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National Report to SCAR for year:	2016					

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AAA						
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2)						
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2)						
3)						
4)						
SERCE						
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Activity	Contact Name	Address	Telephone	Fax	Email	Website
Standing Committees						
SCADM **1)** **2)**						
SCAGI **1)** **2)**						
Other Groups (optional)						
SOOS						

An optional report summarising scientific highlights of the past year may be included below.

Current Projects of the Chilean Program on Antarctic Science (PROCIEN)

INACH CODE	Project Title	Principal Investigator	Institution	e-mail	SCAR-Related	Abstract
RT_19-11+A95:AA95:A127	Isolation of Antarctic microorganisms able to synthesize highly fluorescent semiconductor nanoparticles (Quantum Dots) for biotechnological applications	José Pérez	UNAB	jperezd@gmail.com	MBBA	Applications of nanostructured materials are growing day to day; however, their preparation is still problematic. Current synthesis techniques utilize chemical processes, high temperatures,toxic substrates and the absence of oxygen. Without considering the environmental impact they cause, many of these methodologies are hazardous, expensive and inefficient. Moreover, applications of nanomaterials thus obtained have been limited due to their high toxicity. In this context, using microbial cells to biosynthesize nanoparticles (NPs) should avoid these potential hazards and is likely to improve the properties and applications of such particles. Bacteria are able to generate diverse nanoscale metallic arrangements, including gold, silver, iron and fluorescent particles. In particular, nanostructured semiconductor fluorescent compounds or "quantum dots" (QDs) are highly sought after and have various biotechnological applications. QDs are highly fluorescent NPs exhibiting a narrow emission spectrum directly proportional to particle size. QDs are composed by elements as Cd, Te, Se, Pb, Zn, As and Hg among others. These compounds display cubic crystal structure and function as semiconductors in solar cells and X ray detectors, among many other applications. To date, intracellular synthesis of QDs using microorganisms has been scarcely described and just few examples of CdS and CdSe QDs producer microorganisms have been recently reported. During the last years, our group has been interested in producing QDs by microorganisms. To this end, we developed a "biomimetic" chemical synthesis protocol that simulates conditions found in bacterial cells, requiring only metal substrates and the biological thiol glutathione. With this new protocol, QDs synthesis is achieved at temperature and pH ranges of 37-90 °C and 8-13, respectively. The as produced QDs exhibit spectroscopic properties and biocompatibility levels that favor their applications in biological systems (Pérez-Donoso et al., patent application No. 01596). Based on the conditions described in this method, we recently succeeded in producing fluorescent QDs inside different microorganism and we found that parameters favoring biosynthesis of QDs are temperature, intracellular redox status and the antioxidant defenses. In this context, we hypothesize that Antarctic environment display adequate conditions, as high UV radiation exposure and extreme temperatures, which will favor the development of microorganisms capable to synthesize QDs. The general objective of this proposal is "to isolate Antarctic bacterial strains able to

RT_31-11	Biomagnification and potential effects of Persistent Organic Pollutants (POPs) in the aquatic food web of the Antarctic Peninsula and Patagonia	Gustavo Chiang	C-MERI	gustavochiang@gmail.com	MA	The Persistent Organic Pollutants (POPs) are organic substances of natural or anthropogenic origin, resistant to photolytic, chemical and biological degradation, so they have a high persistence in the environment. Low solubility in water and high lipid affinity, enable them to be bioaccumulated in fatty tissues of organisms, producing toxic effects on reproduction, development and immune function in some animals and plants. These substances include: the hexachlorocyclohexane (HCHs), dichlorodiphenyltrichloroethane (DDT) and bifenilospoliclorados (PCBs). Since 1920's, these compounds have been used in a wide variety of applications, both agricultural and industrial. In recent years, studies in remote areas of the Northern Hemisphere have found high concentrations and high deposition rates of POPs. To explain the presence of these compounds in places where they have never been used, it was proposed in the seventies, tha POPs could migrate through the atmosphere as vapor, attached to aerosol particles and condense at cold temperatures. In the past 20 years this hypothesis was reviewed and discussed by Wania and Mackay (1993), who suggested a process of global fractionation of POPs. Global fractionation theory posits that at low latitudes, warmer temperatures favor evaporation of these compounds from the surface of the earth, while at high latitudes, where temperatures are low, increases the deposition from the atmosphere, ie, cold condensation. Although there is information that supports this hypothesis, mainly in the northern hemisphere, it was recognized that lack extensive background information and history in the southern hemisphere. Antarctica and the Southern Chilean Patagonia, geographical features provide ideal conditions for research in relation to the cycles of POPs in the Southern Hemisphere, its bioavailability and potential impacts on biota. According to the above, this research aims to contribute to the knowledge gap that exists in the biomagnification and deleterious effects of POPs in biota in Antarctica and the Southern Chilean Patagonia, by measuring concentrations of these compounds through food webs in both areas. To this end, we propose the analysis of residues in biota using chromatographic analysis techniques also were used passive samplers for water and sediment in order to establish the bioavailability of POPs. Likewise, the use of biomarkers will help us to define the different degrees of sensitivity of species in the food web and the possible effects of exposure to and accumulation of POPs. Using
AN_02-12	Antarctic Plant Ecophysiology: Unraveling the biological consequences of climate change on plant populations of the Maritime Antarctic	León Bravo	UFRO	labravo@gmail.com; leon.bravo@ufrontera.cl	AnT-ERA	Limiting factors for plant development in the Antarctic Peninsula such as: low summer temperature, short growing season and low liquid water and soil availability are being dramatically modified by the accelerated regional warming (average air temperature increases 2.6°C over the last 50 years). This environmental change is correlated with a significant increase in plant size, coverage and population number of Deschampsia antarctica and Colobanthus quitensis. In spite of several publications describing the effects of regional climate change on Antarctic plant populations, there is limited information on the eco-physiological and biochemical basis that explain growth and expansion of these plant populations. Thus, the general objective of this proposal is: 1. To create an international research core-group in Plant Ecophysiology to study and divulge plant responses to increase temperature and CO2 in order to unravel the biological basis for plants population expansion under the current climate change scenario in the Maritime Antarctica. The specific Research objectives are: 1. To study the effect of warming on seed maturation, germination, plant establishment and growth in the field and laboratory. These effects will be associated with plant physiological performance at different plant levels: freezing tolerance, nutrient uptake, plant metabolism and carbon balance. 2. To study the effect of water availability on plants exposed to local warming in the field and in the laboratory. 3. To evaluate the interaction between warming and CO2 enrichment under laboratory and biotron conditions. 4. To study the effect of warming on microbiological diversity of the vascular plants rhizosphere and associate warming driven changes in the micro-biota diversity with soil nutrient availability. Field and laboratory experiments will be conducted applying an increase in the air temperature (3-5°C) over two growing seasons. Because of their complexity, harsh Antarctic conditions (such as extremely high winds) and logistic difficulties in the field, the studies on the combination of increased temperature and CO2 enrichment will be conducted under growth chamber and BIOTRON where field conditions will be recreated. The studies will focus on understanding the effects of these treatments at the reproductive (seed formation, maturation, and germination), plant growth and development, metabolic (photosynthesis and respiration), and nutritional levels (changes in soil nutrient availability and plant nutrient uptake). Besides, the influence of warming treatments on
FP_03-12	Phylogeography and evolutionary history of the species *Neobuccinum eatoni* (Mollusca, Neogastropoda) in the Southern Ocean	Angie Díaz	UMAG	angie.ddl@gmail.com	AntEco	Unavailable

