LMG 19-01: 30 Dec. 2019 – 12 February 2019, PAL LTER Cruise 27
Weekly Science Report 3

LTER: Land-Shelf-Ocean Connectivity, Ecosystem Resilience and Transformation in a Sea-Ice Influenced Pelagic Ecosystem on the Western Antarctic Peninsula
&
Physiological Ecology of "Herbivorous" Antarctic Copepods
&
Biological and physical drivers of O_2 saturation and net community production variability at the Western Antarctic Peninsula

Week 3 overview (Deborah Steinberg, Chief Scientist):

In Week 3 (13-19 Jan.), we deployed the birder team on Avian Island for the annual census and sampling of the Adélie penguin colony there. We then sampled the 200 grid line, with regular station operations at representative coastal, shelf, and slope stations. We completed our second Process Study as well, with sampling and experiments (details in individual reports below) at both an outer slope station (200.180) and at two Marguerite Bay coastal stations (**Fig. 1**). We conducted day vs. night depth-stratified MOCNESS tows to assess zooplankton diel vertical migration in the outer slope and the coastal Marguerite Bay submarine canyon. In Marguerite Bay, we also compared a deeper canyon station (200.000) with a shallower more coastal station (200.-040). We also had a rendezvous with the R/V *N.B. Palmer* to deliver two gliders that we brought on our cruise for Dr. Andrew Thompson (their shipment did not make it in time for their cruise). We then made our annual visit on January 19 to the British Antarctic Survey (BAS) Rothera Base on Adelaide I., and hosted British and Dutch scientists on a day cruise to carry out joint water sampling and calibration casts with the CTD at two of our three regular stations in Ryder Bay. This was a shortened sampling and science exchange compared to previous years, as Rothera's new pier is under construction which made visit logistics more complicated than usual.

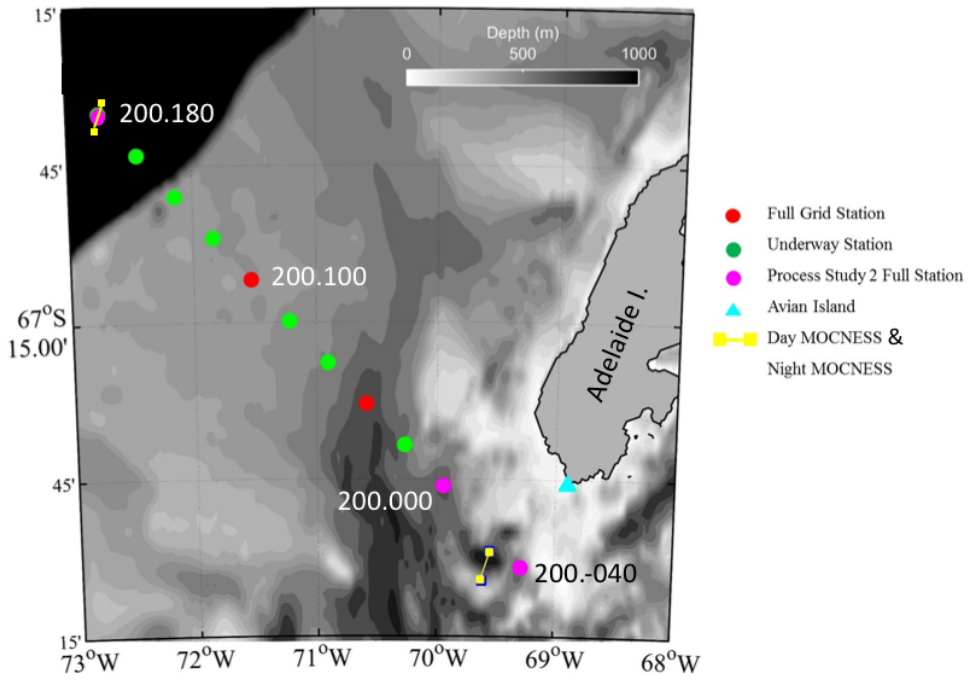

Figure 1. Map of 200 line grid stations, Process Study 2 stations, and MOCNESS tow track across deep canyon in Marguerite Bay.

