:24) was preserved in RNAlater for Dr. Leocadio Blanco Bercial. This was stored in the freezer and shaken occasionally throughout the duration of the cruise. It is stored at -4 on land. Deep sea fish were preserved in ethanol for Dr. Robbie Smith (BAMZ). One set was from the surface at night (R_005 and R_006; 5/21 2100 and 2200) and a second set was from depth (MOC_005; 5/22 9:00). After preservation they were refrigerated and the ethanol was changed 24 h after collection.

12. Outreach

12.1. Social Media

Aside from helping with all the operations on deck and in the lab Kaitlin Noyes spent a large portion of the cruise collecting images and experiences to translate to the DataNugget course

module that will be developed as part of the NSF outreach for this project. She also arranged an Instagram takeover of the National Marine Educators page and maintained a twitter presence throughout the cruise. As of Tuesday June 11th the feeds had the following stats:

Instagram

<https://www.instagram.com/natlmarineed/>

#zoopgroup #zoopFieldNotes

<https://www.instagram.com/biosstation/>

Statistics: 868 likes and videos 149 views

Twitter

<https://twitter.com/BIOSstation?lang=en>

<https://twitter.com/senseofplace3>

#zoopgroup #zoopFieldNotes

Statistics: 34 likes, 14 retweets and videos 194 views

12.2. High School Teacher

As part of the cruise we brought along Paul Wight, a high school teacher from Saltus Academy, Bermuda. Paul is developing a module for his Oceanography course from this experience and was provided day and night CTD datasets so the students could compare the vertical profile using real data. The course will culminate in a student project focused on “Mankind and the Ocean”.

12.3. BIOS REUs and Interns

Marcus Rewan was a summer student at BIOS’s Ocean Academy Programs and was invited to participate as a precursor to his summer internship. He directly collected samples, including DNA and bacterial probe that he will analyze for his project.

Lindsey Cunningham joined the project with Susanne Neuer from ASU. She collected aggregates and water column DNA samples that she will use for her internship project.

13. Cruise Participants

The cruise was lucky to have a thoroughly lovely group of people who worked round the clock to get all the work done. I am incredibly grateful for all of their efforts, particularly as everyone became rock stars of identifying female *P. xiphias* despite it being the first time most had really looked at a copepod.



First	Last	Institute (project	shift
Amy	Maas	BIOS (ZDR)	Day
Hannah	Gossner	BIOS (ZDR)	Day
Emma	Timmins-Schiffman	UW (ZDR)	Day
Lindsey	Cunningham	ASU (ZDR + SN)	Day
Susanne	Neuer	ASU (ZDR + SN)	Day
Andrea	Miccoli	BIOS (ZDR)	Night
Ann	Tarrant	WHOI (ZDR)	Night
Brook	Nunn	UW (ZDR)	Night
Nora	McNamara-Bordewick	WHOI (ZDR)	Night
Brittany	Widner	WHOI (BIOSCOPE)	CTD
Dan	Lowenstein	WHOI (BIOSCOPE)	CTD
Shannon	Doherty	U. Miami (BIOSCOPE)	Day
Kaitlin	Noyes	BIOS (ZDR)	Day
Paul	Wight	Saltus (outreach)	CTD
Marcus	Rewan	BIOS	CTD

14. Event Log

The R2R event logger was used during the cruise but it inexplicably did not document latitude and longitude. The event log was reconstructed from the bridge log.