FI_01-12	Seismic facies variability and sedimentation processes in small bays and fjords of the Danco Coast, Antarctic Peninsula	Cristián Rodrigo	UNAB	cristian.rodrigo@unab.cl	CFCT	Antarctica is undergoing several changes in its environment, being the most notorious those related to sea ice extent and duration, the collapse of ice shelves, the ice mass loss, the increase of air and sea water temperature, among others. It is important to know and assess such changes due to the natural connection to the entire world since Antarctica is the major driver of Earth's climate and sea level. The Antarctic Peninsula is one of the most dynamic and responsive of the region, so it is expected that the evidences of these changes will be clearer and faster in that area. How will the Antarctic environment change over the 21st Century? And, how sensitive is the area of the Antarctic Peninsula to the climate change and ocean warming? Are some question of the new SCAR Programs, but the spatial and temporal scale pattern of the fluctuations is subject to considerable debate, therefore to accomplish the aims is necessary to study all possibles scales in time and space, including locals or specific provinces. We believe that knowing climatic and oceanographic fluctuations in the past, we can help with data to adjust the current climate models. Variations of the glacier fronts that lead in fjords and bays establish clues to determine the changes in climate in the past. These changes and others can be recorded in marine sedimentary sequences. Therefore, knowledge of glaciomarine or glacimarine environments and the associated sedimentary processes, give an important background to establish climatic and oceanographic correlations that would permit understand the environmental evolution of the Antarctic Peninsula. The transitional subpolar-polar glaciomarine environments which should contain a gradient change signals from warmer (South Shetland Islands) to colder areas (the polar area), in which changes may be more apparent in recent decades, so we focus in current and recent sedimentation processes considering small scales in time and space. We propose to study the unexplored and similar small and shallow bays and fjords of the Danco Coast, that show a simple geometry and a limited ice drainage, to interpret the recent and actual sedimentary processes and detect the variability of the sedimentation styles along the coast. To reach the above mentioned we will do geophysical surveys and sediment sampling in 8 representative bays and fjords of the Danco Coast, to obtain the depositional sequence records using a portable parametric subbottom profiler (20 and 200 KHz) and thus to obtain the seismic facies variability, and bathymetry to model the morphology. In addition a high frequency side scan sonar will be used in shallow
FI_03-12	Recent high-resolution climate reconstruction at the northern Antarctic Peninsula - glacio-geochemical investigations at Plateau Laclavere ice cap	Francisco Fernandoy	UNAB	francisco.fernandoy@unab	CCA	The Antarctic Peninsula (AP) is a region highly susceptible to the recent climate variability. Changes of the AP climate are larger than those on a global scale and hence of particular importance for our understanding of the global climate system. However, little is known about the natural and postindustrial climate variability at decadal to centennial scale, their causes and interactions with atmosphere and ocean. Here, we propose to drill several firn cores and a medium-depth ice core (about 150m) at the ice cap of Plateau Laclavere (1030m asl), northern AP. A unique glaciogeochemical record will be obtained on seasonal, annual and decadal timescales to reconstruct the temporal-spatial climate variability and climate forcing of the last century and beyond. Our previous work documents that this location is suitable for drilling and relevant for the region. Air temperature, accumulation and sea ice records will be derived and extended to the pre-instrumental period based on the geochemical composition of the ice. Elevated accumulation rates ensure that a high-resolution (seasonal to monthly) record is stored in the ice cap. Stable water isotopes (as well as physical properties of the core) will gather a first age model of the climate variability, which will then be refined by ion geochemistry and radiogenic isotopes. Since this will be the first ice core at the most northern tip of the Peninsula, new information on moisture sources, transport patterns and intensification of atmospheric modes will be derived from combined isotope and atmospheric circulation models. The firn/ice core data will be compared to existing ice cores, forcing modes and stable isotope data sets and lead to an improved understanding of the regional climate signal and, in combination with geophysical methods, add information on the stability of the West Antarctic Ice Sheet. This proposal is within the scope of broader-scale international programs such as ITASE (International Trans Antarctic Scientific Expedition) dedicated to the past 200-1000 years of Antarctic climate change, and part of the Polar to Tropical Connection Initiative (PTC), a virtual institute which aims to identify past and present climate signals and quantify the transfer of heat, moisture, salt and tracers (aerosols, pollutants) between Antarctica and the Tropics

RT_06-12	Fildes Peninsula Resistome: Is there any contribution of antimicrobial resistance genes from waste waters?	Helia Bello	UdeC	hbello@udec.cl	MBBA	On Earth, all the microorganisms, among them the bacteria, appeared around 3.5 billion years ago and still constitute one of the living organisms with the highest capacity of adaptation and response to a variety of stimuli. Some of them have a pathogenic role, which has resulted, specifically for the bacteria, in the development of multiple molecules with antibacterial properties for the efficient control of infections caused by them. Unfortunately, the wide and at times inappropriate use of these compounds, in man as well as in animals and agriculture, has been exerting a strong selective pressure that, as a consequence, derived in the dominant presence of bacterial strains resistant to towards the most frequently used antibacterial agents. Thus, one of the main Public Health problems in the world is the treatment of infectious diseases produced by circulating multiresistant and pan-drug resistant bacteria, mainly in hospitals, causing serious social and economic problems. The bacterial resistance to antibacterial is not a recent phenomenon since there are some studies that have demonstrated that antibiotic resistance was present before the advent of antibiotics. However, this phenomenon is by no means unexpected, since most antibiotics are produced by soil microorganisms. In this context Antarctica is considered to be one of the most remote places having pristine environments or low pollution level from anthropic origin, but is indeed a very fragile ecosystem, a fact to be carefully considered since the Antarctic tourism as well as the arrival of people to establish in the continent for relatively prolonged periods is increasing. One of the most intriguing problems is the possibility of introduction of foreign microorganisms into the environment through the disposal of untreated sewage from some stations of different nationalities established during prolonged periods. For this reason, the interest related to the presence of antibiotic-resistant bacteria in the Antarctic environment has increased and several authors have reported the isolation of strains of multiresistant bacteria. These facts have stimulated the interest in identifying the source of these microorganisms, as well as of their carrying of antibacterial resistance genes, a property that might reflect their human origin. On the other hand, it must also be considered that despite the treatment of sewage waters for disposal to the environment, epidemiological risk remains, since the treatment does not eliminate antibiotic resistance genes or antibiotic residues, important examples reflecting the emergency of a new type of environmental pollution. By the reasons exposed above, the aim of our research is to identify the antibiotic
RT_09-12	Selection and identification of microbial consortiums with high acidogenic and methanogenic activity from Antarctic sediments, for application to psychrophilic wastewater anaerobic digestion under temperate to cold climates	Léa Cabrol	PUCV	lea.cabrol@gmail.com	MBBA	In the international context of energetic crisis, the necessity to develop renewable, efficient and clean energy sources is a challenging concern. In addition, there is an increasing need for wastewater sanitation development, especially in developing countries. Anaerobic Digestion (AD) can be a solution to both of these problematic concerns, as it enables the simultaneous degradation of organic matter in contaminated wastewaters, and energy recovery through gaseous biofuels, either as intermediate product (hydrogen) or as end product (methane). While hydrogen production from wastewater is still an emerging lab-scale technology, methane production through AD is now a consolidated technology with efficient full-scale applications. However, AD is a mesophilic process which presents low efficiency, low stability and serious failure when operated at low ambient temperatures or for low-temperature wastewaters (below 20°C), i.e . under the normal conditions of wastewater discharge in cold to temperate countries. Low temperature operation affects all DA steps from hydrolysis to acidogenesis and methanogenesis, by reducing drastically the activity rates. Due to the expected crucial role of AD in the coming decade, it appears necessary to develop and implement solutions for increasing its performance and stability under low temperatures. To date, mesophilic sludge is currently used as inoculum, without taking into account its cold-tolerance or sensitivity. As a result, the main strategies to enhance biogas production at low temperatures involve high inversion and operation costs (heating or configuration change). Nevertheless, the fundamental role of the microbial component in cold-adaptation and/or tolerance has been stressed, suggesting that the use of psychrophylic or psychrotolerant adapted consortium would be an attractive solution for stable and efficient LTAD (low-temperature anaerobic digestion), without further cost requirement. The low temperature influences the community structure, the activity of particular groups, and the distribution of carbon flow, for example through acetoclastic or hydrogenotrophic methanogenesis. It is not clear yet whether high-rate LTAD requires the development of psychrophilic or psychro-tolerant populations, nor to what extent mesophilic sludge can become psychro-tolerant. Prolonged psychrophilic cultivation of mesophilic biomass can establish a well-functioning psychroactive methanogenic consortium, which is however inferred to work at sub-optimal performance when exposed to low temperatures. In the

RT_14-12	Actinobacteria diversity in Antarctic ecosystems and assessment of the biotechnological potential of their secondary metabolites	Leticia Barrientos	UFRO	lbarrientos@ufro.cl	MBBA	This project aims to characterize the biotechnological potential of secondary metabolites from a variety of Antarctic Actinobacteria. To achieve this goal, traditional and molecular techniques used for sampling and isolation of microorganisms, dependent and independent of culture, will be employed. The metabolites produced by selected Actinobacteria will be isolated and characterized to finally achieve the identification and characterization of these bioactive metabolites having industrial importance. The project will involve the collaboration of a leading Australian researcher and his working group. It will also employ highly sophisticated analysis techniques such as the use of high performance liquid chromatography coupled to mass spectrometry and nuclear magnetic resonance. The results are expected to contribute to the knowledge of this group of microorganisms that are known as producers of a variety of biologically active molecules obtained through a long evolutionary and adaptive process, having potential application in industry. Antarctica is one of the few places on Earth that does not have a history of long-term human contact and offers a unique opportunity to develop scientific research in one of the purest and less characterized environments on the planet. These extreme weather conditions have conditioned their biodiversity. To successfully thrive in low temperature, psychrophilic organisms have evolved a complex range of structural and functional adaptations in regard to reproduction, metabolism and survival, allowing them to survive low and even subzero temperatures. Within the predominant organisms in extreme cold environments, prokaryotes are the largest reservoir of undescribed biodiversity and have great potential for the discovery of new biologically active natural products. Among them, the Actinobacteria are widespread in terrestrial and aquatic ecosystems where they play a crucial role in the recycling of refractory biomaterials. In recent years they have been characterized as the most prolific producers of novel compounds with potential biotechnological use. Similarly, at this time significant technological advances have occurred in chemistry of natural resources and microbiology, allowing the isolation and characterization of efficient bioactive compounds, which in turn implies promising prospect for the search and characterization of these natural products. The importance of this research lies in the fact that both the market and the wider community, urgently needs new products useful in the therapy industry, human
MA_01-12	Environmental Antarctic Monitoring Center	Claudio Gómez	UMAG	claudio.gomez@umag.cl	MA	Unavailable
CO_01-13	Protocol to select paint schemes to protect structural steel against atmospheric corrosion in areas of Chile with high environmental corrosivity	Rosa Vera	PUCV	rvera@ucv.cl	MA	This Project focuses on one of the most important problems generated as a result of technological development: the corrosion. Industrialization inevitably requires manufacturing metals and alloys that during its life be exposed to environments where corrosion phenomena, soon or later, these will return to its natural state, a process that is done with the formation of corrosion product, as rust in the case of steels. Historically the problem of corrosion has been solved after occurrence, in other words, the damage is repaired, however, does not apply preventive actions before damage, this situation can be changed by research projects focusing on preventive protection of corrosion. For decades, researchers have developed differents corrosion protection methods, which have been seriously considered in some manufacturing sectors, especially in developed countries, where it has become aware of the problem, How has become aware? Simple, reading studies where the cost of corrosion, in different and varied industrial sectors, was quantified. Indeed only in the United States, in 2001, the direct cost of corrosion would have been at least 276 billion dollars (3.1% of GNP) and adding indirect costs (productivity losses, delays, production downtime for repairs and liability for accidents) the total cost of corrosion amount to $ 552 billion per year, its means, 6,2% of GNP. In Chile, although GDP is lower than in the US, we could assume that the costs caused by corrosion processes could be relatively similar, at least in percentage. In our country, the problem exists and is exacerbated by the extent of its coastal zone and increased the content of pollutants in some regions and with certain microclimates. Chile, throughout its territory, has areas with different categories of environmental corrosivity, classified according to ISO 9223 in categories from C1 to C5 (data recently obtained in the project corrosion map of Chile, INNOVA-CORFO 09CN14-5879) [1] These different weather conditions generate different corrosion behavior of materials exposed to the atmosphere, (Approximately 70% is carbon steel) which are, consequently, strongly dependent on the environment, therefore, considering weather and environments, the methods of protection will not have the same performance in all areas. One of the most commonly used protection methods for structures exposed to the atmosphere is painting, it is generally applied on the material in three layers, which forms a paint scheme formed by: a first primer layer, an intermediate layer and a