Individual component reports:

C- 021: Physical Oceanography Component-LTER (Doug Martinson, Lamont Doherty Earth Observatory; PI; Elizabeth Shadwick O-270, Virginia Institute of Marine Science; PI)

Field Team Member: Naomi Manahan

Downloading data from the recovered 300.100 mooring sensors was the main focus during this week. A note of recognition to Ducklow team member Shawnee Traylor, who single-handedly scrubbed approximately 480 meters of biofouled line to ensure it can be reused in future years! Data extraction from the SeapHOx instrument, which monitors pH and oxygen levels, was successful for the majority of the year. We were also able to extract CO_2 data from the CO_2 Pro instrument. These observations from 2018 will allow for a better plan for 2019 data parameters. Lastly, the temperature and pressure sensors that were located throughout the vertical water column at 16 discrete locations were successfully downloaded and the mooring team is excited to take a deeper look at the changing water masses throughout 2018. See **Fig. 2** for an example of subsurface temperatures extracted from a single sensor located just below the ocean surface from January 2018-January 2019 at station 300.100. We are looking forward to deploying another mooring at 300.100 in a little less than two weeks.

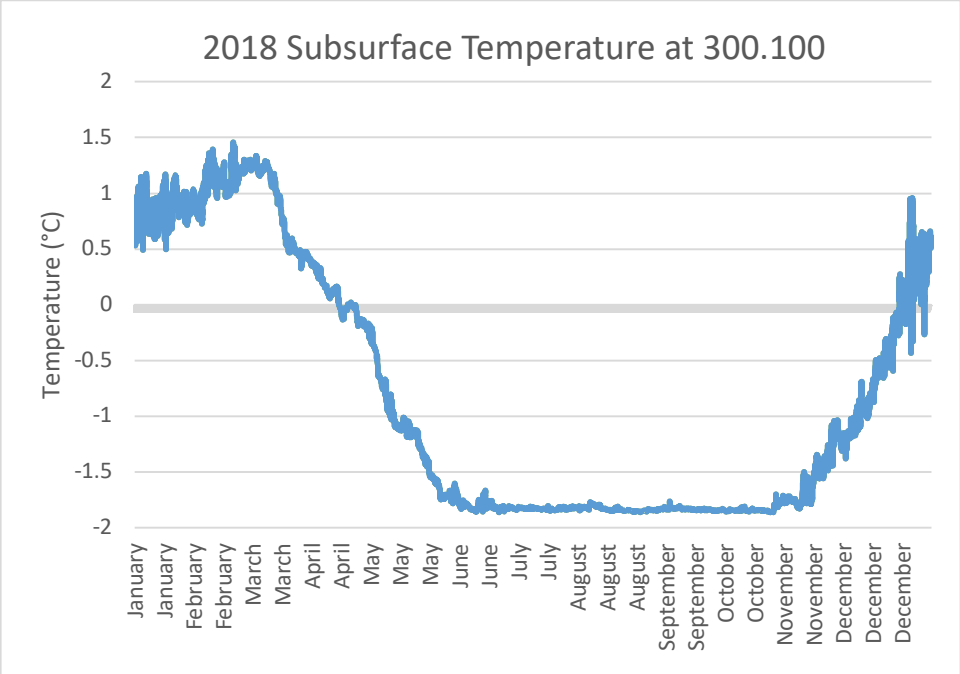

Figure 2. Temperature record from a subsurface temperature & pressure sensor moored at 300.100 from January 2018-January 2019.

C-045: Microbial Biogeochemistry Component-LTER (Hugh Ducklow, Lamont Doherty Earth Observatory; PI)

Field Team Members: Naomi Manahan, Rebecca Trinh, Shawnee Traylor, Johanna Ruff, Srishti Dasarathy

This week we continued sampling along the 300 line and 200 line of the LTER grid. **Fig. 3** shows the results from real-time analysis of bacterial abundance via flow cytometry and leucine incorporation rates thus far in our sampling locations. Leucine incorporation rates and bacterial abundances along the LTER grid stations show a peak in bacterial abundance at shelf station 300.100, despite normal- to low rates of leucine incorporation. Station 200.-040 (in Marguerite Bay) had the highest leucine incorporation rates, suggesting excellent conditions for bacterial production despite lower levels of bacteria per milliliter of surface seawater. There were high leucine incorporation rates and bacterial abundance at the 500 line shelf and coastal stations.