Date	Local Time	Event	ID	Lead Scientist	Winch	Depth (m)	Wire Out	Lat (N)	Long (W)
5/20/2019	12:58	Deploy CTD	C001	Widner	D5	790	803	32 30.167	64 30.147
5/20/2019	14:00	Recover CTD	C001	Widner	D5	790	803	32 10.743	64 30.740
5/20/2019	14:30	Deploy MOCNESS	MOC_001	Maas	C7	600	600	32 10.469	64 30.451
5/20/2019	16:08	Recover MOCNESS	MOC_001	Maas	C7	600	600	32 08.633	64 29.012
5/20/2019	18:42	Deploy MOCNESS	MOC_002	Maas	C7	150	170	32 10.622	64 30.361
5/20/2019	19:12	Recover MOCNESS	MOC_002	Maas	C7	150	170	32 10.136	64 30.030
5/20/2019	20:52	Deploy Reeve	R_001	Maas	D4	200	200	32 10.451	64 30.036
5/20/2019	21:46	Recover Reeve	R_001	Maas	D4	200	200	32 09.805	64 29.496
5/20/2019	21:54	Deploy Reeve	R_002	Maas	D4	200	200	32 09.791	64 29.491
5/20/2019	22:54	Recover Reeve	R_002	Maas	D4	200	200	32 09.131	64 29.024
5/20/2019	22:59	Deploy Reeve	R_003	Maas	D4	200	200	32 09.123	64 29.018
5/20/2019	23:56	Recover Reeve	R_003	Maas	D4	200	200	32 08.500	64 28.640
5/21/2019	0:26	Deploy Reeve	R_004	Maas	D4	200	200	32 08.477	64 28.596
5/21/2019	1:10	Recover Reeve	R_004	Maas	D4	200	200	32 07.866	64 28.185
5/21/2019	4:08	Deploy CTD	C002	Widner	D5	1000	1029	32 10.484	64 29.677
5/21/2019	5:23	Recover CTD	C002	Widner	D5	1000	1029	32 11.640	64 30.422
5/21/2019	6:25	Deploy MOCNESS	MOC_003	Miccoli	C7	600	730	32 10.615	64 30.263
5/21/2019	7:46	Recover MOCNESS	MOC_003	Miccoli	C7	600	730	32 09.175	64 29.415
5/21/2019	11:04	Deploy CTD	C003	Doherty	D5	200	202	32 16.462	64 30.128
5/21/2019	11:41	Recover CTD	C003	Doherty	D5	200	202	32 16.602	64 29.401
5/21/2019	13:03	Deploy MOCNESS	MOC-004	Miccoli	C7	600	619	32 24.373	64 28.777
5/21/2019	14:27	Recover MOCNESS	MOC_004	Miccoli	C7	600	619	32 23.390	64 27.704
5/21/2019	16:42	Deploy CTD	C004	Widner	D5	1000	1020	32 34.259	64 38.779

5/21/2019	18:00	Recover CTD	C004	Widner	D5	1000	1020	32	33.782	64	38.055
5/21/2019	20:56	Deploy Reeve	R_005	Maas	D4	200	200	32	35.614	64	35.203
5/21/2019	21:59	Recover Reeve	R_005	Maas	D4	200	200	32	34.311	64	34.861
5/21/2019	22:14	Deploy Reeve	R_006	Maas	D4	200	200	32	33.938	64	34.761
5/21/2019	23:16	Recover Reeve	R_006	Maas	D4	200	200	32	31.981	64	34.112
5/22/2019	1:14	Deploy Reeve	R_007	Maas	D4	200	200	32	33.387	64	33.609
5/22/2019	2:19	Recover Reeve	R_007	Maas	D4	200	200	32	32.342	64	33.814
5/22/2019	2:24	Deploy Reeve	R_008	Maas	D4	200	200	32	32.259	64	33.821
5/22/2019	3:37	Recover Reeve	R_008	Maas	D4	200	200	32	31.722	64	33.277
5/22/2019	7:26	Deploy MOCNESS	MOC_005	Miccoli	C7	600	750	32	31.722	64	30.261
5/22/2019	8:57	Recover MOCNESS	MOC_005	Miccoli	C7	600	750	32	29.991	64	30.626
5/22/2019	10:54	Deploy CTD	C005	Doherty	D5	790	850	32	28.509	64	31.698
5/22/2019	12:12	Recover CTD	C005	Doherty	D5	790	850	32	29.184	64	32.088
5/22/2019	13:20	Deploy MOCNESS	MOC_006	Maas	C7	600		32	30.080	64	33.126
5/22/2019	14:50	Recover MOCNESS	MOC_006	Maas	C7	600		32	31.342	64	32.747
5/22/2019	16:50	Deploy CTD	C006	Widner	D5	1000	1015	32	34.207	64	38.653
5/22/2019	18:12	Recover CTD	C006	Widner	D5	1000	1015	32	34.715	64	39.138
5/22/2019	21:00	Deploy Reeve	R_009	Maas	D4	200	200	32	34.171	64	38.701
5/22/2019	21:59	Recover Reeve	R_009	Maas	D4	200	200	32	35.210	64	38.380
5/23/2019	2:08	Deploy Reeve	R_010	Maas	D4	200	200	32	10.416	64	47.369
5/23/2019	3:10	Recover Reeve	R_010	Maas	D4	200	200	32	11.485	64	47.298
5/23/2019	3:23	Deploy CTD	C007	Neuer	D5	500	517	32	11.666	64	47.330
5/23/2019	4:10	Recover CTD	C007	Neuer	D5	500	517	32	12.456	64	47.787
5/23/2019	7:06	Deploy MOCNESS	MOC_007	Miccoli	C7	600	680	32	09.789	64	47.450
5/23/2019	8:39	Recover MOCNESS	MOC_007	Miccoli	C7	600	680	32	11.617	64	46.291
5/23/2019	10:44	Deploy CTD	C008	Doherty	D5	500	520	32	12.371	64	46.763
5/23/2019	11:32	Recover CTD	C008	Doherty	D5	500	520	32	12.157	64	46.602
5/23/2019	13:04	Deploy MOCNESS	MOC_008	Maas	C7	600	650	32	13.903	64	40.693
5/23/2019	14:30	Recover MOCNESS	MOC_008	Maas	C7	600	650	32	14.830	64	29.470