FR_01-13	Coping with warming of Southern Ocean: invertebrates responses to thermal stress conditions	Marcelo González	INACH	mgonzalez@inach.cl	AnT-ERA	The Antarctic ecosystems are undergoing the effects of global climate change. Consequently, Antarctic ecosystems are changing, some at a rapid rate while others are relatively stable. The ocean surface temperatures in the Antarctic Peninsula have increased by approximately 2°C. In addition, the increasing ocean surface pCO2 in the polar ocean could be enhancing the stress on the Antarctic marine ecosystem. Several marine invertebrates have some molecular adaptations like an antifreeze protein, but others don't have the capacity to cope with the warming temperatures. At a molecular level, this situation is related to incapability to express the heat shock proteins which are involved in cellular protection. On the other hand, the relatively high oxygen solubility at cold-sea water temperatures, produce an elevated tissue oxidative stress. In this way, Antarctic marine invertebrates may be detrimental of other marine organisms if they can not express these stress proteins or if they expressed constitutively other proteins associated with stress like antioxidants proteins. The role of these stress proteins is not completely understood in these stenothermal invertebrates because the molecular information is limited and their association is not well known in their physiological mechanism. This proposal will be focused in performing physiological measurements and molecular characterization of the thermal stress response in two Antarctic marine invertebrates (Sterechinus neumayeri and Glyptonotus antarcticus). The aim of this application is to provide explanations of how thermal stress could globally affect the physiological response including metabolism measurements like oxygen consumption,and gene and protein expression linked to thermal stress and antioxidant defense. The specific aims of this proposal are: 1. To perform a physiological measure related to metabolic rate during thermal stress. 2. To carry out an Express Sequence Tag (EST) program of the tissues of the Antarctic sea urchin and isopod. 3. To evaluate the expression patterns of different genes encoding antioxidant enzymes and heat shock proteins (HSP 70 and 90) by qPCR. 4. To evaluate the HSP protein expression and antioxidant enzymes like superoxide dismutase, catalase and NKEF by immunological techniques. In this proposal, we will try to establish if these two key species are capable to over-express the heat shock proteins and antioxidant enzymes in the context of global climate change. In addition, the genome information that will be produced for us will help increase our knowledge about the other genes involved in cold adaptation and
FI_01-13	Understanding glacier response to climate change in Chile	Shelley MacDonell	CEAZA	shelley.macdonell@gmail.c	CCA	Throughout Chile and the Antarctic Peninsula, glaciers in all climate settings have shown overwhelming retreat patterns over the last few decades. It is thought that glaciers in northern Chile have been retreating in response to diminishing precipitation, whilst glaciers in the Antarctic Peninsula have retreated due to increasing temperatures. By contrast, glaciers in central Chile, have responded to perturbations in both temperature and precipitation. Although these geographical differences have been documented we do not understand the underlying causes of the geographical variations in glacier behaviour. Developing a knowledge and understanding of these processes is critical in Chile because the glaciers are distributed over a vast latitudinal range from 27ºS to the Antarctic Peninsula. This study aims to understand current glacier-climate relationships for different glacier settings in the Chilean region, and to use this understanding to predict future responses to climatic changes. To address the principal aim, this study will use mass and energy balance models at three sites, each with differing climatic signals along a latitudinal gradient. The first site, the Guanaco Glacier, is situated in northern Chile, and is a cold-based glacier that experiences a cold, dry climate. The Universidad Glacier is situated in central Chile, and is a temperate glacier. This site is on average warmer than the other two sites. Finally, the Ecology Glacier on King George Island near the Antarctic Peninsula represents a cold and wet location. Meteorological data from each site will be used to drive an energy and mass balance model to understand both glacier-climate interactions and ablation rates from each glacier type. Standardised parameterisations of surface temperature, incoming longwave radiation, albedo, turbulent heat fluxes and subsurface heat flux will be tested and/or developed so as to suit all three glacier types. The final modelled results will be verified using surface lowering data, eddy covariance data, and snow chemistry analysis for both point and distributed models. Once a reliable model has been constructed, it will be used to predict the response of each glacier to future climate change following the A2 and B2 climate scenarios. In addition to predicting changes to glacier ablation rates, changing glacier geometry will also be assessed using volume-scaling and flow modelling methods. Direct original outcomes from this study include: the development of a standardised energy and mass balance model for use on different glacier surfaces; the validation of surface temperature, incoming longwave radiation, albedo, turbulent heat flux and subsurface heat flux parameterisations on three glacier types; a new site in the CEAZA

FI_02-13	Photosintetic responses to warming as consequence of the climate change in populations of Antarctic plants from different latitudes in the Maritime Antarctic	Patricia Sáez	UdeC	patrisaezd@gmail.com	AnT-ERA	Warming is one of the most important characteristics of climate change, increase temperatures are already evident in the Antarctic, being this especially important given that ambient temperature is the main factor governing ecosystem processes and biodiversity in this region. Within of these processes, photosynthesis is one of the most affected by environmental changes and is considered as one of the most heat-sensitive processes. The increased temperature may affect the photosynthesis; warming leaves by above their thermal optimum, potentially to a point where electron transport or enzyme associated are labile. Thus is likely that the factors that limit the photosynthesis and the energy proportion drawn towards photosynthesis will be affected. Deschampsia antarctica and Colobanthus quitensis are the only two vascular plants that have colonized the Antarctic. In general, these plants are frequently exposed to low temperature and events of high light intensity, which may induce photo-inhibition. In this way the study of the mechanisms associated with light management is of major importance to understand the possible effects of warming on antarctic plants physiology. Regarding warming, has been proposed that its trend in Antarctic is higher in some areas, thus plants growing in most southern regions exposed to lower temperatures, are also exposed to greater warming trend, this differences within the Antarctic gradient could elicit different responses to warming. The increase in temperature due to warming, could favors the oxidative capacity of Rubisco, it means that reduces their carboxylation specificity factor. However, as the antarctic plants grow usually under sub-optimal temperatures for photosynthesis, being this limited by the low temperatures in field, it is likely that increase in temperature product of climate change resulting in an increase in specificity factor of Rubisco for carboxylation and a reduction in photosynthetic limitations. Given the greater warming trend in the south, this tendency could be higher plants coming from more southern conditions. On this basis it is hypothesized that: Plants from boreal populations of Maritime Antarctic have higher photosynthetic capacity and lower photoprotection than southern populations; these differences are explained by an acclimation response to temperature and not due to genotypic variations. In specific it is hypothesized that: 1. Warming will increase the energy partitioning toward photosynthesis, therefore populations that experience a higher photosynthetic enhancement will also exhibit a higher decrease in their capacity to dissipate the excess of absorbed light energy and a higher reduction in the antioxidant protection
FI_03-13	Addressing global warming scenarios in freshwater ecosystems using aquatic insects as model organisms in sub- Antarctic and Antarctic regions	Tamara Contador	UMAG	tamara.contador@yahoo.c	AnT-ERA	Polar and subpolar regions in both the Arctic and Antarctic evidence significant climatic warming. Antarctica and sub-Antarctic regions have become a focus of studies on environmental responses to regional and global change. Freshwater ecosystems in these regions are highly dynamic, and their responses to climate change may be more immediate and evident than in their terrestrial counterparts. In particular, Antarctica's freshwater ecosystems, although small and isolated, provide habitat for a unique biodiversity of small invertebrates. These organisms may currently be confronting drastic changes in their environments, with marked consequences to life cycles and geographic distributions. Long- term studies on Navarino Island (55oS) in the Magellanic sub-Antarctic ecorregion are beginning to suggest that climate change already is significantly affecting development and seasonality patterns of stream insects and causing changes in the phenology of the aquatic community. A more complete research approach, involving various spatial and temporal scales, is now needed for predicting the potential effects of climate change under various scenarios on freshwater organisms, populations, and ecosystems. The proposed project will involve Navarino Island (55oS) in the Magellanic sub-Antarctic region and King George Island (62oS) in the Antarctic region. Fine-scale spatial variation in freshwater environments will involve changes in voltinism patterns in one widespread species, Parochlus steinenii (Chironomidae: Diptera), along the steep temperature gradients in two freshwater streams on Navarino Island as well as laboratory determinations of upper thermal limits and lower thermal limits of two species found only at high elevations and two species found only at low elevations, respectively. Large-scale spatial variation involves comparing voltinism patterns of P. steinenii between the two streams on Navarino Island (55oS) and two on King George Island, seven degrees to the south. Results will provide the basis for modeling shifts in species life histories and microgeographical distributions over longer time periods following different climate change scenarios. Predictions will be tested, following the current project, by decades-long monitoring. Combined with our previous investigations, the proposed work will enable the formal establishment southern South America's first long-term monitoring program of freshwater ecosystems, at Omora Ethnobotanical Park LTSER site on Navarino Island, and in Antarctic watersheds as well. Our results will be shared with the general public through workshops about freshwater

