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**RESPONSE TO CLIMATE CHANGE:
PHYSIOLOGY AND ADAPTATION OF
ANTARCTIC AND SOUTHERN OCEAN LIFE -
A TRIBUTE TO GUIDO DI PRISCO**



Cinzia Verde

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ABSTRACTS SUBMITTED TO THE (CANCELLED) SCAR 2020 OSC IN HOBART

Temperature but not carbon dioxide, stimulates growth in Southern Ocean phytoplankton

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Southern Ocean phytoplankton have been shown to overcome the low light and low iron (Fe) environment through genomic and physiological adaptations. Together, these adaptations allow the efficient use of light and Fe to photosynthesize optimally in this cold polar region. Through biological and physical processes, the Southern Ocean (SO) accounts for approximately 40% of global carbon fixation. Model projections indicate that light, temperature, Fe and CO₂ (thus pH) in the Southern Ocean are likely to change simultaneously in the future due to changing climate. Although prior investigations have constrained the response of SO species to changes of individual environmental variables, multiple species responses to concurrent changes is unclear. This study adds to a growing research focus which aims to understand how marine biota will respond to climate changes over the coming century. It also aims to uncover underlying adaptations that allow SO phytoplankton to fix and export carbon in spite of cold temperatures, low light and growth limiting iron concentrations in this region. The evidence presented discusses the evolutionary ramifications for dispersal into the SO and suggests different evolutionary histories of SO diatoms isolated from the same location.

Climate change and chemical ecology: Determination of natural products in two species of Bryozoans, *Himantozoum* (*Himantozoum*) *Antarcticum* (Calvet, 1909) and *Chartella Tenella* (Hincks, 1887)

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The marine environment is exposed to global change and one of its effects is the increase of the water temperature, affecting all marine living species, even changing their metabolism. Many benthic organisms produce secondary metabolites (natural compounds) which are used as a defensive system against predation, competitors, microorganisms, pathogens, fouling, etc. In our study, our goal is to determine if there are variations in the natural product composition of two species of bryozoans when temperature is higher than usual. Therefore, two species of bryozoans were selected, representative of two different environments, "*Himantozoum* (*Himantozoum*) *antarcticum*" (Calvet, 1909) from Antarctica, and "*Chartella tenella*" (Hincks, 1887), from the Mediterranean Sea. The experiments consisted in keeping the animals at three different temperatures, 15°C, 20°C, and 25°C for the species "*C. tenella*", and 0°C, 5°C, and 10°C for the species "*H. antarcticum*". The experiments were done in filtered seawater aquaria, with a total of 40 organisms, 20 of each species for a total of two weeks for the Mediterranean samples and four weeks for the Antarctic samples. After organic extraction and clean-up of the samples, the determination of the different compounds was done using chromatography techniques coupled to ultraviolet-visible and a mass spectrometry detector (HPLC-MS). Chromatogram profiles show different composition between bryozoan extracts coming from the two environments, and samples kept at different temperatures present different chemical pattern, and therefore an effect of temperature on bryozoan natural products is observed.

Microbial diversity and role in carbon cycling at the Southern Ocean Time Series (SOTS) site, sub-Antarctic zone

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The Southern Ocean plays a critical and disproportionate role in global climate regulation, buffering the impact of anthropogenic climate change. Of the world's oceans it absorbs ~40% of the CO₂ and ~75% of the excess heat generated by human activities. Microbes form the majority of the biomass in the Southern Ocean and are key drivers of carbon and nutrient cycling. However, these microbial ecosystems are relatively unexplored and baseline data from which to measure how microbial diversity and function will respond to environmental change is extremely limited.

The present research focuses on the Southern Ocean Time Series (SOTS) site within the sub-Antarctic Zone (~142°E, 47°S). Time series observations from the SOTS moorings are crucial to understanding the ecosystem processes that impact carbon cycling; providing a rich, biogeochemical dataset. Microbial ecology studies of environmental samples collected from SOTS over three field seasons are combined with physicochemical observations to build, for the first time, a baseline picture of the microbial community against which future changes in ecosystem structure and function can be measured.

This talk will reveal the diversity and function of the SOTS microbial ecosystem and begin to highlight the community's role in carbon cycling. It will investigate the function of these microbial communities in carbon cycling by measuring rates of remineralisation of particulate organic carbon and changes in community structure during remineralisation. From this basis, the potential impacts of climate change on microbial carbon cycling in the Southern Ocean will be discussed.

Branchial osmoregulatory response of *Notothenia rossii* upon temperature and salinity changes

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Antarctic fish are strictly marine and have evolved in stable thermohaline conditions. Recent climate changes have contributed to rises in water temperature and forecast models indicate the rate of such changes will increase in coastal regions of maritime Antarctica, leading to further ice melting and freshening of shallow waters in enclosed areas.

Notothenia rossii were collected in shore waters from King George Island, and acclimated from natural temperatures (0-2°C) to 4-8°C and from 32‰ to 20 and/or 10‰ by addition of freshwater to recirculating tanks, over a period of up to 10 days. Blood samples were used for osmolality and ion-contents, and gills were preserved for determination of NaK-ATPase (NKA) activity, gene expression and for histology and fluorescence immunohistochemistry (FIHC).

Reduced salinity resulted in lower osmolality and decreased NKA activity showing limited hyperosmoregulatory ability. This was accompanied by modifications in the expression of genes coding for ion-transporters (NKA, NKCC, CFTR, NHE), water channels (aquaporins) and tight junction membrane barrier proteins (claudins). FIHC shows these fish present a typical distribution of chloride cells in the gill filament, with abundant levels of NKA and NKCC in sea- and brackish water, but do not appear to efficiently upregulate NHE in brackish water. Additionally, high temperature further reduced osmolality, mainly due to reduced sodium and chloride, increasing the osmotic gradient between extracellular fluid and seawater and resulting in up-regulated branchial NKA activity, thus contributing to the energetic demands.

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Antarctic sponges and climate change: are they winners rather than losers?

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Research assessing the effects of warming on Antarctic species have shown that the limited capacity of many Antarctic organisms to cope with climate change. Experimental studies at individual/molecular levels have demonstrated that some Antarctic species are sensitive to even small changes in water, also having significant effects at the community level. Antarctic sponges are important members of Antarctic benthic communities, being dominant in abundance and playing important functional roles. Based on previous knowledge on Antarctic organisms along with evidence from studies on sponges from other latitudes, it has been thought that sponges have a very limited or no capacity to cope with warming. Studies conducted on Antarctic sponges around Doumer Island, Palmer Archipelago (western Antarctic Peninsula) provide new insights about the potential resilience of some sponges to warming scenario and other climate change stressors, suggesting that not all Antarctic sponges might be “losers” as previously thought. Results show that sponges have some capacity to cope with small increases in temperature, showing genomic complements and hosting highly stable bacterial communities (in terms of community structure and predicted functional patterns) despite being exposed to abnormal seawater temperatures (3°C) and high rates of temperature increase (0.15°C day⁻¹). Previous research has reported a considerable plasticity in seasonal and metabolic plasticity in Antarctic sponges, which along with the potential role of their symbionts providing capacity to sponge hosts to cope with rapid environmental change, suggest they may improve the chances of more sponge species to become winners under the climate change scenario.

Survival in the Southern Ocean with Little or No Antifreeze Proteins

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Antifreeze glycoprotein (AFGP) is long regarded as an adaptive evolutionary innovation that crucially enabled the Antarctic notothenioids to colonize and diversify in the freezing Southern Ocean. Lacking this adaptive trait would seem paradoxical and incompatible with life for these endemic fish. However, two nototheniid species appear to be exceptions – *Lepidonotothen squamifrons* and *Pleuragramma antarcticus* (Antarctic silverfish). We investigated the biochemical and molecular bases of this peculiar trait alteration. *L. squamifrons* completely lacks active AFGPs in its blood. *P. antarcticus* has minimal circulating concentrations of AFGPs (~1mg/mL) versus its highly fortified (upwards of 30mg/mL) relatives. We sequenced the genome of these two species to isolate and characterize the AFGP loci for potential genotypic changes or defects. *L. squamifrons* has drastically reduced AFGP genotype, but some coding sequences (cds) appear intact. Tests for AFGP mRNA expression showed transcriptional silence likely caused the absence of the active protein. In contrast, *P. antarcticus* genome appears to contain large numbers of AFGP cds. However, closer scrutiny reveals much of them are non-functional SSR-like fragments scattered throughout the genome. The canonical AFGP family and its actual coding capacity will be clear when high quality assembly of the silverfish genome is complete. How does *L. squamifrons* survive without any AFGPs? In field and in lab tests suggest that *L. squamifrons* seek non-freezing bottom water layer to avoid freezing. It may serve as an adaptive model for notothenioid survival in a warming sea.