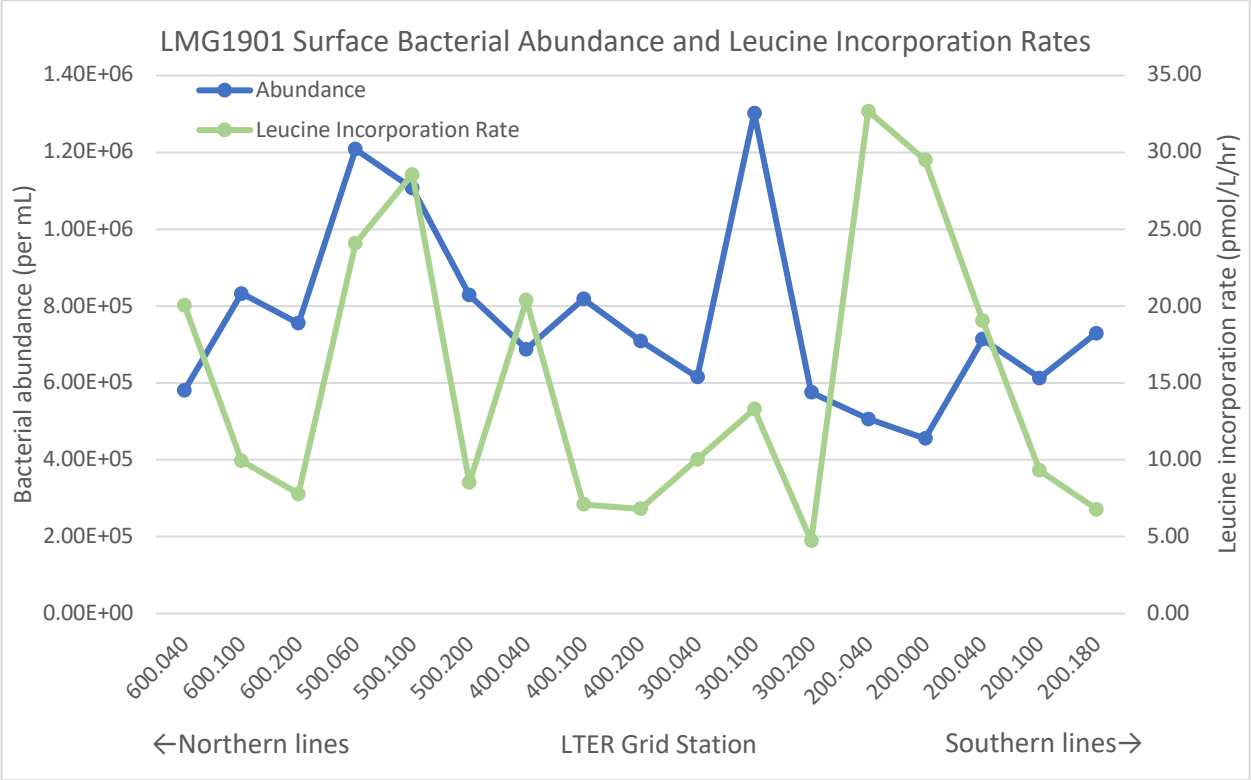

Figure 3. Leucine incorporation rates and bacterial abundances along the LTER grid stations from north to south along the Western Antarctic Peninsula.

In addition to our time series sampling, PhD student Rebecca Trinh was able to successfully perform krill fecal pellet experiments examining the bacterial production associated with krill fecal pellets. See **Fig. 4** for a photo of Rebecca working to isolate krill from a large net tow to collect their fecal pellets.