FP_03-13	The metagenomes and metatranscriptomes of microbial communities at the Arctic and Antarctic Ocean surfaces: which metabolic processes and principal actors drive these ecosystems and how will climate change modify them?	Beatriz Fernández	UChile	biotica@gmail.com	AntEco	Microorganisms occupy virtually every habitat and their metabolisms shape the environment and the biogeochemistry of the planet, ensuring the recycling of elements such as carbon (C) and nitrogen (N). In the marine environment, biological N2 fixation and N uptake are crucial processes for atmosphereocean-atmosphere cycling of N. About 61% of the total N added to the biosphere is produced by biological N2 fixation, a strictly prokaryotic and energetically expensive process in which N2 is reduced to NH3. This equals ~250 Tg of 'new' N per year, of which ~140 Tg originate from the oceans. Most of the N2 fixation in the oceans is performed by cyanobacteria and, although it has generally been associated with warmer tropical and subtropical surface waters, it has been observed that the process of N2 fixation can also occur at temperatures near 0°C. Since N2 fixation was assumed not to take place in polar seas, their quantitative contributions to this global budget and to the N-budget of the polar food webs themselves, remains unknown. Such processes probably take place over the top 2-3 meters of the ocean surface over the 23-24 millions of km2 of Arctic and Antarctic sea ice. However, large differences are expected between an ice-covered and a non-ice-covered ocean, because channels in the ice contain brine water with microbial communities quite different from those in seawater. Recently, a high diversity of cyanobacterial and heterotrophic bacterial nifH genes from Fram Strait and the Greenland Sea has been reported (Díez et al., 2012). However, our knowledge about diversity, distribution and activity of microorganisms related to the nitrogen cycle, and in particular diazotrophs in the marine polar regions, is very rudimentary. This proposal intends to investigate the N2 fixation and N uptake in samples collected in several expeditions already conducted in the Arctic Ocean (2012) and in the Southern Ocean (2013), as well as in new expedition to the Southern Ocean (2014). It is the first time that in situ experiments were performed using stable isotops of N in central Arctic Ocean and Antarctic marine waters. In the present research project, DNA (metagenome) and RNA (metatranscriptome) collected from seawater and ice brine samples both in the Arctic and Antarctic Oceans will be sequenced and analyzed in order to investigate microbial actors and their metabolic processes, and in particular those associated to the nitrogen cycle (nitrogen fixation; nitrate and ammonium assimilation). In that sense, the metatranscriptome sequencing and expression of the main genes involved in those
FP_04-13	Effect of endophytic fungi onthe ecophysiological performance and biochemical responses of *Deschampsia antarctica* under the current scenario and in one of simulated global climate change	Rómulo Oses	CEAZA	romulo.oses@ceaza.cl	AnT-ERA	Plants have been confronted with changing environmental conditions, forcing them to adapt to selective pressures (eg., extreme temperatures, insufficient water, and salinity) in stressful environmental. Although there have been significant advances in understanding plant stress responses, much remains to be determined concerning the mechanisms by which plants adapt to abiotic stress and the effects on diversity and ecological distribution. Recently, it has been demonstrated that specific fungal endophyte in symbiosis with their host plant may contribute to or are responsible for plants adaptation to stress, enhancing effects on plant performance, biochemical responses and fitness under stress environments. Since all plants are symbiotic with endophytic fungi, the potential role of symbionts in the adaptation of plants to environmental stresses has been studied. The Antarctic continent is considered one of most stressful ecosystem on Earth for plant life. The establishment and survival of Antarctic plants occurs under severe environmental conditions such as cold temperatures, low water availability and limited organic nutrients in soil, hindering plant performances and spread. It has been proposed that positive symbiotic association between plant and fungal endophytes would be a key factor for the adaptation and higher performance especially under stressful environments. According to this, should be expected that fungal endophyte - plant symbiosis play a key role in the adaptation and survive of plants especially when the environmental conditions are stressful like those found in Antarctic ecosystem. Recent reports have shown that the occurrence of symbiotic association between fungal endophytes and antarctic vascular plants is consistent. However, despite of research that show positive association between plant and fungal endophytes, further investigations is need to understand the potential fungal endophytes in the adaptation and performance of Antarctic plant species. Considering that climate change models predict an increase in water and nutrient availability and a rise of temperature, among others factors, its turn relevant to assess the effect of fungal endophytes on Antarctic plant performance under current and future global change scenario. The aim of this study will be to evaluate the effects of fungal endophytes on physiological performance, fitness-related traits and biochemical responses in Deschampsia antarctica plants under current and simulated global climate change conditions. This work will be conducted in both field and controlled conditions in order to address the following questions:

RT_01-13	Photobiont selectivity and specificity in the genus Caloplaca (lichenized Ascomycota): comparisons between southern Chile and Antarctic communities	Reinaldo Vargas	UMCE	reinaldovargas@gmail.com	AntEco	Lichens are formed by the obligated association of a mycobiont with a photobiont, and the establishment of a functioning symbiosis requires a mycobiont to meet and associate with a suitable free-living photobiont or to arrest already lichenized photobiont cells from another thallus. Giving its dual nature, the distribution of a lichen species, understood as compatible interacting partners in a unit or holobiont, rests on the ecological and adaptive advantage resulting from the association between the different partners, while the availability in a given place of either biont might be modulated by ecological constrains, such as temperature, water availability, presence of a suitable substrata, among others. In cold areas of Southern Chile in the Magallanes Region, several Caloplaca species known to occur in maritime Antarctica are present. Their distribution seems to be related to the connection between the land masses during the Late Cretaceous, with further spreads to areas with similar ecological conditions when Patagonia and the Antarctic Peninsula separated around 120 mya. With this the availability of partners may have modulated the present distribution of this group of lichens along the southernmost part of southern America, and generated lineage-specific associations between myco- and photobionts that may be shared along a latitudinal gradient from Magallanes to maritime Antarctica. To understand these patterns of distributions of the different bionts in Caloplaca species in the mentioned gradient, taking into account the range of taxonomical partners compatible to each biont (or selectivity), which may modulate the specificity of their association, we will examine phylogenetic associations among lineages of Caloplaca species and its algal partners of the genus Trebouxia. We will also study the geographic variability along southern Chile and Maritime Antarctica of the algal associations within Caloplaca species to seek evidence for ecological dominance of algal lineages and we will test for favored dispersal patterns in Caloplaca species to assess the advantages on the transmission of the algal partner. Results from this study will allow us to understand the diversity and distribution of lichens on a long range basis and the way in which lichen mycobionts associate to their photobionts in cold areas of southern South America. Also, our results will help us to understand the large distributional ranges of many lichens under the view of their re-
RT_04-13	Does dietary overlap, feeding selectivity and growth change in Antarctic ichthyoplankton at different time scales? A biophysical study in Chile Bay, Greenwich Island, South Shetland Islands during austral summer season	Mauricio Landaeta	UV	landaeta.mauricio@gmail.c	AntEco	Trophic interactions in the plankton at temporal scales smaller than seasonal have been scarcely studied in the nearshore marine Antarctic environment. The adjacent coastal ocean is affected by a series of meteorological and oceanographic processes, like wind and tides, which interact with the water column producing turbulent mixing. Marine planktonic organisms found in the water column, from phytoplankton to fish larvae, may modify their composition and abundance at such temporal scales, and therefore trophic interactions of the ichthyoplankton may also vary, changing their diet composition or the prey size. Fish larvae (Bathylagids, myctophids, notothenioids) collected in the coastal zone of the South Shetland Islands during the austral summer season show different morphs, varying their morphology as well their morphometry (proportion of mouth, snout and/or eye diameter in relation to the body length). This situation suggests that different feeding tactics may arise in the larval fish assemblage that, eventually, may reduce the intespecific competence for food in a period of time which the feeding availability is the largest in Antarctica. As working hypothesis we suggest that during the summer season temporal variability occurs at different scales (tidal, weekly) of the abundance of phyto- and microzooplankton triggered by meteorological and oceanographic forcing, which leads to changes in the feeding habits, selectivity and diet overlap in the ichthyoplanktonic assemblage in Bahía Chile, Greenwich Island, South Shetland Islands. To test this hypothesis we will describe the bio-physical coupling of feeding habits, selectivity and dietary overlap of fish larvae collected in Bahía Chile, Greenwich Island, South Shetland Islands during austral summer 2014 and 2015. As specific goals, we propose: 1) To measure meteorological (wind direction and intensity, solar radiation) and oceanographic (temperature, salinity, density) features of the atmosphere and the water column of Bahía Chile, Greenwich Island, during the sampling period (December 2013-February 2014 and December 2014-February 2015); 2) identify and quantify the abundance and diversity of phyto-, micro- and mesozooplankton from Bahía Chile during the sampling period to estimate potential prey field for ichthyoplankton; 3) to determine the adaptation to the Antarctic environment of fish larvae based on the interespecific and ontogenetic variability of their diet composition and feeding success at Bahía Chile, Greenwich Island, during austral summer 2014 and 2015; 4) to determine the age and growth of larval/juvenile