Effects of benzophenone-3 on temperate and polar microalgae under future warming scenarios

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Benzophenone-3 (BP-3) is an organic ultraviolet (UV) filter which is commonly found in various sunscreen products as a type of UV protectant. With the increased awareness of skin cancer, the usage of sunscreens had increased dramatically. The amount of BP-3 that was found in water bodies raised concerns on the effects of this chemical towards aquatic organisms. Moreover, the impact of global warming is becoming more apparent in recent years. In this study, a total of four microalgae from polar (*Chlorella* UMACC 400 and *Chlorella* UMACC 401) and temperate (*Chlorella pyrenoidosa* and *Chlamydomonas reinhardtii*) regions were used to investigate the interactive effects of BP-3 (0, 100, 200, 300, 400 mg/L) and temperatures (ambient, ambient + 4°C, ambient + 8°C) for 72 hours. The cell size, specific growth rate (μ), photosynthetic pigments (chlorophyll-a, chlorophyll-b, carotenoids) and biochemical composition (carbohydrate, protein, lipid) were measured to assess the impacts of BP-3 on microalgae under future warming scenarios. The results showed that high concentration of BP-3 (200, 300 and 400 mg/L) affected growth, photosynthetic pigments and biomass of microalgae. However, the two temperate microalgae exposed to 100 and 200 mg/L of BP-3 at 26°C (ambient + 8°C) resulted in increased in photosynthetic pigments and biomass. However, this was not observed in the polar microalgae. Further investigation is required to understand mechanisms used by these microalgae to cope with multiple stressors.

Long-term trend in reproductive cycle underpins inter-annual variation in the gametogenic development of an Antarctic marine invertebrate

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Reproductive success is an important measure of fitness, determining an animal's resilience to change and predicting population continuity and survival. Patterns in reproductive cycles and their drivers remain challenging to interpret since it is often the interplay between multiple factors that is responsible for regulating reproductive performance. This study investigates the long-term reproductive ecology of an abundant Antarctic sea urchin, *Sterechinus neumayeri*, by characterising the seasonal and inter-annual variability observed, and the key patterns that underpin reproductive allocation. The reproductive cycle of *S. neumayeri* was investigated over a seven-year period (2012- 2018) using monthly measurements of investment in gonad tissue and observations of gametogenic development. Seasonal and inter-annual variation in reproductive condition were also explored in relation to the changing environment. Our analyses identified significant annual increases in gonad index over the length of the time series. This suggests a long-term signal that varies on a decadal-scale which may underpin the seasonal and annual variability observed in reproduction. We hypothesise this trend is driven by the interplay between local and regional environmental factors. However, both gonad index and oocyte size co-varied with small changes in seawater temperature, which fluctuated by less than 2°C. These findings suggest that temperature plays a critical role in regulating reproductive performance in Antarctic marine invertebrates. In addition, this study underscores the need for future research that utilises long-term biological time series to better describe and reliably predict faunal responses to climate change, especially in terms of variability and consequences for reproductive performance.

Consequences of marine heat waves on the energetics and functioning of Antarctic marine invertebrates

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Extreme climate events, such as marine heat waves (MHW), are forecasted to escalate in many areas of the climate system under future global change scenarios. However, the implications of MHWs on the biological patterns and processes of marine organisms are relatively understudied in comparison to the effects of gradual temperature shifts. The difficulty of studying MHWs results from their unpredictable nature and past infrequency, where most studies to date have focused on the effect of gradual climatic trends. This study investigates how MHWs affect biological functioning in the Antarctic marine environment using a functionally important and abundant invertebrate, the sea urchin, *Sterechinus neumayeri*. Animals collected directly from the field were exposed to three rates of warming, 1 day/°C, 2 days/°C and 3 days/°C, until their thermal maximum temperature was reached. During warming, basic functioning, including ability to feed, food absorption efficiency, righting ability and metabolic rate were monitored. Initial findings suggest that despite thermal maximum temperatures occurring at > 9°C above ambient, functioning began to deteriorate when temperatures were increased by only a couple of degrees above ambient in all treatments. Our results show that although this species appears robust to warming in terms of lethal limits, it is in fact still highly sensitive, in terms of basic functioning, to just small changes in temperature, which will ultimately affect long-term survival of the species. This study highlights the need to consider the sub-lethal effects of short-term warming as incidences of MHWs continue to increase across the globe.

A chicken-and-egg dilemma: hemoglobin-and-red blood cells in white-blooded icefishes?

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Antarctic icefishes fascinate physiologists and evolutionary biologists because of their unique white blood lacking hemoglobin. The presence of mature erythrocytes in the icefish blood has, however, been controversial. Thus a chicken-and-egg dilemma still remains: Which came first? The loss of the capacity to make mature erythrocytes or the loss of hemoglobin genes?

To address this conundrum, we questioned the initiation of erythropoiesis in icefishes and characterized the morphology of erythropoietic cells in notothenioid peripheral blood.

Histological analyses of head kidney sections identified a few immature erythropoietic progenitors (proerythroblasts) in icefish, indicating that icefishes hematopoietic marrow still initiate an erythropoietic program, although attenuated. Morphological analysis of erythropoietic cells in blood smears from 13 red-blooded notothenioid and nine icefish species revealed that icefish proerythroblasts were morphologically undistinguishable from those of their red-blooded relatives. The most advanced erythropoietic cells observed in icefish blood were morphologically similar to, but smaller than, maturing erythroblasts in red-blooded species. Together, results suggest that erythropoiesis in icefish arrests at an intermediate stage of erythrocyte maturation. The peripheral blood of dragonfishes, the sister lineage to icefishes, contained mature, but circular, erythrocytes. Genomic analyses of published notothenioid genomes revealed potentially deleterious mutations in erythrocyte membrane skeletal genes, mimicking human spherocytosis and elliptocytosis conditions.

Our analysis therefore suggests either that the most recent common ancestor of icefishes and dragonfishes possessed abnormally shaped erythrocytes or that relaxed selection on components of the cytoskeleton independently led to alterations in erythrocyte shape and formation in dragonfishes and in icefishes.

Deciphering the molecular mechanisms at play in the acclimation of the Antarctic sea urchin *Sterechinus neumayeri* to future climate change scenario

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Global warming is threatening marine Antarctic fauna, which has evolved in isolation in a cold environment for millions of years. Facing increasing temperatures, marine Antarctic invertebrates can either tolerate or develop adaptations to these changes. Adaptation in Antarctic ectotherms will require at least hundreds of years. On a shorter time scale, their survival and resistance capacity to warming will be driven by the efficiency of their phenotypic plasticity. Successful acclimation to higher temperature has been shown possible in a limited number of marine Antarctic invertebrates. This acclimation to future climate change scenarios is mainly studied using the C_{max} method, which links animal physiology and thermal ecology. Although powerful to determine whether these taxa could successfully acclimate to out-of-range temperatures, traditional methods do not disentangle all the underlying biological, physiological and sub-cellular mechanisms at play. The aim of this study was to unravel the molecular mechanisms underpinning acclimation to different ocean warming scenarios in the Antarctic sea urchin *Sterechinus neumayeri* and to determine whether it is capable to adjust for maintenance of homeostasis under warming conditions. A combination of genomic, physiological and behavioral-based approach was used on individuals acclimated to three experimental temperatures: control (ambient temperature in summer, ca. 1°C), control +2°C and control +4°C, corresponding to warming predictions by the end of the century. Altogether our results showed an important regulative effort after acclimation to ocean warming with notable adjustments of major energy sink processes (e.g. proteins and RNA synthesis).

Global paleoclimate change and the loss of erythrocytes by Antarctic icefishes

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Understanding adaptation to environmental change is of fundamental importance to predicting the evolvability of species in the Anthropocene. Antarctic icefishes (Channichthyidae) lost the ability to produce red blood cells as the Southern Ocean (SO) cooled and dissolved oxygen concentrations rose, providing a test case for analyzing the evolutionary genomic responses to environmental change and the potential for species resilience as the SO now warms. By integrating paleoclimate records with an extensive phylogenomic dataset, we demonstrate relaxation of purifying selection across erythrocyte-associated genetic regions following a rapid decline in global temperatures and the formation of stable ice sheets. Acceleration of variation in erythrocyte-associated regions continues in modern Antarctic notothenioids, including red-blooded species. For example, we detected predicted deleterious variation in the beta-spectrin gene of red-blooded dragonfishes, one of which has spherocytic erythrocytes like those observed in humans with mutations in this gene. Despite loss-of-function mutations in a few key erythrocyte-specific genes, we show that most of the erythroid genetic toolkit has been maintained in icefishes. Interestingly, there is a bias in the accumulation of drift in putative gene-regulatory regions flanking genes expressed late in erythropoiesis. Together, results indicate that erythropoiesis in icefishes is blocked late in erythrocyte differentiation, consistent with the presence of proerythroblasts in icefishes. Our results provide a comprehensive phylogenomic perspective of the genetic changes in icefishes that led to loss of erythrocytes and a framework for understanding the potential for their adaptive resilience as the SO warms. Supported by US NSF PLR-1444167 (H.W.D.).