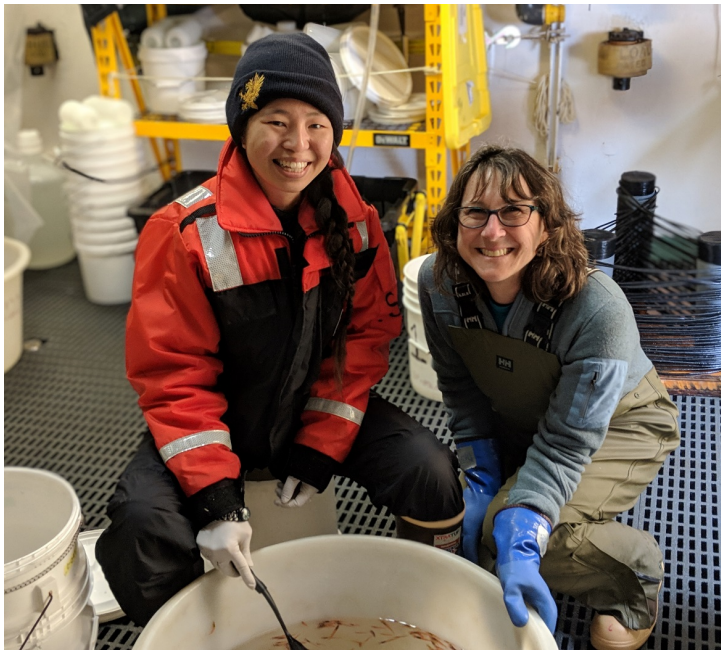

Figure 4. PhD student Rebecca Trinh (left) and Chief Scientist Debbie Steinberg (right) are all smiles after their successful zooplankton net tow. Rebecca is working long hours in the Aquarium Room to isolate krill from a net tow she recovered earlier that day. During this cruise, she has completed two successful experiments as part of her PhD dissertation that require around-the-clock attention, in addition to working 12-hr days overseeing the night shift for the Ducklow team.

B-461: Biological and physical drivers of O_2 saturation and net community production variability at the Western Antarctic Peninsula (Nicolas Cassar, Duke U., PI)

Field Team Member: Alexandria (Alex) Neibergall

The Equilibrator Inlet Mass Spectrometer (EIMS) has been taking continuous underway O_2/Ar measurements since we left Palmer Station. These measurements are used to estimate Net Community Production in the mixed layer along the cruise track. This week along the 200 line (as last week along the 600, 500, 400, 300 lines) at each grid station I took duplicate 60ml water samples at 7 depths between the surface and 500m, to obtain a roughly linear depth profile. These samples will be analyzed for dissolved N_2O concentration. Obtaining an N_2O gradient from depth to the mixed layer will allow us to account for vertical mixing of anoxic or suboxic deep water that may affect O_2/Ar measurements taken from the EIMS.

I also took duplicate 4L water samples at each grid station from a Niskin bottle fired at 5m depth. I also took duplicate samples at most underway stations on the 600 - 200 lines, totaling 90 samples so far. These samples were filtered through a .22µm Stervix filter and will be used for 16S/18S amplicon sequencing to characterize the microbial community. I will continue to take duplicate 4L samples at grid and underway stations on the 100, 000, and -100 lines. I will also take opportunistic samples along the ice edge or in areas where we see notable changes in the O_2/Ar measurements from the EIMS. The data taken on this cruise will be used to examine the relationship between microbial community composition and NCP along the WAP.

C-019: Phytoplankton Component-LTER (Oscar Schofield, Rutgers, P.I.)

Field Team Members: Nicole Waite (lead), Emily Slesinger, Samantha Schofield, Hailey Conrad, Kim Thamatrakoln

We continued to sample the LTER grid, completing the 200 line and our second process study in the Marguerite Bay area. There has been an increase in chlorophyll concentrations and a switch from the cryptophyte and dinoflagellate dominated phytoplankton community we observed in the north, to a diatom and *Phaeocystis* dominated system as we entered the southern WAP (**Fig 5**). There has also been an increase in cell size as we've moved south (**Fig 6**).

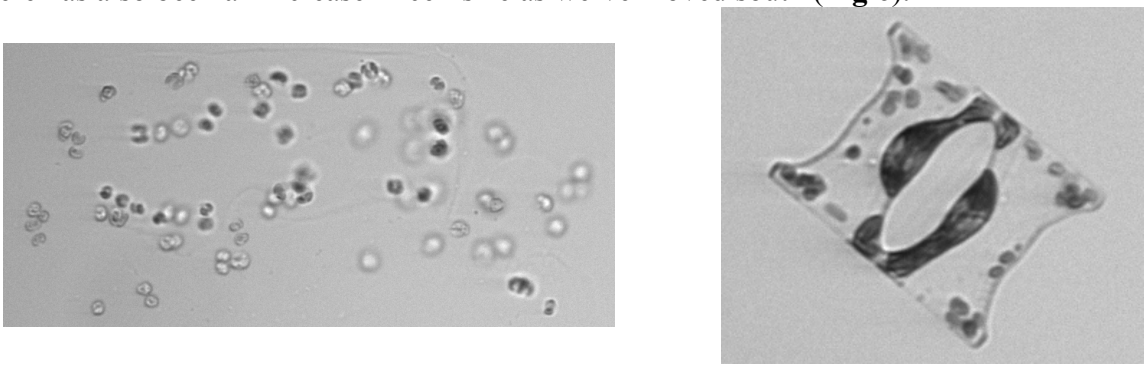

Figure 5. Photo of *Phaeocystis* (left) and the diatom, *Eucampia*, collected at Process Study 2.