Appendix 1 Summary of MOCNESS tow data

Tow	Day	Time	Loc.	Lat (N)	Long (W)	Notes	Files
MOC-001	05/20/19	14:00	HYDRO	32° 10.317'	64° 30.310'	1 open, 3 closing, 1 normal 1 open cod end. Came up totally tangled. Preserved one copepod for Leo	AE1910_01MOCNESS.csv AE1910_01MOCNESS_net.txt
MOC-002	05/20/19	18:30	HYDRO	32° 10.643'	64° 30.390'	1 open cod end, 1 closing, 1 open set up tested as an alternative	AE1910_02MOCNESS.csv AE1910_02MOCNESS_net.txt
MOC-003	05/21/19	06:00	HYDRO	32° 10.689'	64° 30.293'	TS3 samples; new set up working	AE1910_03MOCNESS.csv AE1910_03MOCNESS_net.txt
MOC-004	05/21/19	13:00	NE	32° 24.363'	64° 28.749'	TS4	AE1910_04MOCNESS.csv AE1910_04MOCNESS_net.txt
MOC-005	05/22/19	07:30	NE	32° 31.592'	64° 30.307'	TS7; electronics failure; Fish for Robbie	Electronics Failure AE1910_05MOCNESS_net.txt
MOC-006	05/22/19	13:30	NE	32° 30.127'	64° 33.194'	TS8; remainder of the sample in RNA later for Leo	Electronics Failure
MOC-007	05/23/19	07:00	S	32° 08.950'	64° 47.354'	TS11	AE1910_07MOCNESS.csv AE1910_07MOCNESS_net.txt
MOC-008	05/23/19	13:00	SE	32° 13.948'	64° 40.649'	TS12	AE1910_08MOCNESS.csv AE1910_08MOCNESS_net.txt

Appendix 2 Summary of Reeve tow data

All Reeve net tows were completed in a W pattern with the wire descending at 20 m/min then coming up to a middle depth at 5 m/min, going down again at 5 m/min and coming back to the surface at 20 m/min.

Tow	Day	Time Start	Time Stop	Loc.	Lat (N)	Long (W)	Notes	ODI file
R_001	05/20/19	20:53	21:46	HYDRO	32° 10.435'	64° 30.018'	Used to set up C1, TS1	5C10004.dat
R_002	05/20/19	21:56	22:52	HYDRO	32° 09.730'	64° 29.441'	Used to set up C1	5C10004.dat
R_003	05/20/19	23:01	23:55	HYDRO	32° 09.071'	64° 29.985'	Used to set up C1	5C10004.dat
R_004	05/20/19	00:05	01:15	HYDRO	32° 08.434'	64° 28.581'	Used to set up C1, TS2	5C10004.dat
R_005	05/21/19	20:59	21:59	NE	32° 33.650'	64° 34.754'	TS5, fish for Robbie	6C10004.dat
R_006	05/21/19	22:22	23:19	NE	32° 33.707'	64° 34.759'	TS5, fish for Robbie	6C10004.dat
R_007	05/21/19	01:17	02:15	NE	32° 33.387'	64° 33.609'	TS6, misc. for Susanne, remainder for Shannon	6C10004.dat
R_008	05/21/19	02:27	03:30	NE	32° 32.259'	64° 33.821'	Misc. for Susanne, remainder for Shannon	6C10004.dat
R_009	05/22/19	20:58	22:00	NE	32° 34.141'	64° 38.701'	TS9, C2 samples (no ODDI data)	NA
R_010	05/23/19	02:08	03:10	SW	32° 10.416'	64° 47.369'	Used for TS10 (no ODDI data)	NA