Climate change induced shifts in sea ice algae nutrient content: Species, community and trophic implications.

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The polar regions are experiencing a reduction in sea ice extent, yet the biological ramifications of these changes remain largely unexplored. Understanding the implications on sea ice algae is particularly important, as they provide up to 26% of total primary production in seasonally ice-covered waters and up to 50% in perennially ice covered waters. As sea ice algae are limited by a range of environmental factors, including water temperature, salinity and light availability, the ongoing environmental changes in the polar regions will shape the algal community composition, phenology and macromolecular composition. Combined, these effects alter the nutrients supplied to higher trophic levels and even small changes at the production level can have large cascading effects on higher trophic organisms in the short polar food webs. This study traces the changes in community composition and individual physiologies of sea ice algae as a result of environmental change. Specifically, we use FTIR microspectroscopy to perform single-cell analyses to investigate how sea ice algae shift in carbon partitioning between the macromolecular storage of proteins, lipids and carbohydrates in response to natural variation in temperature, salinity and light. This phenotypic plasticity exists to satisfy physiological requirements, such as increasing lipid accumulation in response to increases in salinity, in order to facilitate osmoregulation. However, this plasticity on a broad scale alters the nutrient availability to higher trophic levels, affecting modifications in nutrient transfer through the polar marine systems. Through tracing these changes, this study improves our understanding of the biological ramifications of sea ice decline.

The stress axis and response to acute stressors in *Notothenia rossii* acclimated at different temperatures

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Antarctic fish evolved in a stenothermal environment, subject to very small fluctuations in temperature throughout their life (−1°C - 2°C). Their ability to respond to increased temperature is uncertain. We aimed at evaluating the mechanism and capabilities of the HPI axis in Antarctic fish in three sets of experiments. Four groups were placed at 2°C. Upon a standard stress test (SST: chasing+netting +1min air exposure) fish were returned to tank and sampled after 1,4,24h. Six groups were acclimated to 2,5,8°C for 10-days. At this point the control group of each temperature was sacrificed. The other group received SST and sacrificed 90-min after. Plasma and tissue samples were collected for cortisol and stress-related genes and the interrenal used in-vitro to determine sensitivity to ACTH. Eight groups at 2°C were injected with drugs involved in blockage or stimulation of cortisol release/action (saline, cortisol, dexamethasone, metyrapone, spironolactone, mifepristone) and then kept at control or transferred to 6°C and sampled after 36 hours. After SST cortisol peaks between 1-4 hours and reduces to basal between 24-48 hours. Temperature influenced the cortisol response to SST. At higher temperatures cortisol levels in non-stressed group are as high as in fish subjected to SST. Interrenal sensitivity at high temperature showed little response to ACTH, suggesting low sensitivity and/or exhaustion. Manipulation of the HPI-axis showed these fish to respond in a way similar to what has been reported in other fish families in temperate or tropical environments. Supported by FCT through Propolar and grants PTDC/BIAANM/3484/2014 and CCMAR/Multi/04326/2019.

Microbial diversity and community structure across space and depth in Gerlache Strait (Western Antarctic Peninsula)

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The Gerlache Strait presents several environmental changes from natural fluctuations and anthropogenic impacts, such as glacier melting/retreat, lowering of the seasonal ice-sheet and one of the fastest rates of temperature increase. As microorganisms play a vital role in the element cycling in the pelagic system, this study aimed to analyze the taxonomic composition, diversity and community structure of Bacteria and Archaea of the Gerlache Strait, besides inferring their functionality and understanding the impacts of environmental factors in these communities. A total of 38 samples were collected from the euphotic zone to deep waters during the austral summers of 2013, 2014 and 2015. The region V4 of the 16S rRNA gene was sequenced using the Illumina platform and bioinformatics tools were used for data analysis. The observed OTUs varied from 306 to 631, and bacterial taxa (90.4%) prevailed over archaea (9.6%). These microorganisms were clustered according to depth (categories below or above 100 m) and temperature (below or above 0°C). An increase in the archaeal diversity, mainly Marine Group II and Nitrosopumilus, was observed with depth. Regarding bacteria, there was a higher relative abundance of Deltaproteobacteria and Cyanobacteria at lower temperatures. The relative abundance of Gammaproteobacteria and Deltaproteobacteria was higher below 100 m deep, while for Alphaproteobacteria, Oxyphotobacteria e Bacteroidia were relatively more abundant in the euphotic zone. Since temperature is a key driver of microbial communities in the maritime Antarctica, climate-driven change will possibly shift the microbial community structure disturbing biogeochemical cycles, especially the sulfur and nitrogen.

Assimilation and turnover rates of specific lipid compounds in dominant Antarctic copepods: CSIA, a cutting-edge tool to reveal ecophysiological adaptations in polar oceans during times of climate change

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The study revealed species- and stage-specific differences in lipid accumulation of the dominant Antarctic copepods, the primarily herbivorous *Calanoides acutus* (copepodids CV, females) and the more omnivorous *Calanus propinquus* (females), storing wax esters and triacylglycerols, respectively. Feeding carbon-labelled diatoms to these copepods, ¹³C signatures elucidated assimilation and turnover rates of total lipids as well as specific fatty acids and alcohols. The ¹³C incorporation was monitored by compound-specific stable isotope analysis (CSIA). CV stages of *C. acutus* exhibited an intense total lipid turnover and 55% of total lipids were labelled after nine days of feeding. In contrast, total lipid assimilation of female *C. acutus* and *C. propinquus* was clearly lower with 29% and 32%, respectively. The major dietary fatty acids 16:0, 16:1(n-7) and 20:5(n-3) showed high turnover rates in all specimens. In *C. acutus* CV copepodids, the high rates of the de novo synthesized long-chain monounsaturated fatty acids and alcohols 20:1(n-9) and 22:1(n-11) indicate intense lipid deposition, whereas these rates were low in the females. These high-resolution data of lipid assimilation and turnover provide a much better understanding of lipid metabolic pathways. Lipid accumulation of zooplankton key species, especially herbivores, is a crucial process in polar oceans buffering the extreme seasonality of primary production. These life history traits are well synchronized with seasonal events. However, environmental change at high latitudes may decouple e.g. light- and temperature-controlled processes and thus result in a mismatch situation of primary and secondary production impacting lipid biosynthesis of herbivores.

Potential disruption of gelatinous zooplankton to subantarctic ecosystem function caused by climate change

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Due to the formation of intermediate and mode waters in the subantarctic Southern Ocean, the region is considered to be an important deep ocean carbon sink. Common zooplankton in this area such as krill and copepods play a noteworthy role in the downward carbon flux, for example by producing carcasses. In autumn 2019, a bloom of the pelagic tunicate *Pyrosoma atlanticum* was observed in the subantarctic Southern Ocean, far from its normal subtropical home. Pyrosome bloom frequencies are thought to increase under marine heatwave conditions, which may lead to increasing numbers in the subantarctic Southern Ocean as the warm East Australian Current extends further south. During this study, pyrosomes exceeded the biomass of other common zooplankton, so we investigated their potential contribution to downward carbon transport and compared the results to krill. We measured bacterial remineralisation of pyrosome and krill carcasses. Further, we analysed their sinking velocity in a settling column and estimated the transport to the deep Southern Ocean. Due to their high biomass and abundance in the water column, pyrosome carcasses were a hotspot for bacterial activity. Additionally, the fast sinking speed and relatively high carbon content indicate their importance in the subantarctic carbon flux. We will finish this talk by exploring the possible impacts of increasing pyrosome abundance could have on the subantarctic ecosystem biodiversity and overall function.