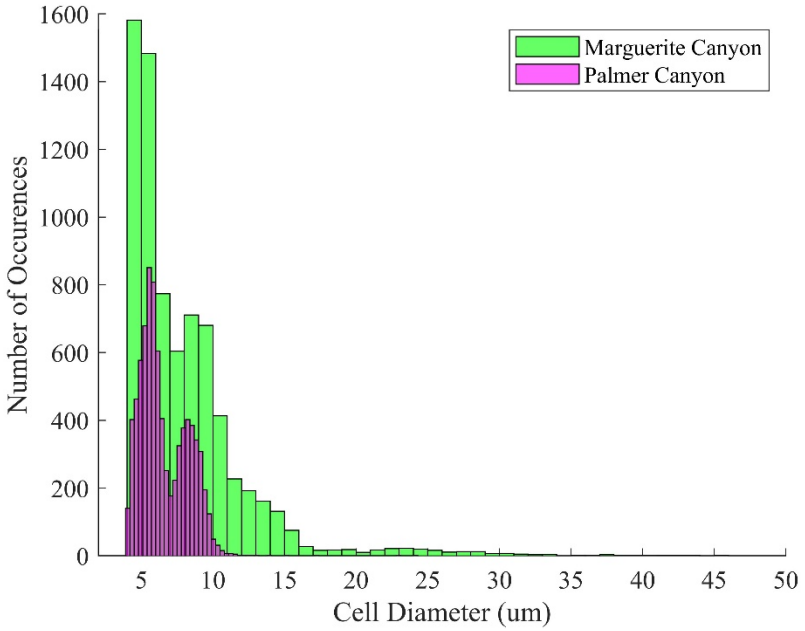

Figure 6. Histogram of phytoplankton cell diameter in Palmer Canyon (pink) and Marguerite Canyon (green), showing a shift to larger cells in Marguerite Canyon in the southern WAP.

Our incubation experiments are progressing, and we began a third incubation during Process Study 2. For these experiments, we have been incubating triplicate, 33L bags in flow-through incubators. Using the Imaging Flow Cytobot, we have been following the abundance of 'large' diatoms (larger than ~8-10 μm; **Fig 7**). We are interested in following the dynamics of a diatom

bloom, from formation to collapse, and specifically are interested in the role that viral infection plays in bloom termination. Little is known about the role viruses play in diatom bloom dynamics in polar regions. During the incubation, we are collecting an array of samples for downstream analysis, including biogenic silica (a proxy for diatom-specific biomass), POC/PON, dissolved nutrients, eukaryotic metatranscriptome analysis, and quantification of free, extracellular viruses (using targeted quantitative PCR). The data from our first incubation, using subsurface water collected at Palmer Deep on Jan 6, 2019, show that after ~ 1 week the diatoms started to bloom and are growing at growth rates that are typical for this region (~0.4 d-1) (**Fig. 8**). We have collected samples at two time points (day 7 and 12) and will collect additional time points during the bloom demise.

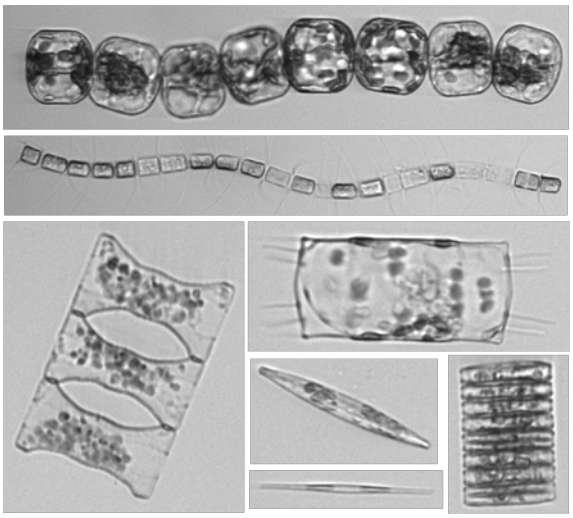

Figure 7. Photographs of large diatoms growing in incubation experiments acquired with the Imaging Flow Cytobot.