Appendix 3 Summary of CTD data.

Cast 001, Local 12:50

We used the star-ODDI pressure sensor alongside the seabird pressure sensor because after this cast we were planning on removing the seabird pressure sensor (putting it on MOCNESS). This was to calibrate. We ended up not having to, but it was a fun test! 30 second soaks. CTD run by Brittany Widner. Water was sampled by WHOI team + friends, with the exclusion of DNA for Susanne Neuer (SN), POM for Shannon Doherty (SD) and water for experiments for the project (AEM – sampled by Kaitlin Noyes).

#	DEPTH	DOC/ DON	DAPI	Probe	FCM	NUTS	NH4	Urea	Cyanate	POC/ PON	DNA (SN)	POM (SD)	water (AEM)
1	sfc	x	x	x	x	x	x	x	x	x			
2	20										x		
3	20	x	x	x	x	x	x	x	x	x			
4	40										x		
5	40	x	x	x	x	x	x	x	x	x			
6	75											x	
7	100											x	
8	120												x
9	120												x
10	120												x
11	120										x		
12	120	x	x	x	x	x	x	x	x	x			
13	200											x	
14	300											x	
15	300										x		
16	300	x	x	x	x	x	x	x	x	x			
17	400	x	x	x	x	x	x	x	x	x	x		
18	400											x	
19	500	x	x	x	x	x	x	x	x	x			
20	500										x		
21	600	x	x	x	x	x	x	x	x	x			
22	600											x	
23	600										x		
24	790	x	x	x	x	x	x	x	x	x			

Cast 002, Local 1250

CTD run by Brittany Widner. Water was sampled by WHOI team + friends.

#	DEPTH	DOC	new HR DOM	HR DOM	DAPI/ probe	FCM	DNA	NUTS	NH4	Urea	Cyanate	POC/ PON
1	1	x	x	x	x	x	x	x	x	x	x	x
2	1											
3	40	x	x	x	x	x	x	x	x	x	x	x
4	40											
5	80	x	x		x	x	x	x	x	x	x	x
6	80											
7	110	x	x	x	x	x	x	x	x	x	x	x
8	110											
9	150	x	x		x	x	x	x	x	x	x	x
10	150											
11	200	x	x	x	x	x	x	x	x	x	x	x
12	200											
13	250	x	x		x	x	x	x	x	x	x	x
14	250											
15	300	x	x		x	x	x	x	x	x	x	x
16	300											
17	500	x	x	x	x	x	x	x	x	x	x	x
18	500											
19	600	x	x		x	x	x	x	x	x	x	
20	600											
21	800	x	x		x	x	x	x	x	x	x	
22	800											
23	1000	x	x	x	x	x	x	x	x	x	x	
24	1000											

Cast 003, Local 1250

CTD run by Shannon Doherty. Water was sampled by Shannon and Kaitlin

#	DEPTH	POM (SD)	Water (AEM)
1	25		
2	25		
3	25		
4	25		
5	25		
6	25		
7	25		
8	25		
9	25	x	
10	25	x	
11	50	x	
12	50	x	
13	75	x	
14	75	x	
15	100	x	
16	100	x	
17	120	x	
18	120	x	
19	120		x
20	120		x
21	150	x	
22	150	x	
23	200	x	
24	200	x	

Cast 004, Local 1645

CTD run by Brittany Widner. Water was sampled by WHOI team + friends.

Seas slightly choppy, has clouded over as Subtropical Storm Andrea is approaching. We repositioned to North of Bermuda and hope to sample there tomorrow also, if sea state allows. Bottle 18 was accidentally fired just shy of 500 m while the CTD was moving.