Shifts in ascidian distributions in response to rapid glacial retreat in Marian Cove, King George Island, WAP

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Impacts of tidewater glacier retreat on epibenthic megafauna were investigated in Marian Cove, a small tributary embayment of KGI where tidewater glaciers have retreated about 2 km over the last six decades and ~45% of its bottom turned into ice-free area. The benthic communities were investigated from almost entire water depths (10-90 m) at four selected sites with varying distances from the glaciers using a remotely operated vehicle (ROV). Analysis showed that filter feeders, particularly ascidians were the most diverse (14 out of 63 taxa captured in the ROV images) and the most abundant (~128 inds./m²) taxa, contributing most (~64%) to the differences of the total epibenthic assemblages, suggesting a utility of ascidians as a sentinel taxon for assessing climate impacts. Furthermore, the ascidian distributions were well differentiated by the distance from the glacier front and also with water depths. The two opportunistic species *Molgula pedunculata* and *Cnemidocarpa verrucosa* predominated (>90% of density) at all depth close to the glaciers, while more diverse taxa (14) occurred at 50-90 m in the remote site (3.5 km from the glacier), indicating a shift in habitat stability. Sediment analysis supported the idea that ascidian shifts were primarily related to habitat stability. Given the fact that the distance was proportional with the time elapsed after the retreat, the ascidian shifts seemingly reflected successional processes over the long-term period in the past, which in turn would be expected to project future changes.

Manganese co-limitation of phytoplankton in the Southern Ocean

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The Southern Ocean (SO) plays a critical role in global biogeochemical cycles and climate. The SO is the largest High Nutrient Low Chlorophyll (HNLC) area, where phytoplankton growth is thought to be limited mainly by iron (Fe) concentrations. But, other trace metals, such as manganese (Mn) potentially co-limit phytoplankton growth in HNLC areas. Mn is an essential micronutrient due to its roles in photosynthesis and in the scavenging of reactive oxygen species. However, its biogeochemistry remains poorly constrained.

A recent voyage following the SR3 transect, between Tasmania and Antarctica, measured incredibly low Mn concentrations over most of the section, including the lowest Mn concentrations ever measured in the SO. This suggests that SO phytoplankton communities may have a low requirement for Mn or that Mn limitation is pervasive. In subsequent voyages to the Southern Ocean Time Series (SOTS) site, located in Subantarctic waters, south of Australia, we performed Fe and Mn addition incubations on natural phytoplankton communities during austral spring and autumn.

Results showed different seasonal responses of the phytoplankton communities to Fe and Mn additions. In spring, only the addition of both Fe and Mn resulted in significant biomass increase, suggesting Fe-Mn co-limitation. This result was not observed in autumn. Flow cytometry, along with carbon and Fe uptake measurements provided additional information on the communities involved and the physiological effect of Fe-Mn co-limitation. Overall, our findings provide physiological insights on how these Subantarctic phytoplankton communities cope with changes in natural conditions.

Functional diversity reveals novel insights into the distribution of Southern Ocean squid

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Squids play an important role in the Southern Ocean ecosystem, as their prevalence in the diet of many top predators and their voracious feeding nature potentially exerting a top-down control on their prey species. These species are documented for circumpolar distribution and show higher numbers of squid species relation to various fronts of the Antarctic circumpolar current, presumably driven by regional oceanographic conditions. However, such knowledge is mainly built on species richness and associated occurrence-based measures, and yet information about their diversity taking into account species traits appears to be the most necessary. Here, we provided comparisons of a biodiversity distribution measure based on richness with metrics that incorporate species functional traits. We used squid occurrence data from the SCAR Biogeographic Atlas of the Southern Ocean and Global Biodiversity Information Facility (GBIF), and calculated functional diversity indices that summarize community diversity with respect to four traits, encompassing body size, feeding ecology, maximum living depth, and phylogeny. The richness of functional groups closely resembled the pattern in species density. In contrast, functional diversity of the squids showed markedly different patterns to the species density and functional group richness. Both maximum living depth and phylogeny contributed most to the pattern of functional diversity. In addition to previous “hotspot” regions, new hotspots of squid diversity were predicted for areas along the Subantarctic Zone and Antarctica. These findings imply a more complicated distribution of the Southern Ocean squid, possibly contrasting with well-known latitudinal gradients in richness.

The role of viruses in marine polar environments and their response to change

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Viruses are the most abundant life form on earth with an estimated total abundance in the oceans of ~10³⁰. They are responsible for 10-30% of bacterial mortality, known to control harmful algal blooms and can reduce photosynthesis by up to 78%.

In Prydz Bay, eastern Antarctica, their abundance at all depths was closely correlated with both chlorophylla and bacterial abundance. Metagenomic analyses of surface seawater from the Scotia Ridge and Prydz Bay, identified bacteriophages of the Caudovirales, especially the Podoviridae, as the most abundant. Microalgal viruses belonging to the Phycodnaviridae family, which contains most microalgal viruses, especially Phaeocystis viruses, were also identified.

Sea ice algae communities comprises a globally significant photosynthetic biofilm. While their microalgal and bacterial constituents are well characterized, there is very little information on their associated viral communities or on the virus-bacteria and virus-algae interactions within them. While high levels of interaction might be expected because of the high density of cells, infection rates, particularly of microalgae, have been found to be low. It remains unclear whether this is a result of environment characteristics, developed resistance or because of the small number of studies.

We are investigating how ocean acidification and other climate change forcings will change infection rates in ice edge blooms and sea ice ecosystems.

Effect of ocean acidification and temperature on physiology and energetics of Antarctic krill

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Antarctic krill (*Euphausia superba*) is a key species in the Southern Ocean, forming an important link between primary producers and higher-level predators. A commercial fishery for krill has existed for almost 50 years, due to their high biomass and swarming behaviour, and because of its commercial and ecological importance krill are one of the best studied crustacean species. During the last several years, general concepts of krill biology and life history have changed considerably as more information is collected from the field and laboratory experiments; however, there are still only a handful of published studies examining the effects of ocean acidification (OA) on krill. Until now, there have been no long-term experiments focusing on krill and their physiological and energetic responses to OA combined with increased temperature. There is currently a gap in the knowledge as to whether krill can adapt to the changes occurring in their ecosystem, and, if they can, if a “tipping point” will arise at which adaptation can not occur. Through laboratory-based experimentation, krill physiological responses were monitored over 1.5 years. These responses included growth, reproductive maturity, metabolic activity and lipid storage. Understanding the effects of increased exposure to CO₂ and temperature on the physiological responses of krill will allow Southern Ocean fisheries management, led by the Commission for the Conservation of Antarctic Marine Living Resources, to parameterise existing Southern Ocean ecosystem models and continue fishing for the species in a sustainable manner.

Responses from sub-Antarctic phytoplankton communities to short-term trace metal incubations in early austral spring and links with the biogeochemical signature of sea ice

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Phytoplankton (PL) growth in the Southern Ocean (SO) buffers the effects of rising atmospheric CO₂ and is thought to be limited by micronutrients (e.g. Iron). Formation of winter sea-ice is thought to store trace metals (TM) which are released in spring and summer, providing PL with necessary micronutrients for growth. During the SCALE 2019 expedition in the Atlantic sector of the Southern Ocean we assessed if PL growth is limited by TM during early austral spring in the sub-Antarctic and marginal sea ice region. The influence of “non-limiting” nutrients (e.g. Al) was also investigated as recent studies suggested that Al may have beneficial growth effects on PL 1,2,3. Ice cores from the marginal ice zone indeed show higher concentrations of TM and Chl-a compared to in situ waters. The phytoplankton community response to addition of TM compared to control in short-term incubations was evaluated from chl-a concentration, flow cytometry, and phytoplankton photo-physiology. Results suggest that phytoplankton communities may not have been limited by TM at the time of sampling. Further, Al only additions had a negative effect on PL community structure. It is possible that the early melts of sea-ice from the marginal ice zone are a potential source of trace metals beyond their threshold limiting concentrations.

1 Zhou et al. (2018) doi: 10.1016/j.jinorgbio.2017.09.022

2 Liu et al. (2018) doi: 10.1016/j.marpolbul.2018.02.011

3 Zhou et al. (2018) doi: 10.1007/s10533-018-0458-6

Antarctic krill microbiota and its relationship with climate change through a metagenomic approach

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Antarctic krill is one of the most abundant organisms on the planet and lives only in the Antarctic region, it is the main food of many organisms and is the basis of the food chain in Antarctica, it feeds mainly on phytoplankton but can feed on other organisms as well as waste or decomposing organic matter. Its diet is very versatile and it is known that it has a great metabolic capacity mediated by microorganisms, these microorganisms have adapted to the conditions of the host as well as the physical or environmental environment being an important source of genes and bioactive compounds for the industry. This study aims to identify the main microbial patterns that make up the microbiota of the Antarctic krill through a metagenomic approach aimed at 16S RNAr genes and establish what are the relationships established with the main oceanographic variables such as sea temperature, dissolved oxygen, salinity and pH, as an instrument for assessing the effects of climate change in the area between the Bransfield Strait, Joinville and surrounding Elephant Island in the Antarctic Peninsula. Finally, it should be noted that this study is part of the ANTAR XXVI and XXVII scientific expeditions developed by the Peruvian state during the southern summer 2019-2020.