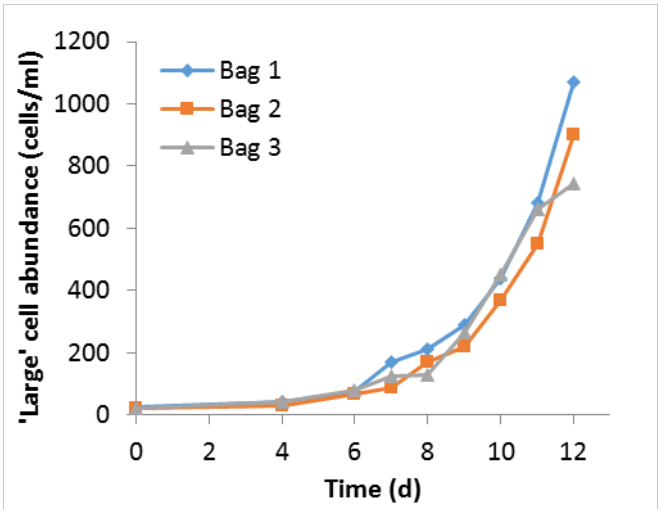

Figure 8. Abundance of 'large' cells (>8-10 µm) over time in days for Incubation 1, started at Palmer Deep, showing the start of a bloom after ~1 week.

C-020: Zooplankton Component-LTER (Debbie Steinberg, VIMS; PI)

Field Team Members: Deborah Steinberg, Joe Cope, Patricia Thibodeau, Joshua Sacks, and Samuel Malmquist

We concentrated our operations along the 200 line, and at the 3-day process study situated in Marguerite Bay. In addition to our regular station operations, we conducted day and night sampling of zooplankton distribution at discrete depth intervals using the MOCNESS (Multiple Opening-Closing Net Environmental Sensing System) to investigate depth distribution and diel vertical migration of zooplankton at the slope process study station, as well as the inshore Marguerite Bay canyon station. Tows were successful and we will process the samples at our home institution.

We also conducted four more experiments along the 200 line and at Process Study stations measuring rates of fecal pellet production by *Euphausia superba* to continue our time series of the role that different zooplankton taxa play in particle export in the WAP.

Patricia Thibadeau, a Ph.D. Candidate in Steinberg's lab is conducting experiments for her 3rd consecutive year with an open ocean snail, the shelled pteropod *Limacina helicina antarctica* (**Fig. 9**). Tricia is interested in determining how increasing temperatures and shifting food availability affect pteropod metabolism (specifically, respiration and excretion). She has been conducting a series of these experiments monitoring *Limacina* metabolism along the PAL LTER grid. New this year, Tricia has conducted continuous respiration monitoring experiments (**Fig. 10**) to determine potential circadian rhythms in pteropod respiration as well as better interpret results from experiments conducted the past two years.