RT_06-13	Phylogenetic Diversity and Bioactive Potential of Gram-Positive Bacteria Associated with Marine Macroalgae from Antarctica	Sergio Leiva	UACH	sleiva@uach.cl	MBBA	The surface of marine macroalgae is a protected and nutrient-rich habitat that harbors a dense, complex and highly dynamic microbial community, in which bacteria are the dominant colonizers. Despite the critical importance of epiphytic bacterial communities for macroalgal development, knowledge of bacterialalgal interactions is still fragmentary and the mechanisms are poorly understood. Although Gram-positive bacteria are receiving increasing attention as a rich source of pharmacologically significant bioactive compounds, there is still a lack of understanding and knowledge about the taxonomic diversity, ecophysiology and bioactive potential of marine Gram-positive bacteria, especially those associated with living surfaces. This collaborative study addresses the question of what is the phylogenetic diversity and bioactive potential of culturable Gram-positive bacteria associated with the surface of marine macroalgae in Antarctica. Our objective is to test the hypothesis that a variable distribution of Gram-positive bacteria and secondary metabolites gene clusters occur amongst different species of macroalgae. To our knowledge, this will be the first comprehensive study of algae-associated Gram-positive bacteria in Antarctica. We will study six species of macroalgae (Chlorophyta, Rhodophyta and Phaeophyta) with an emphasis on those endemic to Antarctica. Our approach will use a combination of selective culturing techniques, advanced molecular-based methods and chemical analysis of bioactive metabolites to assess the phylogenetic diversity and potential of epiphytic Gram-positive bacteria for the production of novel secondary metabolites. Even if this work does not support the hypotheses, the understanding of biodiversity of the microbial community associated to living surfaces in Antarctica will be greatly increased. Outcomes from this research will include a better understanding of the microbial biodiversity in Antarctic environments. However, this research has potential significance beyond the Antarctic ecosystem, for it will broaden the database of microbial communities on algal host species and may lead to the discovery and development of several classes of novel marine natural products that inhibit growth of drug-resistant pathogens. Results will also set the stage for future studies directed to (a) unravel the role of Grampositive bacteria in macroalgae-microbe interactions, (b) the identification of new lead compounds that can be used to treat bacterial infections caused by antibiotic-resistant bacteria and (c) understand how the macroalgae and the associated microbial community respond to environmental perturbations and changing
RT_07-13	Studies of diversity, adaptations and applied potential of yeasts colonizing Antarctic terrestrial habitats	Marcelo Baeza	UChile	mbaeza@u.uchile.cl	MBBA	The present project is focused in the study of yeasts communities that colonize terrestrial habitats in the Chilean Antarctic territory. The main goal is to increase the knowledge of the Antarctic yeasts diversity and their adaptations mechanisms, and additionally to evaluate their potential as a source of economically important metabolites. In spite of the essential ecological roles of yeasts in cold ecosystems, our knowledge about them is still limited. The microfungal communities of terrestrial environments at the Antarctica have been scarcely investigated. In this project, two independent expeditions are planed to collect soil and water samples: one to the islands of the South Shetland Archipelago and the other to the Antarctic Peninsula. The yeasts will be recovery from the samples using different culture conditions and characterized physiologically. The molecular identification and typing of yeast isolates will be made using ribosomal DNA markers and the cytochrome oxidase I gene. The genetic characterizations of yeasts also include dsRNA elements and circular plasmids, which could be additional tool for yeast typing. These genetic elements will be characterized to establish if dsRNA molecules are mycovirus and the properties of DNA plasmids. Viruses in psychrophilic yeasts have not been described and are interesting for evolutionary studies. On the other hand, the plasmid could constitute potential “raw material” to develop vectors for psychrophilic yeasts, a valuable tool to perform molecular studies on this kind of microorganisms. Furthermore, metagenomic analysis will be performed with the samples using the rDNA marker, in order to determine the full extent of the non-cultivable yeasts. To evaluate the adaptations of yeast to Antarctic conditions, the isolates will be analyzed in relation to the production of metabolites that have been described as important in response to different stresses, and in their ability to use and compete for nutrients. These analyses include the production of extracellular hydrolytic enzymes (lipases, esterases, cellulases, etc.), and anti-freeze proteins, antimicrobial, and UVabsorbing compounds. Furthermore the metabolites will be evaluated in their potential to be applied in industrial productive process. The development of the present proposed research will contribute to the knowledge about yeast diversity and their adaptation mechanisms to the extreme conditions of Chilean Antarctic region. In this sense the discovery of unknown/undescribed or unusual yeasts, proteins, enzymes, etc., is very interesting in diverse fields of basic

RT_08-13	Study of viral and bacterial diversity in seawater and Antarctic fish species: Finding of natural reservoir of salmonid pathogen	Marcelo Cortez	USACH	marcelo.cortez@usach.cl	AntEco	The growing need for animal protein has led to accelerated growth in animal production techniques, among these aquaculture. Aquaculture in Chile has experienced rapid growth, establishing Chile as the second most important salmon producer worldwide. Despite the country's geographic advantages and pathogen control measures like vaccines and the use of antibiotics, intensive production conditions and the introduction of foreign species like the Atlantic salmon have resulted in outbreaks of viral and bacterial diseases that have caused enormous economic losses, spreading throughout the Chile's waters and infecting wild fish that live near production areas. An example is the emergence of the infectious salmon anemia virus (ISAV), which in 2008 provoked what has been termed the "salmon crisis", with major economic and social consequences. Initially the salmon industry was located in the Los Lagos Region, but the ISAV outbreak and subsequent restructuring of the industry resulted in the relocation of fish farms further south to the Aysen and Magallanes Regions. Surprisingly, viral and bacterial pathogens have adapted to conditions of lower temperatures and have established themselves 1,000 kilometers to the south of where they were initially detected some years previously. There have been recent outbreaks with usually high levels of virulence at temperatures below 8ºC. The overuse of antibiotics and vaccines have resulted in pathogens developing mechanisms of reservoirs in wild and escaped species, with pathogens being found in wild fish in waters around salmon production centers. Despite its isolation, Antarctica is less than a thousand kilometers from Cape Horn and can be exposed to salmon viruses owing to ocean currents; migration of infected fish or migrating birds that have consumed infected fish. To the above must be added the almost 200 million salmon seeded annually along the Chilean coast, there is the possibility that some of these viral pathogens have migrated to Antarctic waters and have found a niche where they remain as reservoirs. Given the lack of scientist reports describing fish pathogens in Antarctic waters, we have the opportunity to contribute to Antarctic sciences with a study focused on the abundance and diversity of Antarctic organisms through the isolation of new pathogens, as well as the possibility of reporting the presence of microbiological agents already present in salmon production in the southern continental Chile. Given all of the above, we propose the following hypothesis: "Seawater from the bays of King George Island, Greenwich Island (South Shetland), Cape Legoupil and several
RT_11-13	Evolutionary history of the Antarctic pearlwort Colobanthus quitensis (Caryophyllaceae): Population genetics, phylogeographic patterns, and adaptive differentiation	Cristian Torres	UBíoBío	crtorres@ubiobio.cl	AntEco	Nowadays, with the exception of the recently human-introduced Poa annua (Poaceae), the flora of the Maritime Antarctic includes only two species of vascular plants: Colobanthus quitensis and Deschampsia antarctica. Interestingly, C. quitensis is within the vascular plants with the more extended range of distribution worldwide (from México to the Antarctic continent). Although the environments (from highelevation in the Andes to coastal low-elevation shores in the Antarctic) in which C. quitensis inhabit seem to be homogeneous, both their abiotic and biotic conditions can drastically change. On the other hand, while some authors have suggested the Tertiary relict status of these Antarctic plants, others have claimed that it is a recent Holocene immigration. Although there is no concluding evidence (fossil record) supporting the Tertiary relict status of this species in Antarctica, molecular data could shed light on this enigma. On one side, D. antarctica and C. quitensis could have migrated to Antarctica in the Holocene or Late Pleistocene (after the Last Glacial Maximum, LGM) through bird-aided long-distance dispersal. Nonetheless, the possibility of Antarctic relicts during tertiary cannot be dismissed. Interestingly, a growing body of evidence strongly suggests that terrestrial biota is an old endemisms that survived glaciation of the Antarctic continent and the sub-Antarctic islands. For the south hemisphere, an important number of studies have shown that populations that were located at high-latitudes in ice-free areas –where icesheets were broadly extended during the LGM– did maintain relatively high levels of allelic richness and genetic diversity comparing to northern populations located in ice-sheet free zones that served as refugia (near 40ºS giving support to the multiple refugia hypothesis). In this scenery, different predictions can be made regarding the evolutionary history of C. quitensis. Undoubtedly, these contrasting sceneries would have very different consequences on the distribution of the genetic diversity (population structure), on the geographical patterns of genetic diversity (phylogeography), and, on the potential of adaptation to different environments across its range of distribution (evolutionary ecology). The main goals of our proposal is to assess the evolutionary history of C. quitensis, –in a broad sense– by evaluating: (i) how its genetic diversity is distributed within and among populations (population genetic approach), (ii) how historical processes have influenced the contemporary distribution of C. quitensis across its southern range of distribution and to establish whether geographical patterns of