Evaluating the effects of ocean warming and freshening on the physiology and transcriptomic response of the Antarctic limpet *Nacella concinna*

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Antarctic coasts are highly vulnerable environments where temperature have remained very constant for millions of years. These unique environmental conditions have generated a large number of stenotic species that could be highly sensitive to future projections of climate change. We investigated the effects of increasing seawater temperature and decreasing salinity on the physiological and transcriptomic performance of the subtidal Antarctic limpet *Nacella concinna*, collected at Fildes Bay, King George Island. Adult limpets were exposed to an orthogonal combination of five temperatures (1, 4, 8, 11, 14 °C) and two salinities (20, 30) for a 60-day period. A drastic increment in mortality was observed with seawater warming and 100 % mortality was recorded in limpets exposed to 14, 11 and 8 °C, both salinities. At 4°C, sub-lethal effects were observed with a negative scope for growth associated with a mild up-regulation of genes involved in oxidative stress (e.g. glutathion peroxydase). At 1°C (control), a positive scope for growth was observed in both salinities and no mortality was recorded. However, an important regulation of limpets transcriptome was observed with an up-regulation of stress-related proteins (chaperons) and a down-regulation of genes involved in carbohydrate and ATP metabolism. Scope for growth was negatively affected by the interaction of ocean warming and freshening which inhibited the expression of chaperons (HSP). The stenothermal character of *N. concinna* demonstrate the limited ability to cope with the most severe models of global warming and freshening projected for the Antarctic and Magellan regions by the end of the century.

The hypoxia response in *Notothenia coriiceps*

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We sought to determine if the evolution of Antarctic notothenioid fishes in a cold, oxygen-rich environment has diminished their capacity to mount a robust molecular response to hypoxia. *Notothenia coriiceps* were held at normoxia (10 mg L⁻¹ O₂) or hypoxia (2 mg L⁻¹ O₂) for 12 hours. Protein levels of the master transcriptional regulator of oxygen homeostasis, hypoxia-inducible factor-1 α (HIF-1 α), were quantified in nuclei of heart ventricles using western blotting. Changes in gene expression in heart ventricles, as well as in brain, liver, and gill, were quantified using RNA-Seq. Although protein levels of HIF-1 α increased in heart ventricles in response to hypoxia, the expression of only 22 genes increased, none of which are known to be regulated by HIF-1 α . Liver displayed the largest molecular response to hypoxia with the expression of 664 genes significantly changing, including an upregulation of genes in the MAP kinase and FoxO pathways, and ones involved in glycolytic metabolism and vascular remodeling, indicative of a canonical molecular response to hypoxia. Overall, the molecular response to hypoxia appears diminished in some tissues, but not absent, in Antarctic notothenioid fishes.

Impacts of ocean acidification on key members of shallow water Antarctic communities

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Macroalgae form dense undersea forests on hard bottoms along the northern portion of the western Antarctic Peninsula (WAP). Macroalgae support huge densities of amphipods which are the most numerous animals in the forest communities. Prior work from our group has shown that some species of amphipods will be impacted more by ocean acidification than others. However, the results demonstrated that longer term studies were needed on multiple members of the macroalgal-associated amphipod assemblage to understand which species may be relative 'winners' and 'losers' in future oceans. We performed a 60+ day long experiment with amphipod assemblages from macroalgae at several sites near Palmer Station on southwest Anvers Island. Amphipods and their associated host macroalgae were held under ambient, near-future, and more distant-future pH levels. The amphipods were at the same density per unit biomass of their hosts as they had been in nature. Relative winners and losers were identified at the end of the experiment. These data will inform a follow-on experiment comparing 'winners' and 'losers' to understand what amphipod characteristics are likely to contribute to relative fitness in the future Southern Ocean along the WAP.

Are Antarctic mollusks prepared for an invasion of shell-crushing predators?

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In marine environments where shell-crushing predators are very scarce, such as in coastal zones of the Antarctic, shelled species should have thinner and less complex shells, given low selection pressure for thicker shells or harder material. This study assessed natural variation in the shell strength and the vulnerability of the dominant Antarctic limpet *Nacella concinna* to a novel shell-crushing predator. Limpets from the intertidal and subtidal rocky shores of King George Island (Antarctica) were collected and the breaking strength of their shells determined using an electronic tension/compression device. Shells from intertidal limpets had 66% greater breaking strength than subtidal ones, presumably due to higher mechanical forces experienced there. Limpets from the subtidal environment were also transported to southern Chile where they were exposed to a shell-crushing predator, the southern king crab (*Lithodes santolla*). 83% of the limpets were consumed within 24 h, the crabs broke the shell without apparent difficulty. When limpets were exposed to water-borne cues of the crab for a 8-month period, there was no change in shell strength. Despite abundant evidence of shell plasticity in mollusks, our results demonstrate that this species does not modify shell mechanical properties in response to the presence of crushing predators, at least, not as a rapid response. This key Antarctic species thus appears extremely vulnerable to bioinvasions of shell-crushing predators, and further efforts to estimate the vulnerability of this and other species are needed to predict the magnitude of possible changes in Antarctic marine communities. FONDECYT 1180643, FONDAP-IDEAL 15150003

Evolution of globin genes in red-blooded and white-blooded Antarctic notothenioid fish

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As Antarctic waters chilled, notothenioid ancestors adapted to cold, oxygen-rich waters followed by the evolution of icefish, which lack functional hemoglobin genes. Some icefishes also fail to express cardiac myoglobin, but all appear to retain other globin genes: cytoglobin-1, cytoglobin-2, globin-x, and neuroglobin. Functions of the corresponding proteins, however, remain poorly understood, but may include oxygen storage and protection against oxidative stress. To test the hypothesis that these minor globins evolved features related to cold hyper-oxygenated water and hemoglobin loss, we performed phylogenomic analyses, addressed evolutionary selective pressures, and followed gene expression patterns in both temperate and Antarctic notothenioids, including icefishes. Genomic analyses identified conserved synteny, gene sequences, and protein domains for all four genes. Evolutionary analyses revealed sequence divergence between temperate and Antarctic species, suggesting evolution associated with cold adaptation. Cytoglobin-1, Cytoglobin-2, and Globin-x showed additional residue changes in icefishes, suggesting sequence evolution related to hemoglobin loss. Finally, expression analyses showed that all four globin gene expression patterns evolved with cold adaptation, and that cytoglobin-1 and cytoglobin-2 displayed additional changes in expression patterns in white-blooded Antarctic fish. We conclude that these four globins evolved as fish adapted to chilling waters, potentially providing additional protection from oxidative stress. Globin expression patterns also evolved, as cytoglobin expression increased in white-blooded fish compared to red-blooded Antarctic fish, which might provide icefishes with supplemental oxygen storage capacities. Together, these findings suggest that evolutionary modifications in globins may have contributed to the success of Antarctic notothenioid fish.

Temperature response of active microbiome from perennial cave ice

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Icy habitats investigations unraveled the impact of climate changes on the glacier melting leading to microbiome exposure to higher temperatures when changing habitats. Our survey provides pioneering data on the heat-shock response of ice-contained microbial communities focused on their structural and functional diversity.

Shotgun metatranscriptomic analysis of the 900 years-old ice microbiome from Scarisoara cave (Romania) submitted to a three-day 4-25°C heat-shock cycling treatment followed by incubation at 4°C up to 14 days constituted the first characterization of the active microbial community from ice habitats. Both rRNA and mRNA data revealed a major variation of the microbial composition immediately after heat-shock, suggesting a dissimilar resilience of ice microbial taxa and functional response at gene transcription level after glacier melting. Among the dominating bacterial representatives, Firmicutes, Actinobacteria and Chlorobi were mostly affected, while Archaea, scarcely present in this habitat, showed a 9-fold decline of relative abundance after heat shock cycles. Fungal community appeared to be the most disturbed by the thermal shock, mainly Basidiomycota and Ascomycota taxa, while Blastocladiomycota and Chytridiomycota phyla were more adapted to temperature variations. Microeukaryotes mostly represented by heterotrophic flagellates showed a high recovery potential after heat-shock exposure. The functional response implied an upregulation of the genes coding for chaperones, polymerase sigma factor, enzymes of the TCA cycle, and implied in carbon and nitrogen regulation and cellular motility.

This first report on the presence of an active microbiome in perennial ice accumulated in caves contributes to understanding changing environments and their ecological impact due to ice melting.