#	DEPTH	DOC	new HR DOM	HR DOM	DAPI/ probe	FCM	DNA	NUTS	NH4	Urea	Cyanate	POC/ PON
1	4.2	x	x		x	x	x	x	x	x	x	x
2	4.2			x								
3	40	x	x		x	x	x	x	x	x	x	x
4	40			x								
5	80	x	x		x	x	x	x	x	x	x	x
6	80											
7	115	x	x		x	x	x	x	x	x	x	x
8	115			x								
9	150	x	x		x	x	x	x	x	x	x	x
10	150											
11	200	x	x		x	x	x	x	x	x	x	x
12	200			x								
13	250	x	x		x	x	x	x	x	x	x	x
14	250											
15	300	x	x		x	x	x	x	x	x	x	x
16	300											
17	500	x	x		x	x	x	x	x	x	x	x
18	500			x								
19	600	x	x		x	x	x	x	x	x	x	
20	600											
21	800	x	x		x	x	x	x	x	x	x	
22	800											
23	1000	x	x		x	x	x	x	x	x	x	
24	1000			x								

Cast 005, Local 1250

CTD run by Shannon Doherty. Bottle 12 leaked. DNA was sampled by Susanne Neuer (SN), POM by Shannon Doherty (SD) and water for experiments for the project (AEM – sampled by Kaitlin Noyes).

#	DEPTH	DNA (SN)	POM (SD)	Water (AEM)
1	sfc			
2	20	x		
3	20	x		
4	40	x		
5	40	x		
6	120	x		
7	120	x		
8	120			x
9	120			x
10	120			x
11	120			x
12	200	x		
13	200	x		
14	300	x		
15	300	x		
16	300			
17	400	x		
18	400	x		
19	500	x		
20	500	x		
21	600		x	
22	600	x		
23	600	x		
24	790		x	

Cast 006, Local 1645

CTD run by Brittany Widner. Water was sampled by WHOI team + friends.

This is supposed to be identical to yesterday. Same spot same time. But the chl profile looks totally different than yesterday. I opted to sample the same depths even though we basically missed the DCM. There are three chl bumps at ~50, 100, 135. There has been a little tropical depression last night/today. Not sure if that is why it is different.

#	DEPTH	DOC	new HR DOM	HR DOM	DAPI/probe	FCM	DNA	NUTS	NH4	Urea	Cyanate	POC/PON
1	1	x	x		x	x	x	x	x	x	x	x
2	1			x								
3	40	x	x		x	x	x	x	x	x	x	x
4	40			x								
5	80	x	x		x	x	x	x	x	x	x	x
6	80											
7	115	x	x		x	x	x	x	x	x	x	x
8	115			x								
9	150	x	x		x	x	x	x	x	x	x	x
10	150											
11	200	x	x		x	x	x	x	x	x	x	x
12	200			x								
13	250	x	x		x	x	x	x	x	x	x	x
14	250											
15	300	x	x		x	x	x	x	x	x	x	x
16	300											
17	500	x	x		x	x	x	x	x	x	x	x
18	500			x								
19	600	x	x		x	x	x	x	x	x	x	
20	600											
21	800	x	x		x	x	x	x	x	x	x	
22	800											
23	1000	x	x		x	x	x	x	x	x	x	
24	1000			x								

Cast 007, Local 0330

CTD run by and sampled by Susanne Neuer. All bottles fired at 150 m and used for roller tank experiments

Cast 008, Local 1250

CTD run by Shannon Doherty. POM sampled by Shannon Doherty (SD) and water for experiments for the project (AEM – sampled by Kaitlin Noyes).

#	DEPTH	POM (SD)	Water (AEM)	Notes
1	25	x		
2	25	x		
3	25	x		
4	75	x		
5	75	x		
6	75	x		
7	100	x		
8	100	x		
9	100	x		
10	DCM		x	
11	DCM	x		
12	DCM	x		
13	DCM	x		
14	200	x		
15	200	x		
16	200	x		
17	350	x		
18	350	x		
19	350	x		
20	350	x		
21	500	x		Brittany
22	500	x		
23	500	x		
24	500	x		