RT_12-13	Campylobacter in Antarctica: diversity, origin and effects on wildlife	Daniel González	UdeC	danigonz@udec.cl	AnT-ERA	The study of infectious agents in wild animals in Antarctica and the ecology of the diseases they cause is important for assessing long-term viability of animal population in this unique ecosystem. In the current application, we focus on the multihost bacterium Campylobacter jejuni (and related species) and the consequences this putative pathogenic species has on Antarctic wildlife. Species of Campylobacter have a broad host range and have been isolated from many organisms and environments in the world. They are the most common causes of bacterial gastroenteritis globally, with C. jejuni being the most virulent in regards to human health. Infection can result in post infectious complications such as reactive arthritis and the severe neurological disorder Guillain-Barré syndrome. In fact it is considered one of the most important emerging pathogens in many parts of the world with a huge health cost burden to the society. Wild birds have been suggested to play an important role as a reservoir, and may affect Campylobacter epidemiology as an intermediate between the human and wildlife interface, subsequently spreading these bacteria great distances through the landscape. In fact Campylobacter have recently been described in the Antarctic territory, were human activities have been increasing over the last few years. Therefore, the overall aim of this project is to generate knowledge about the ecology of Campylobacter species in Antarctica, especially regarding human-associated taxa such as C. jejuni and C. coli. We want to study which animal hosts that carry these bacteria, and to characterize the spatial distribution of these pathogens across the Antarctic Peninsula and the South Shetland Islands, and assess the importance of the birds' health status on the prevalence and severity of infection. Preliminary studies conducted by our research groups have identified the presence of C. jejuni in Antarctic birds, and genotyping results confirmed them to be of a probable human origin. Based on these preliminary results, we hypothesize that Campylobacter infect native birds in Antarctica, but that pathogen prevalence varies between different geographic locations according to the anthropogenic influences. Specifically, higher prevalence is in those bird colonies with close proximity to humans related activity, including military and scientific bases, and tourist routes. Further, we would like to test the hypothesis that body condition of birds affects the likelihood of Campylobacter infection. Some Campylobacter strains have the capacity to incorporate sialic acids in their lipooligosaccharide (LOS) structure on the bacterial surface. This feature has been
RT_13-13	Polyphenols isolated from antarctic Lichens as inhibitors of tau aggregation	Carlos Areche	UChile	areche@uchile.cl	MBBA	Alzheimer´s disease (AD) is a neurodegenerative disorder involving extracellular plaques (amyloid -β) and intracellular tangles (NFTs) of tau protein. So far, targets for AD therapy have considered immunization against Aβ42 and compounds that inhibit the Aβ fibrils formation, which have failed in improving cognitive functions, even though they reduce the burden of amyloid plaques. Actually, the studies for tau immunization show improvement of cognitive functions. On the other hand, there are several data indicating that tau is necessary for Aβ- neurotoxicity. Interestingly, NFTs formation correlates with neurodegenerative process, but recently data have pointed that earlier multimeric aggregates can be responsible or at least in part of memory impairment in transgenic mice overexpressing tau. Moreover, tau aggregation inhibitors have shown an important activity against fibrils formation of tau protein, diminishing the deleterious effects of cognitive disorders and the progression of disease. Besides, the current therapeutic strategies are aimed to look for natural phytocomplexes and polyphenolics compounds that can be able to either inhibit or disaggregate tau filament formation. Despite this, there are few molecules emerging in order to prevent tau aggregation. Although possibly effective, natural drugs targeting against tau have not been approved yet. Lichen substances from Chilean Antarctic has not been tested for the treatment of cognitive disorders, but others polyphenolics compounds including fulvic acid already have proven to be effective in vitro. Therefore, we will investigate the effects of lichens substances as lead compound, on the aggregation using in vitro data. Specific aims of this project are: (1) To isolate phenolic compounds from lichens and to investigate their effects on tau aggregation in vitro. In this context, we propose to carry out biophysical/biochemical studies in order to elucidate whether tau is affected in a structural manner when is treated with polyphenols. (2) To study the effects of polyphenols on human neuroblastoma cells (SH-SY5Y) that stable express tau pathogenic mutation P301L diminishing the level of phosphorylation. These studies will give a general insight to increase our understanding in preventing pathological tau aggregation and/or disassembling pre-aggregated oligomeric forms of tau. The funding we are applying would be of critical importance for continuing these very promising studies, and would allow us to search and discover new natural compounds able to prevent tau aggregation, and oriented to create new insights for the treatment of Alzheimer´s disease.

RT_17-13	Antifreeze proteins purified from psychrophilic Antarctic microorganisms	Patricio Muñoz	FBiociencia	pmunoz@bioscience.cl	MBBA	Water is one of the most essential components of living cells. It is the medium for biological reactions, allowing the transport of molecules, pH regulation and stabilization of macromolecular structures. Limited accessibility due to physical state changes from aqueous phase to ice crystal could be detrimental for functioning and survival of organisms. Many cold-adapted microorganisms that experience regular phases of low temperature and freezing, increase their survival at sub-zero temperatures by producing some protein molecules called antifreeze proteins (AFPs). These antifreeze proteins (AFPs) were initially characterized in marine fishes and described as freezing protectors. In fish AFPs substantially drop the freezing point of blood or hemolymph in a non-colligative manner to help them to survive sub-zero temperatures to which they are naturally exposed. AFPs can lower the freezing temperature of a solution containing ice without significant influence on the melting temperature of the ice. They are 200 to 300 times more effective at freezing point depression than ideal solutes, being evident when they are present in relatively high concentrations. In order to measure antifreeze activity, the difference between freezing and melting temperatures is used and it is called thermal hysteresis (TH). AFPs have been identified and described and purified from different sources. These include snow molds and sea ice diatoms and recently few bacteria can be mentioned. Despite this, little is known about the proteins responsible for bacterial recrystallization inhibition activity. Studies have reported the relationship between past climates in glacier ice and microbial life. Diversity of patterns of glacier microbial populations have been found in ice layers, indicate they were generated under different climate conditions. Polar regions with their continuous low temperatures force the evolution of AFPs among populations of extremophilic bacteria that live on them. Purification of AFPs from cold-adapted Antarctic bacteria and studies on their mode of action may provide insight into the complexity of the cellular machinery involved in stress adaptation. This study proposes to identify and purify AFP(s) from antarctic microorganism(s) and to evaluate their activity. This work may have interesting potential biotechnological applications and certainly contributes to the development of Antarctic innovative research.
RG_02-13	Historic and recent colonizers: genetic and phenotypic variability and phylogenetic relationships of *Colobanthus quitensis* and *Juncus bufonius* in the context of regional changes in Antarctica	Marely Cuba	UdeC	mcuba@udec.cl	AnT-ERA	Global warming is affecting the Antarctic ecosystem more than any other ecosystems in the world. The Antarctic terrestrial ecosystem is simple and has very low diversity; only two vascular plants are considered native, Deschampsia antarctica and Colobanthus quitensis. Furthermore, in recent times it has experienced an increased human activity, due to scientific and touristy activity in the region. Both activities have become a reducing agent for natural biological isolation, making the Antarctic ecosystem vulnerable, and enhancing the risk of establishment for non-native species, mainly in coastal areas and in ice-free areas, all of which points out a potential increment in terrestrial diversity, which could result in the development of a more complex ecosystem. The extreme abiotic conditions in the Antarctic continent affect growth, physiological performance and reproduction of plants, leading to conditions that restrict life. Regional warming leads to temperature increase and higher water and nutrient availability. These could help increase the colonization of native as well was non-native species, mainly for those species with high genetic and phenotypic variability, which are key characteristics for the adaptation to the polar environment. The probability of success for nonnative and invasive species depends on the number of propagules, on the likelihood for establishing and on the extension that settled species are capable to cover and modify in the local ecosystem. Recently a newly arrived plant has been reported in the Antarctica, Juncus bufonius, without being able to specify its origin. Only one nonnative species (Poa annua) has been able to establish under current Antarctic abiotic conditions. P. annua, throughout its distribution, has shown a high reproductive capacity and phenotypic variability which is due possibly to gene structuring. It has been reported that the “Antarctic” P. annua originates from various sources of introduction, indicated by its high genetic diversity. The polymorphism level, genetic variability and the relationship between populations of the species, contribute to the identification of its possible geographical origin, as well as the phenotypic performance which may have under new environmental conditions. Those characteristics, in the case of native species, allow knowing the gene variability and therefore the potential different levels of phenotypic responses for adaptation and competition given a climate scenario that favors the entrance and dispersion of species that can alter its habitat.