Not dead, just dormant: Building a physiological basis to understand susceptibility of an Antarctic copepod to climate change

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The calanoid copepod, *Boeckella poppei*, is broadly distributed in Antarctic maritime lakes that are undergoing rapid structural alterations due to climate change. This copepod species occupies the highest trophic level of these lakes, and produces embryos capable of remaining dormant for centuries when conditions are inhospitable for active life-stages. However, little is known about the biology of dormancy in *B. poppei*. Understanding the mechanisms responsible for the dormant stage is necessary to predict the effects of climate change on Antarctic freshwater zooplankton. This study is the first to examine dormancy mechanisms and post-dormancy development in *B. poppei*. Pre-emergent development in *B. poppei* was characterized after exit from the dormant state using morphological features visible by light microscopy. The number of nuclei increases during pre-emergent development as yolk platelets are depleted. This indicates that yolk stores must be conserved during dormancy. If yolk must be preserved, then the embryos must downregulate metabolism while dormant. It is known that intracellular acidification in brine shrimp embryos downregulates metabolism during anoxia-induced dormancy. A similar acidification is expected in embryos of *B. poppei* because embryos in lake sediments are likely to encounter anoxic conditions. To test this, intracellular pH during resurrection from dormancy was monitored with ³¹P-NMR. Intracellular pH alkalinizes during post-dormancy development, indicating that pH is acidic during dormancy. In summary, embryos of *B. poppei* must downregulate metabolism while overwintering, and this appears to be achieved using intracellular acidification.

Coccolithophore response to environmental variability in the subantarctic zone and their role in the carbonate pump: lessons from the SONaR-CO2 project

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Coccolithophores are an important component of the present and past Southern Ocean biogeochemical cycles, however their contribution to calcite production and export and their response to ongoing environmental change are largely unknown. The Marie Curie Action SONaR-CO2 aims to shed light on these issues by analysing the coccolithophore assemblages preserved in unique water column time-series collections and sediment samples from the Australian and New Zealand sectors of the Subantarctic Zone. We found that peak relative abundances of heavier *Emiliana huxleyi* coccoliths occurred at times of maximum annual TCO₂ concentrations in all the time series analysed. These results challenge the view that ocean acidification will necessarily lead to a replacement of heavily-calcified coccolithophores by lightly-calcified ones in subpolar ecosystems. Secondly, we estimated that coccolithophores account for about half of the annual carbonate export to the deep sea in the Subantarctic Zone. Notably, although *E. huxleyi* numerically dominates the assemblages, less abundant but larger species account for a greater contribution to the CaCO₃ flux. Combination of our results with previous studies suggests that future southward migration of oceanic fronts will result in increasing CaCO₃ export but, eventually, ongoing ocean acidification will overwhelm those changes. Lastly, comparison of coccolith morphometric parameters of modern (sediment traps) and pre-industrial (surface sediments) *E. huxleyi* assemblages revealed important differences between them. Although the signal preserved in the sedimentary record is partially obscured by carbonate dissolution, our results indicate that pre-industrial Holocene *E. huxleyi* assemblages were more calcified than present populations.

Antarctic intertidal macroalgae under increased temperatures induced by Climate Change: would they thrive?

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The Antarctic Peninsula is one of the regions to be most affected by increase in sea surface temperatures (SSTs) mediated by Climate Change. Temperature is one of the most important factors mediating diversity and distribution of macroalgae, although there is still no consensus as to the likely effects of higher SSTs, especially for polar seaweeds. Some available information suggests that potential strategies to withstand future increases in SSTs will be founded upon the glutathione-ascorbate cycle and the induction of chaperone-functioning heat shock proteins (HSPs). The intertidal green, red and brown macroalgae species *Monostroma hariotii*, *Pyropia endiviifolia* and *Adenocystis utricularis*, respectively, from King George Island, Antarctic Peninsula, were exposed to 2 °C and 8 °C for up to 5 days (d). Photosynthetic activity (α ETR and ETRmax, and EkETR), photoinhibition (Fv/Fm) and photoprotection processes (α NPQ, NPQmax, and EkNPQ) provided no evidence of negative ecophysiological effects. There were moderate increases in H₂O₂ and lipid peroxidation with temperature, accompanied by stable levels of total glutathione and ascorbate, with mostly higher levels of reduced ascorbate and glutathione than oxidized forms in all species. Transcripts of *P. endiviifolia* indicated a general upregulation of antioxidant enzymes and HSPs under warmer temperature, although with different levels of activation with time. This investigation suggested that Antarctic intertidal macroalgae may be able to withstand future rise in SSTs, perhaps slightly altering their latitudinal distribution and/or range of thermal tolerance, by exhibiting robust glutathione-ascorbate production and recycling, as well as the induction of antioxidant enzymatic machinery and the syntheses of HSPs.

Ecophysiological and whole transcriptome responses of the rare Antarctic aquatic moss *Drepanocladus longifolius* to increased temperatures projected for Climate Change

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Drepanocladus longifolius is a rare aquatic bipolar moss, recently described in the Antarctica. In King George Island, Antarctic Peninsula, *D. longifolius* grows in inner lakes below 5 meters depth under daily and seasonally extremely changing environmental conditions, as those related with light and temperature. To address the molecular basis behind stress response and potential adaptation to future conditions of Climate Change, *D. longifolius* was sampled from Kitiash lake and exposed under laboratory conditions to increasing temperatures from 2°C (control) to 8°C for 3 days at 140 $\mu\text{mol m}^{-2}\text{s}^{-1}$ photosynthetic activity radiation (PAR), day/night cycle of 20/4 hours. In ecophysiological response, *D. longifolius* does not suffer consequences in terms of photosynthetic activity, manifested in *in vivo* fluorescence of chlorophyll *a* parameters (*Fv/Fm*, ETR, NPQ). A *de novo* whole transcriptome study, sequencing with Illumina NovaSeq platform 6000, demonstrated the regulation of almost 1,400 genes, of which 626 were downregulated and 764 were over-expressed under 8°C. From the latter, there were related to primary metabolism processes such as carbohydrate metabolism, lipid metabolism, several transcription factors, seed dormancy and maintenance, and stress response associated with light harvesting complex-related proteins, enzymes involved in cell wall reorganization, dehydration and senescence response proteins, and several antioxidant enzymes and heat shock proteins (HSPs). The information suggested that an efficient tolerance response based on the activation of several increased-temperature mechanisms will provide *D. longifolius* efficient ecophysiological and metabolic defenses to counteract increased temperatures expected for the end of the XXI Century, even under the most negative predicted scenarios.

Increased temperatures predicted for Climate Change induce general transcriptomic tolerance responses in the Antarctic intertidal brown macroalga *Adenocystis utricularis*

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Adenocystis utricularis is an ecologically relevant intertidal brown macroalga distributed from the temperate west coast of South America until the Antarctic Peninsula. In the latter, it survives under extreme environmental conditions, which compromise strong desiccation, wave action, and drastic fluctuations in radiation and temperature. In this investigation, *A. utricularis* from King George Island, Antarctic Peninsula, was exposed to 2°C (control) and 8°C for 3 days and 20/4 day/night cycle at 140 $\mu\text{mol m}^{-2}\text{s}^{-1}$ photosynthetic activity radiation (PAR). In ecophysiological response, *A. utricularis* is not subject to affection in photosynthetic activity, measured in terms of in vivo fluorescence of chlorophyll a (Fv/Fm, ETR, NPQ). RNA was extracted and whole transcriptome was studied by RNA-seq using an Illumina NovaSeq 6000 platform. Results demonstrated the regulation of over 640 genes, of which 151 were over-expressed and 496 down-regulated. Represented processes were related to DNA replication, repair and reorganization, fucoxanthin-chlorophyll binding proteins, transcript maturation and translation related proteins. Conversely, repressed genes were associated with ribosomal proteins, ABC transporters, aminoacids metabolism, translation, cytoskeleton reorganization, oxidative stress-related proteins and heat shock proteins (HSPs) together with other chaperones. Considering the general shut down in gene expression occurred upon an increased in temperature exposure, ecophysiological and transcriptomic results suggest that higher temperatures would be beneficial for this Antarctic macroalga's fitness under future predicted negative scenarios of Climate Change.