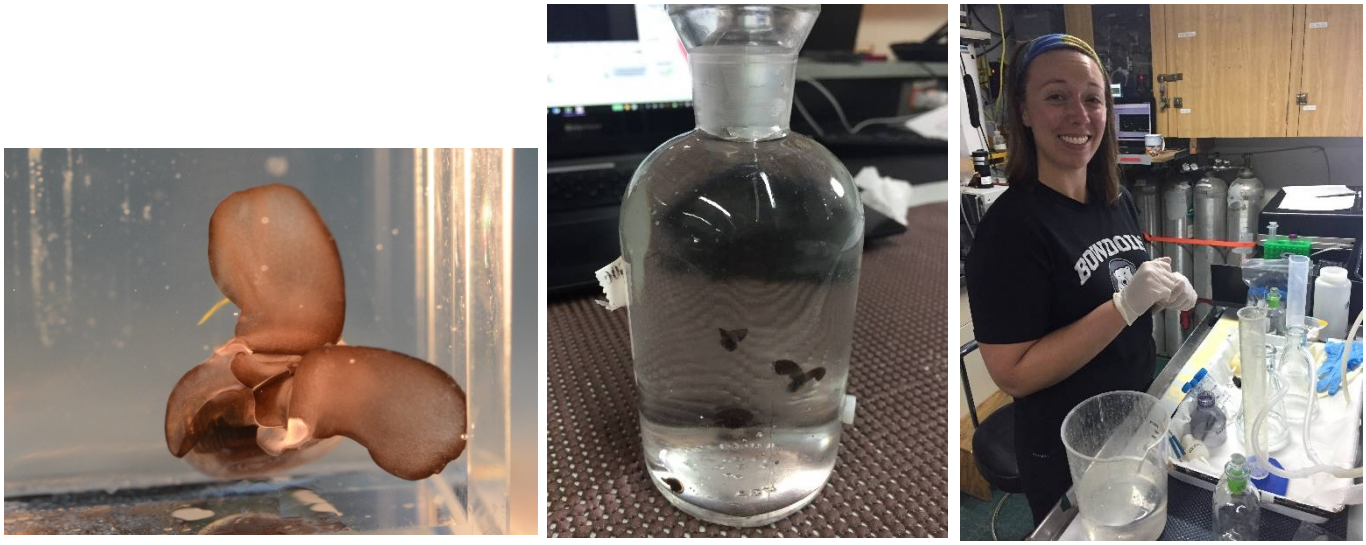

Figure 9. Left to right: Close-up of a swimming *Limacina helicina Antarctica, Limacina* in an incubation bottle, and Tricia Thibodeau processing samples from her experiment.

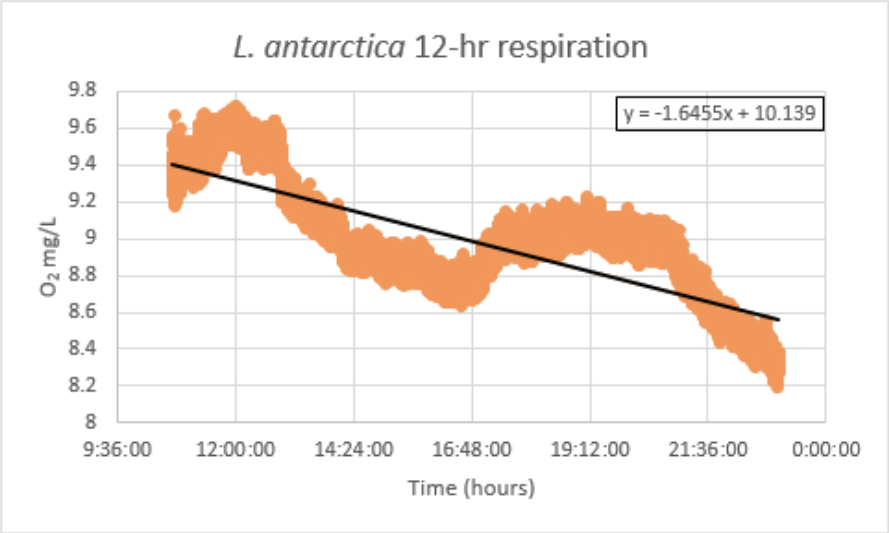

Figure 10. Decrease in oxygen concentration over time in a continuous respiration experiment.

B-258: Physiological ecology of 'herbivorous' Antarctic copepods (Ann Tarrant, Woods Hole Oceanographic Institution; PI and field team member)

This week, live copepods were sampled on three occasions along the 200 line (200.040, 200.-040 process station, and 200.000). Copepods were not sampled from 200.100 because a high abundance of gelatinous zooplankton resulted in poor copepod sample quality. We encountered large numbers of *Calanoides acutus,* with *Rhincalanus gigas* and *Calanoides propinquus* less abundant. Individuals were preserved in RNA later (61 *C. acutus,* 18 *C. propinquus*, and 13 *R. gigas*), and pooled samples were frozen for enzymatic or lipid analysis (20 pools of *C. acutus,* usually 5 animals per sample). These animals were individually photographed for morphometric analysis. Samples were collected from some of the small-scale feeding experiments that began during Week 1 (11 samples containing a total of 23 individuals, various species) and lasted 9-11 days (**Fig. 12**). With the high *C. acutus* abundance, a larger feeding experiment was started that included ~240 *C. acutus.* About 40% of these animals have been sampled after 5 days, and the remaining animals will be sampled next week.

Figure 12. *Calanoides acutus* from fed (left) and unfed (right) feeding treatments after 5 days of shipboard incubation.

C-013: Seabird Component-LTER (William Fraser, PI)

Field Team Members: Megan Roberts and Anne Schaefer

This week with the help of ASC staff we were able to establish our field camp on Avian Island, which we occupied from the morning of the 14th to the 20th of January. Our work at Avian is focused primarily on the breeding success and foraging ecology of Adélie penguins (**Fig. 13**). However we were able to use the limited access to the area to collect samples, and census multiple species for localized population dynamics as well as collect data on foraging. The same data is collected at Palmer and makes for a useful analysis of bird nesting and foraging at two sites with different sea ice characteristics along the WAP.