DT_01-13	Characterization of psychrophilic bacteria isolated from Deschampsia antarctica phyllosphere and their potential protective effect against frost injury to plants	Fernanda Cid	UFRO	fernanda.cid.alda@gmail.c	MBBA	Economic losses caused by frost injuries in production systems worldwide, occurs primarily due to the introduction of exogenous species poorly adapted to freezing temperatures. Plants are differentially affected by low temperatures. Some are not capable of to overcome ice formation in tissues being lethal, while other plants regulate the freezing point depression by the presence of compatible solutes such as sugars and amino acids, increasing the colligative properties of the cellular environment and consequently reaching lower temperatures in their tissues, known as super-cooling. However, plants with the ability to super-cool at freezing temperatures, are affected by the presence of ice nucleation active bacteria (INA), which catalyze ice formation at temperatures between -2 and -6 ° C damaging plant tissues. Psychrophiles (as Antarctica organisms) have developed a wide set of physiological adaptations to undergo freezing or cold temperatures. Among these, antifreeze proteins (AFP) have evolved as an adaptation to extreme cold temperatures to tolerate ice formation decreasing the freezing point of water through a thermal hysteresis. This protein has been identified in various organisms such as fish, fungi, plants and bacteria. Another strategy to adapt to cold temperatures present in psychrophilic plants is the regulation of ice formation in extracellular spaces directed by ice nucleating proteins, reducing the rate at which ice is formed, making it a slow and controlled process that allows cells adjustment to ice crystals formation. Previous studies have shown positive results in the inhibition of ice nucleation activity present in bacteria by fish antifreeze proteins, this project aims to assess the presence of antifreeze activity and ice nucleating activity in bacteria isolated from the phyllosphere of Deschampsia antarctica, make a characterization of these bacteria, inhibition assays and subsequently evaluate its protective effect on plants exposed to low temperature thermal shock.
DT_02-13	Characterization, heterologous expression and improving antimicrobial activity of bacteriocins produced by Antarctic *Pseudomonas*	María Soledad Pavlov	PUCV	msoledad.pavlov@gmail.c	MBBA	The ever growing apparition of antibiotic multiresistant microorganisms, refractarian to conventional antibiotics therapies, highlights the urgent needed to discover and develop antimicrobial agents with new inhibitory mechanisms, that lack of cross resistance with the available now days; it is also necessary to explore strategies of combined treatments, to ensure an efficient antimicrobial therapy in the near future. The antarctic continent, and its adjacent seas, has been proposed in the last decades as an interesting genetic reservoir for the identification of new molecules, due to its unexplored microbial diversity and its extreme environmental conditions. In general, the evolution of the bacteria that inhabit Antarctica, has been actively modulated by a unique set of selective forces that allowed the survival of those organisms that better fit the severities of the Antarctic environment (i.e. low temperatures, low water activity, frost/thawing cycles, among others). This adaptations include particular molecular/celular modifications, as well as the production of secondary metabolites, like extracellular antimicrobial compounds, wich may be particularly advantageous in reduce the intra and inter-specific competition, allowing the dominance of the productor organism. The antibiotics and bacteriocins are among the classical antimicrobial compounds of bacterial origin. The laters, shape a diverse group of antimicrobial peptide/proteins that, due to its abundance, have been described as “the microbial weapon of choice”. Even more, recently it has been attributed a high potential as future therapeutic agents, because they are synthesized in the ribosome, have a defined spectrum action and have the potential to act in nanomolar concentrations. Although, there are describe many bacteriocins produced by Pseudomonas, almost all of them have been isolated from mesophilic strains and almost exclusively from pathogens systems. In the last decade of Antarctic prospections, it have been confirmed that the marine and terrestrial bacteria from several biotopes produce a great diversity of extracellular antimicrobial compounds, that act inhibiting competitors bacteria, being the taxa Actinomycetes and Pseudomonas (γ-proteobacteria) the dominant producers. In this context, I propose in the present research, identify and characterize bacteriocins from Antarctic strains of Pseudomonas, though the identification of antagonistic activities in cultures and the posterior generation of transposed mutants, that allow recognizing the structural gen of the bacteriocins and generating a strategy for the heterologous expression. Moreover, I propose the evaluation of several methodologies of directed

DG_03-13	Identification and characterization of a new mechanism/strategy for tellurite resistance in tellurite-resistant bacteria isolated from Chilean Antarctic Territory	Claudia Muñoz	USACH	c.munoz.villagran@gmail.c	MBBA	In nature, and because they display a variety of resistance determinants, microorganisms are able of adapting to various unfavorable conditions such as salt stress, UV, metals, etc. Metal resistance mechanisms, for example, present in organisms isolated from extreme habitats, such as the Chilean Antarctic Territory, are of great interest to researchers because it can provide genes that might be useful for bioremediation processes, nanoparticle generation, etc. In turn, this knowledge can be used to optimize various industrial processes to be less harmful to the environment. Particularly, it has been observed that various microorganisms isolated from the Chilean Antarctic territory are highly resistant to tellurite, a toxic compound that is distributed as traces in nature. These microorganisms are able to reduce this tellurium oxyanion, however we bet that they may possess new resistance mechanisms (or different strategies) that allow them to grow in the presence of high tellurite concentrations. The aim of this work is to look for new mechanisms / strategies of tellurite resistance in microorganisms isolated from the Chilean Antarctic Territory, using chromosomal/plasmid DNA libraries for identification resistance genes when expressed in a sensitive microorganism. Expected results include the identification of genes that favor clustering, biofilm formation, intracellular sequestration, increased efflux, adsorption and / or decrease in the consumption of tellurite as well as proteins and/or metabolites that increase their synthesis in tellurite-exposed microorganisms.
FR_01-14	Influence of the solar activity on the polar enviroment	Alessandro Damiani	USACH	alessandro.damiani@usac	CCA	The solar-cycle variability has long been believed to have impacts on Earth's climate. Many studies reported a clear dependence on the solar cycle of different parameters, such as the temperature, ozone, water vapor, winds and so on. However, the impact of the solar activity on the Earth's environment is not fully understood. The sun can influence the terrestrial atmosphere through the direct output of electromagnetic radiation and by modulating solar and galactic cosmic rays flux. These sources of natural variability must be carefully understood before we can realistically assess climate changes caused by anthropogenic greenhouse gases. The aim of the present project is to evaluate and monitor the influence of the solar activity on the polar atmosphere, with a special care for the Antarctica and his peninsula, one of the fastest warming areas on the Earth. We plan to develop two main research lines. The first research line concerns the study and monitoring of the ground-based ultraviolet (UV) radiation in Polar Regions and its influencing parameters such as clouds and ozone. In addition to the possible direct influence of the solar extraterrestrial irradiance variability (e.g. 11-years and 27-days solar cycles) on the surface UV, solar signatures can be present in some parameters (e.g. ozone, clouds) able to determine the amount of UV radiation at ground. We propose to exploit available ground and satellite data and reanalysis in order to highlight possible solar cycles signatures in surface UV and clouds. Periodicities in the responses at different latitudes and atmospheric layers will be highlighted by classical analysis such as Wavelet Transform and compared with other internal oscillations (e.g., ENSO, QBO etc.). In the light of recent findings (Frederick and Hodge, 2011), the controversial issue regarding the influence of the cosmic rays on cloudiness will be faced. Moreover in order to achieve continuous data of UV and O3 with high temporal resolution, we propose to install some new radiometers at our platform in Escudero base (King George Island, Antarctic peninsula) and compare the recorded data with other Antarctic locations (e.g., from the National Science Foundation's UV Monitoring Network). The second research line is devoted to investigate and assess the influence of the transient solar activity on the polar atmosphere. Therefore the analysis deals with the impact of the so-called solar energetic particle (SEP) events on the stratosphere/mesosphere and its influence on ozone and other chemical components