Coordination between water flow and photosynthesis in the Antarctic vascular plants in response to increased temperature

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The photosynthetic performance of Antarctic vascular species is strongly determined by their xerophytic anatomical traits. Both, *Deschampsia antarctica* and *Colobanthus quitensis* have thick and dense mesophylls, determining remarkably low values of CO₂ mesophyll conductance (g_m). When these species grow at temperatures close to their optimum for photosynthesis (≈15 °C), g_m increases whilst leaf density (LD) and leaf mass area (LMA) decrease. Since CO₂ and water partially share the diffusion pathways inside leaves, we hypothesized that the leaf anatomical modifications experienced by the Antarctic species in response to warmer temperature, increases their hydraulic conductivity. We evaluated the effect of growth temperature (5, 8 and 15 °C) on several anatomical and hydraulic parameters, as well as their co-variation with photosynthetic performance. At higher temperature, Antarctic plants increased their leaf hydraulic conductivity (K_{leaf}), and the whole plant conductivity (g_{plant}). Increases in K_{leaf} and g_{plant} correlated with decreases in LD and LMA, and with increases in the anatomical hydraulic diameter due to changes in the number and size vessels. The increase in K_{leaf} with temperature correlated with higher stomatal conductance and g_m. Therefore, increases in water and CO₂ flows favored carbon assimilation, resulting in a coordination between the hydraulic properties and photosynthesis in response to temperature. This information is essential to make realistic predictions of the Antarctic plants response to climate change.

Antarctic marine microbiome across space and depth

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It is expected that marine microbes, which are the main drivers of biogeochemical cycles and essential to the food web, will be affected in different ways by changing climate and oceanographic conditions in the western and eastern Antarctic Peninsula. The main goal of this research was to determine the taxonomic composition, diversity and distribution of the microbial communities across different regions and depths of the Southern Ocean. We selected samples from the epi-, meso- and bathypelagic zones of the Gerlache and Bransfield Straits, the areas influenced by the Bellingshausen Sea and the Weddell Sea, north of the Antarctic Peninsula, besides areas near the sea ice edge. By using the Illumina sequencing-based profiling of bacterial and archaeal 16S rRNA genes, 1529 OTUs were identified from a total of 74 samples. In general, the bacterial classes Gammaproteobacteria, Alphaproteobacteria, Flavobacteriia and Cyanobacteria, and the archaeal Marine Group II and Nitrosopumilus corresponded to 90% of the total taxa identified. The sea ice edge and the Weddell Sea presented the most distinctive microbial communities when compared to the other sampling areas. The microbial composition in the meso- and bathypelagic zones was very similar, with high percentages of Oceanospirillales, SAR11, SAR324, Thaumarchaeota and Euryarchaeota. Significant differences in microbial communities were obtained between sampling areas and pelagic zones. This research provides invaluable advances in understanding the spatial dynamics of Bacteria and Archaea in the water column of underexplored areas around the Antarctic Peninsula.

How new scenario of climate change are affecting the Antarctic fish *Harpagifer antarcticus*

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The climate change is modifying the Antarctic area, being the teleosts very sensitive to temperature and freshening. In addition, this temperature increase is changing the oxygen concentration, boosting the probability of fishes facing hypoxia events. These climates changes are affecting important physiological process for teleost fish as energy yielding processes, osmoregulation, oxygen consumption, immune responses and survival. The last 5 years we did experiments with *Harpagifer antarcticus* (Notothenioid), an Antarctic species called the spiny plunderfish. The aim of these studies was to evaluate the physiological responses according to variables of climate change, such as freshening, high temperature and hypoxia. Our results demonstrate that *H. antarcticus* has a CTMax at 18°C. The osmotic, stress and metabolic responses are modified by high temperature, freshening and hypoxia. The immune system (using LPS and POLY:C to stimulate the response) is being modified by high temperature. In addition, that dependence of thermal regimens *H. antarcticus* are changing the prey-item from *Gondogeneia antarctica* to *Cheirimedon femoratus*.

These studies provides information relevant for understanding how the climate change is affecting the physiological and immune response of this Antarctic Notothenioid fish. This work was financed by Fondap-Ideal Grant N°15150003, Fondecyt 1160877, VIDCA-UACH and INACH.

Interactive effects of exposure to metals and elevated temperatures under a warming climate on an Antarctic marine ostracod

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While concentrations of contaminants in Antarctic marine waters are typically low, a number of nearshore sites, such as those adjacent to past waste disposal tips at research stations have increased levels of contaminants, including the metals cadmium, copper, lead, and zinc. To assess the risk associated with mobilisation of these metals in meltwater streams into the marine environment, chronic toxicity of metals to a common Antarctic ostracod (*Bradleya antarctica*) were examined. Tests were conducted at 0°C; representative of current environmental conditions. For copper, two elevated temperatures were also tested (2 and 4°C) to assess potential interactive effects of exposure under elevated temperatures. Ostracods were exposed to metals for 10 weeks, with periodic observations of behaviour and survival throughout the testing period. Sub-lethal behavioural responses were observed in the first week of exposure; however, there was no significant mortality observed up to 10 days. Toxicity increased with exposure time, up to 10 weeks, with 50% Lethal Concentrations (LC50) for these long exposures comparable to those reported for related temperate species over shorter exposures of only 10 days. The response of Antarctic ostracods to metals was therefore delayed, and may in part be attributed to reduced metabolic rate that is characteristic of Antarctic marine invertebrates living at constant low temperatures. Sensitivity to copper increased in tests conducted at the higher temperatures of 2 and 4°C, indicating that, under a warming climate, these Antarctic biota may be subject to elevated risk if exposed to contaminants.

Ocean Acidification Impacts Primary and Bacterial Production in Antarctic Coastal Waters during Austral Summer

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Polar waters are at increased risk of ocean acidification (OA) due to the higher solubility of CO₂ in colder waters. Three experiments examining the influence of OA on primary and bacterial production were conducted during summer at Davis Station, Antarctica (68°35' S, 77°58' E). For each experiment, six 650 L tanks were simultaneously filled with 200 µm filtered coastal seawater and incubated for 10 to 12 days, with CO₂ concentrations ranging from pre-industrial to post-2100. Primary and bacterial production rates were determined using NaH¹⁴CO₃ and ¹⁴C-Leucine, respectively. For all experiments across the summer season, maximum photosynthetic rates (mg C mg chl a⁻¹ h⁻¹) decreased with enhanced CO₂, reducing rates of gross primary production (mg C L⁻¹ h⁻¹). Rates of bacterial production (µg C L⁻¹ h⁻¹) and growth (d⁻¹) were faster under enhanced CO₂ from Days 0-4, but became more similar between treatments thereafter. Conversely, rates of bacterial cell-specific productivity (µg C cell⁻¹ h⁻¹) decreased with enhanced CO₂ suggesting some cell impairment. Initial increases in bacterial production and growth with OA were enabled through reduced grazing pressure associated with fewer heterotrophic nanoflagellates. This emphasises the importance of community-based studies to best elucidate OA effects. Reductions in primary and cell-specific bacterial productivity with enhanced CO₂ occurred at concentrations greater than 2X present day (> 780 ppm) indicating resilience in the system. Decreased primary production under OA conditions may exacerbate global warming through reduced CO₂ uptake via the biological pump, and reduce food availability to higher trophic levels in the Antarctic food web.

Fatty acid content of the Antarctic krill *Euphausia superba* of the Southern Ocean revealed changes under water temperature regimes

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Climate change is as a major threat to biodiversity loss, causing great alterations in marine ecosystems in the Southern Ocean. Antarctic krill *Euphausia superba* is a key species in Antarctic trophic food web presenting a high abundance and a crucial role at the trophic food web. Due to the scarce information in literature about the adaption of species to global warming and environmental change, it becomes crucial to determine and assess the biochemical profile of these species to a better knowledge in the trophic food web. Fatty acid (FA) are molecules with physiological roles and revealed to be good bioindicators of environmental change. In this study FA profile of *E. superba* collected in different sites (cold, warm and transitional waters) across the Antarctic Polar Front was determined to: 1) assess potential changes with water temperature; 2) assess the body condition of the organisms, 3) characterize the diet, and 4) compare the FA profile of *E. superba* with *E. triacantha*. Results highlight *E. triacantha* is more tolerant to warm than cold waters with higher abundance and diversity in FA content in warmer waters. Moreover, *E. superba* presents a more sensitive behavior to the sampling sites than *E. triacantha*. Although different food preferences, carnivorous zooplankton is one of the food sources in the diet of both species. This study highlights that under environmental change scenarios, *E. triacantha* have more potential to cope better in the future, and possibly having a more relevant role in the Antarctic trophic food webs than *E. superba*

Show us your beaks and we tell you what you eat: Different ecology in sympatric Antarctic benthic octopods under a climate change context