Figure 13. Adélie Penguin colonies on Avian Island.

While on Avian, we conducted breeding colony censuses of Adélie Penguins, and weighed and measured crèched (groups of) chicks. Additionally this year, we used a hand-held GPS logger to map all colonies on the island to later determine colony density on Avian I. To better understand foraging, we approached the problem from multiple angles. Diet samples from 27 adult Adélie penguins were collected and two GPS tags were deployed on two different adults to examine discreet foraging runs. These data provide interesting insight into foraging at Avian compared to the Palmer area over a short time scale. For long-term analysis of fish consumption, we collect excrement from sediment traps to extract fish otoliths that have accumulated over the course of the year, and are eventually used to identify to fish species. Skuas often predate Adélie Penguin chicks leaving the feet and skeleton intact. These chick feet were collected for stable isotope analysis. This is used as another means of analyzing diets that covers a longer time span than the diets we collect while on island.

Full island surveys of nesting Southern Giant Petrels, and Blue Eyed Shags were completed (**Fig. 14**). South Polar Skua fecal samples were collected and will be analyzed for fish otoliths to better understand Skua foraging. We collected boli from Blue Eyed Shags, primarily piscavores, to better understand what fish species are found in the general area, and to detect long-term changes in Blue Eyed Shag diets. A marine mammal census was also conducted. The vast majority of marine mammals seen on Avian are Southern Elephant seals.

Figure 14. Blue Eyed Shag on left, and Southern Giant Petrel on right.

We would like to sincerely thank the ASC staff that helped with the camp set up at Avian, and especially thank Sean Bercaw and Debbie Steinberg for their support and help achieve our main goal of establishing the camp at Avian Island.

C-024: Cetacean Biology & Ecology-LTER (Ari Friedlaender, University of California, Santa Cruz, PI).

Field Team Members: Michelle Modest, Ross Nichols

Sightings Operations

Humpbacks were the sole species observed during the 200 line grid transect and in significantly reduced numbers compared to last week/further north. The whales observed this week were seen foraging at the surface using surface lunge feeding, bubble net feeding and taking longer dives where prey could potentially be present at deeper depths. We have seen additional whales performing transiting behavior that presents itself as short surface intervals between temporally short dives. Photo ID was taken on all animals that were present during zodiac deployments and include a dorsal fin photo and matching fluke photo for later identification. Nearshore off of Adelaide island had the highest presence of whales, with diminishing numbers with further distance from shore along the 200 line. On the return to nearshore waters and the survey of Marguerite Bay, whales were essentially absent. 4 orcas were seen offshore of Rothera Station on the 18th, consisting of 1 male and 3 females. Rothera science staff confirmed that this group has been seen consistently throughout the season and were believed to be resident animals. See **Table 1** for our weekly and total sightings statistics, and **Fig. 15** for example sightings photo.

Biopsy operations

Over the last week, our team collected 6 biopsies on humpback whales. 4 of these whales showed bubble net feeding behaviors, and all showed surface lunging. This is indicative of whales foraging on a prey field that is much shallower, and possibly more diffuse. 5 of these samples had skin and blubber, however one of the samples only contained skin. While blubber is needed for some of our hormone analysis, skin samples allow us to use genetic analysis to sex and identify the whale and to perform microbiome analysis of the skin. We can use this sample to identify differences in skin features between different locations of the animal's dorsal area.

Table 1 – Weekly statistics of our sightings from the LMG 1901 from 1.12.2019 – 1.20.2019. Four orcas were seen at Rothera, with a reduction in Humpback whales from the week prior.

	Total Whales Sighted	Total Calves	Total Adults
Humpback	248	4	244
Minke	4	0	4
Orca	10	0	10
Fin Whale	6	0	6
Unknown	41	0	41
Totals	**309**	**4**	**305**

Biopsies	Total Samples
Humpback	13
Minke	0

Figure 15. An Adult Humpback whale surfaces between the LMG and the deployed Zodiac, this photo will be used in our photo ID database to later identify this whale by comparing their scarred dorsal fin to dorsal fins of other adult humpbacks in our system.