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Sympatry can lead to higher competition under climate change and other environmental pressures, particularly in South Georgia region, where the two most common octopod species, *Adelieledone polymorpha* and *Pareledone turqueti*, occur side by side. As both species' beaks are commonly found in predator's stomachs and its ecology is still poorly known due to their elusive behaviour, we studied their feeding ecology through a multidisciplinary approach combining stable isotope signatures (¹³C and ¹⁵N), total mercury (T-Hg) analysis and biomaterials' engineering techniques (Scanning Electron Microscopy, X-Ray Diffraction, micro-Computerized Tomography and Nanoindentation Test). An isotopic niche overlap of 95.6% was recorded for the juvenile stages of both octopod species, dropping to 19.2% in adult stages. Both species inhabit benthic ecosystems around South Georgia throughout their life cycles (¹³C: $-19.21 \pm 1.87\text{‰}$, mean \pm SD for both species) but explore partially different trophic niches during adult stages (¹⁵N: $7.01 \pm 0.40\text{‰}$, in *A. polymorpha*, and $7.84 \pm 0.65\text{‰}$, in *P. turqueti*) (Matias et al. 2019 Mar. Environ. Res.). The beaks of *A. polymorpha* are less dense and significantly less stiff than *P. turqueti* beaks. The T-Hg concentrations in the flesh of *P. turqueti* were higher relative to *A. polymorpha* (0.434 ± 0.128 g-g⁻¹ and 0.322 ± 0.088 g-g⁻¹, respectively). Overall, both octopod species exhibit similar habitats but partially different trophic niches, related to different morphology/function of the beaks. Moreover, both species presented T-Hg concentrations similar to the ones found in northern hemisphere octopod species and may increase under the present climate change context.

A

Abrantes, Fátima 1254
 Ahn, In-Young 799

 Alves, Alexandra 1273, 1606
 Amsler, Charles 672
 Amsler, Margaret 672

B

Baeta, Alexandra 152
 Ballegeer, Anne-Marie 1254
 Bista, Iliana 1297
 Bodrossy, Lev 1436
 Boissonnot, Lauris 299
 Borrull, Sílvia 135
 Bostock, Helen 1254
 Bowie, Andrew R. 409

C

Cabrol, Léa 1376
 Canario, Adelino 1606
 Canário, Adelino 1273
 Cardenas, Leyla 1248
 Cárdenas, César 914
 Cavan, Emma 1436
 Cavan, Emma L. 406
 Cavieres, Lohengrin 1303
 Ceia, Filipe 152
 Celis-Pá, Paula 1092

D

Daane, Jacob 823
 Davidson, Andrew 191
 Davies, Diana 1254
 De Leij, Rebecca 874, 875
 Desvignes, Thomas 1114
 Desvignes, Thomas 1297

E

Ellegaard-Jensen, Lea 102
 Ellwood, Michael 43

F

Fawcett, Sarah 658
 Fernandes, Emmanuel 152

G

Galmés, Jeroni 1303
 Garrido, Bastian 1091
 Gil-Pelegrin, Eustaquio 1303
 Gómez, Iván 1092, 1419
 Gonçalves, Ana 1115
 Gonçalves, Fernando 1115
 Gonzalez, Marcelo 981

H

Hagen, Wilhelm 299
 Halfter, Svenja 1436, 406
 Hallegraeff, Gustaaf 1254
 Haraguchi, Lumi 658

Andrew, Sarah 43
 Anwar, Muhammad Zohaib 102
 Auvinet, Juliette 823
 Auvinet, Juliette 1114
 Avila, Conxita 135

Boyd, Philip 1436
 Boyd, Philip W. 406
 Bravo, León 1303
 BreMiller, Ruth 1114
 Bressac, Matthieu 1436
 Brown, Murray 1092, 1419
 Butterworth, Phil 406
 Butterworth, Philip 1436

Celis-Plá, Paula 1376, 1419
 Chaparro, Oscar 1091
 Chen, Xinjun 1012
 Cheng, C-H. Christina 1666
 Cheng, Christina 525
 Ching Yee, Wong 1596
 Coimbra, Manuel 1115
 Cortina, Aleix 1254
 Couto, Elsa 1606
 Covi, Joseph 779

Detree, Camille 1248
 Détrée, Camille 981
 Detrich III, H William 823
 Detrich III, H. William 1114, 1297
 Duncan, Rebecca 278
 Durbin, Richard 1297

Eriksen, Ruth 1254

Flores, José Abel 1254
 Font, Alejandro 981

Graeve, Martin 299
 Grange, Laura 874, 875
 Gregory, Susan 152
 Guerreiro, Pedro 1273, 1666
 Guerreiro, Pedro M. 1606
 Gusmão, Ana Carolina 982, 1390

Harris, Matthew 823
 Herrera, Karina 1297
 Houvinen, Pirjo 1092, 1419

J

Johnson, Ladd 1091

KKagawa, Shaw 525
Kattner, Gerhard 299
Kawaguchi, So 1559Khim, Jong Seong 799
Kim, Dong-U 799
King, Catherine 432**L**Landes, Audrey 1297
Latour, Pauline 409
Lauridsen, Henrik 1114
Lavelle, Evan 1408
Lavergne, Céline 1092, 1376, 1419Lavin, Paris 102
Lee, Sung Gu 779
Liang, Yantao 266
Lin, Dongming 1012
Louro, Bruno 1273, 1606**M**Maher, Lynsey 191
Marcelo González-Aravena, Marcelo 914
Marques, João 1115
Martínez, Danixa 1666
Marx-Albuquerque, Leandro R. 1114
Matias, Ricardo 152
McClintock, James 672
McCormick, Stephen D. 1666
McMinn, Andrew 266
Melvin, Jessica 1559
Menzel Barraqueta, Jan-lukas 658Mesquita, Andreia 1115
Ming Li, Teoh 1596
Moenne, Alejandra 1092, 1419
Moenne, Fabiola 1092
Mondini, Antonio 102Montes, Angel 1312
Morley, Simon 1248
Moy, Andrew 1254
Mtshali, Thato 658
Muñoz, Jose Luis 1666**N**Navarro, Jorge 981, 1248
Navarro, Jorge M. 1666
Navarro, Nelso 1419
Navarro, Neslo 1092
Niehoff, Barbara 299Nodder, Scott 1254
Northcote, Lisa 1254
Novillo, Manuel 1114
Nunes, Cláudia 1115**O**OBrien, Kristin 1408
Ortiz, Alejandro 1248Oswalt, Hannah 672
Oyarzún-Salazar, Ricardo 1666**P**Pardo, Diego 1092
Pardo, Luis Miguel 1091
Park, Hyun 779
Parker, Sandra K. 1114
Paschke, Kurt 1666
Patil, Shramik 1254
Peck, Lloyd 874, 875
Peguero-Pina, José 1303
Pellizari, Vivian 1390
Pereira, Eduarda 152Pescadinha, Patrícia 1115
Peters, Michael 823
Petrou, Katherina 278
Piatkowski, Uwe 152
Pontigo, Juan Pablo 1666
Postlethwait, John 1297
Postlethwait, John H. 1114
Poulin, Elie 1376
Purcarea, Cristina 102**R**Ramos, Jaime 152
Rayamajhi, Niraj 525
Reed, Katherine 779Rocha, Miguel 152
Rodríguez-Rojas, Fernanda 1092, 1376
Rodríguez-Rojas, Fernanda 1419

Reis, Rui	152	Rondon, Rodolfo	914
Rigual-Hernández, Andrés S.	1254	Roychoudhury, Alakendra	658
Rix, Anna	1408	Ryan-Keogh, Thomas	658
S			
Sáez, Claudio	1092, 1376, 1419	Signori, Camila	982
Sáez, Patricia L.	1303	Silva, Sandra	1273
Samanta, Saumik	658	Silva, Sandra	1606
Sánchez Santos, José Manuel	1254	Silva, Tiago	152
Sancho-Knapik, Domingo	1303	Singh, Asmita	658
Schilkey, Faye	1408	Søreide, Janne	278
Schram, Julie	672	Strzepek, Robert	43, 409
Seco, José	152	Suhr Jacobsen, Carsten	102
Sena, Johnny	1408	Swadling, Kerrie	1559
Sierro, Francisco J.	1254	Swadling, Kerrie M.	406
Signori, Camila	1390		
T			
Teitelbaum, Charles	1114	Trull, Thomas	1436
Thomson, Paul	191	Trull, Tom W.	1254
Townsend, Ashley	432		
V			
Vallejos, Valentina	1303	Varpe, Øystein	278
van den Enden, Rick	191		
van der Merwe, Pier	409		
Vargas-chacóff, Luis	1666	Viljoen, Johannes Jacobus	658
W			
Wang, Min	266	Wilson, Jonathan	1273
Wasley, Jane	432	Wright, Simon	191
Westwood, Karen	191	Wuttig, Kathrin	409
X			
Xavier, José	1115, 152		



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