FR_02-14	Metabolomic responses of the Antarctic mosses *Sanionia uncinata* and *Polytrichum alpinum* to global warming	Gustavo Zúñiga	USACH	gustavo.zuniga@usach.cl	AnT-ERA	The Antarctic Peninsula is the most affected area by global warming. This warming has been correlated with the increase of the size of populations of vascular plants. Antarctic mosses are the dominant species in the maritime Antarctic, wich are affected by warming that affects the region. There are few studies on the mechanisms of tolerance of these species to the environment. Some studies have shown changes in the composition of flavonoids from the leaves as a result of excess light or UV-B radiation in Antarctic conditions. Less information exists on the response to water availability or warming. In additions, no studies linking both stress conditions in the Antarctic environment have been reported. In relation to tolerance of mosses to the environment, we postulate the following hypothesis: Global climate change and seasonal variation throughout the year in most regions of the world should affect the metabolome of organisms, but most metabolomic studies have not considered the effects. We hypothesized that: (1) Metabolomic studies of plants or exposed to different environmental conditions should reveal an organism's flexibility in modulating its metabolome to maintain optimal fitness under different conditions. (2) Seasonal differences in the metabolome of Antarctic mosses should be similar to the shifts that occur in individuals growing under varying conditions of temperature and water availability. The main goal is to chracterize at metabolomic level the physiological and molecular changes induced by temperature increase, UV-B radiation and water availability on two the moss species Saniona unicinata and Polytrichastrumun alpinum. The main challenge of this project is to characterize the changes induced in the
FR_03-14	Response of soil enzymatic and microbial activity to global temperature increase in cold ecosystems of Patagonia and Antarctica	Angela Machuca	UdeC	angmachu@udec.cl	AnT-ERA	The role of enzymes and microorganisms in soil function and biogeochemical cycles has been widely recognised along with their sensitivity to changes in the ecosystems. Predictions from the IPCC in 2007 pointed out that the global increase of temperature will continue to rise if the rate of greenhouse emissions is not decreased, causing temperature change, precipitation and CO2 concentration altering primary productivity of carbon inputs to the soil, and the consequent modification on the rates of carbon and nitrogen decomposition. This research will explore the effect of the global increase of temperature on the soil biological activity of carbon and nitrogen in the cold environment in Patagonia (Chile) and Antarctica, as they are considered exposed ecosystems to the climate change and although research has been conducted on the aquatic ecosystems, the soil-plant relationships have not received enough attention. Contrasting ecosystems in soil organic matter content will be studied, a) peat soil (Aysen Region), b) grassland soil (Aysen Region), c) permafrost soil (Magallanes Region), d) tundra soil (Magallanes Region), e) forest soil (Magallanes Region), d) soils from Antarctica (Arctowsky and Livingstone Island). The ecosystems will be characterized in weather and soil properties, as well as in the exposure to the temporal variation of the temperature. The regional changes in temperature will be monitored and sensitive areas will be identified using satellite images. The effect of the temperature increase on the soil activity will be measured by incubating soils at partial increments of temperature: 0, 5, 10 and 20oC for microbial activity (C-CO2 evolution for 1, 7, 14, 21, and 42 days combined with 0, 30, 60, and 100% of the water-filled pore space), whilst the same temperature range (0-20ºC) will be used to assess the enzymatic activity (β-Glucosidase, β-Glucosaminidase, carboxymethylcellulase, and urease). Additionally, soil microbial biomass and microbial communities will be assessed, as well as the quality of the carbon and nitrogen substrate by measuring physical fractions of the organic matter. The dissolved organic carbon and nitrogen will also be analysed, particularly in peat, and permafrost ecosystems, as they represent the readily available fraction of carbon and nitrogen to trigger microbial activity. The plant-soil relationship will be emphasized under Antarctic conditions as we expect to find better correlation between growth and physiological plant (Collobantus) parameters and soil activity than using fractions of organic matter, due to the paedogenesis of Antarctic soils, and a site in Magallanes will be sampled to contrast results from Antarctic ecosystem. Relationships between soil

FR_04-14	Macroalgal Adaptive Radiation: Potential Links to Ecological Niche Diversity in the Ecoregion of Magallanes and Chilean Antarctica	Andrés Mansilla	UMAG	andres.mansilla@umag.cl	AntEco	The present study is the continuation of our prior investigation, and of the first regional approaches, to establish the region of Magallanes and Chilean Antarctica as a mid- and long-term research site to consolidate the region's biodiversity knowledge base. Most importantly, the present study takes efforts one step further to use occurrence, ecophysiological and molecular data obtained in the first study, and new in-depth environmental characterization and species-occurrence data to model macroalgal distribution ranges (Buckley et al. 2010), estimate species niche of representative macroalgae, and predict their vulnerability and habitat suitability (Tsoar et al. 2007) in the wake of global changes. Antarctica and southwestern South America (or, sub-Antarctic ecoregion), have been identified as two of the only 24 wilderness areas remaining on the planet (Mittermeier et al. 2003). They represent unique natural laboratories that share singular ecological characteristics, such as the endemic rainforest, and the largest ice sheets on Earth, being highly sensitive to past and present global, environmental changes (Turner et al. 2013). These regions host a unique record of the diverse processes that took place before and during the opening of a major gateway between Antarctica and South America: the Drake Passage, and the ensuing period of isolation of the Antarctic continent until its present condition (Dalziel 2012). Both landmasses have alternated terrestrial connection and disconnection intervals since upper Cretaceous (Campanian), modifying the area available for terrestrial biota and the species richness patterns in Antarctica and the sub-Antarctic ecoregion. The response of biodiversity to future scenarios of global change has probably been one of the main focuses of scientific research in the past decade. Species-occurrence data are key for biodiversity analyses. But, identifying the set of factors that determine species occurrence, distribution, and spatiotemporal dynamics under which a species evolved (Brown & Knowles 2012) is complex, as it must consider covarying abiotic and biotic factors, and their interactions in the environment (Phillips et al. 2006). Furthermore, the factors determining species occurrence and distribution are scale dependent (Austin & Van Niel 2011), and often linked with ecosystem process. At small (regional and local) scales, biogeographic studies focus on the many environmental parameters influencing taxa's distribution ranges (e.g., patterns of population dispersion, range contractions/expansions over short temporal scales; Gooina et al. 2010; Fig. 1) or species-specific predictions on patterns of genetic
FI_01-14	Historical and recent biogeographic patterns and processes in Southern Ocean marine mollusks with contrasting developmental modes	Claudio González	IEB	omeuno01@hotmail.com	AntEco	Diversity, abundance and composition of the Southern Ocean's biota are unique ever since the biogeography of this region reflects the complex interactions between abiotic processes (tectonics, oceanography, and climate) and biotic elements since the Eocene. The opening of major gateways permitted the establishment of the Antarctic Circumpolar Current (ACC), the major current system flowing clockwise around Antarctica. The position of the ACC has major repercussions over the distribution of the Southern Ocean marine benthic fauna. Biogeographical revisions of the Southern Ocean marine benthic fauna based on taxonomic lists of major invertebrate groups (e.g. gastropods, bivalves, bryozoans, and pycnogonids) recognized that the number, distribution and boundaries of large-scale faunal provinces are strongly related to the group being considered. However, molecular-based studies in SO benthic invertebrates have detected contrasting biogeographical patterns within particular taxonomic groups. Consequently, large-scale faunal provinces in the Southern Ocean rather than be related to major taxonomic grouping seems to rely upon life-history traits (e.g. bathymetric ranges, developmental modes, larval life span). Other determinants affecting the distribution of the Southern Ocean fauna includes main oceanographic patterns in the region, the stochastic transport of juveniles and/or adults on rafting material, and anthropogenic activities. Current biogeographical studies in the Southern Ocean require combining an array of disciplines into an integrative biogeography in order to have a better understanding the patterns and processes governing the distribution of the marine benthic biota. This proposal aims to examine and compare historical and recent biogeographical patterns in Southern Ocean mollusks exhibiting contrasting developmental modes that are currently distributed in different provinces of this region. For this purpose, this study will include two direct developers' genera (Kerguelenella and Margarella) and two broadcast-spawners' (Nacella and Yoldia) ones. In order to discard the effect of deep-sea connectivity, the analyzed groups are restricted to continental shelves in different provinces of the Southern Ocean provinces (Antarctica, South America, and sub-Antarctic Islands). Molecular-based analyses will be performed to further understand the processes involved in the origin and diversification of these groups in Antarctic and sub-Antarctic waters at different temporal scales. Therefore, this proposal aims to decipher the role

FI_02-14	Evaluating the role of Antarctic root-endophytes on the ecophysiological performance, environmental tolerance and yield in Lettuce crops	Marco Molina	UTalca	marco.molina@ceaza.cl	MBBA	Future climate variability is recognized as one of the most challenging environmental problems over the next century. Consensus scenarios of future climate variability stress the need to develop the adaptive capacity of the agricultural sector. Sustainability strategies alone are not likely to feed the world during the next decades. All global models agree that climate change will make Central and Central-Southern regions of Chile more arid. In the Central area, the expected decreases in precipitation between 25 and 35% for the year 2040 and 2070 respectively, coupled with increasing temperatures of about 2 to 4 ºC could displace current climatic zones further South. In general, studies of Chile forecast future yield reductions for a number of crops including corn and wheat, and that in the more arid zones such as Northern and Central Chile, climate change could lead to the salinization and desertification of agricultural land. The scarcity of water resources and the increased salinization of soil and waters are the primary cause of crop loss worldwide and will soon become even more severe as desertification involves progressively additional regions of the world. Although the temporal frame necessary for plant adaptation to environmental stresses is unknown, the adaptive processes are considered to be regulated mainly by plant genome. However, most studies do not consider the fact that all plants in natural ecosystems are thought to be symbiotically associated with microbial endophytes (e.g., fungi) and these endophytes can have profound effects on plant performance and fitness under stress environments. Currently, it is a well recognized fact that symbiosis is a common and fundamental condition of plants in nature. An example of these microbial associations corresponds to symbiosis between host plant and fungal endophytes. In agree with literature is important to consider fungal endophytes–plant symbiosis as part of an approach to study adaptation responses of plant in stressful environments and more interesting to explore their role on crops performance under new scenarios imposed by global change as the increase of desertification. The Antarctic continent is considered one of most stressful ecosystem on Earth for plant life. The establishment and survival of Antarctic plants occurs under severe environmental conditions It has been proposed that positive symbiotic association between plant and fungal endophytes would be a key factor for the adaptation and higher performance especially under these stressful environments. According to this, fungal endophytes are expected to play a key role in the adaptation and survive of plants especially when the
FP_01-14	Physical controls of biological hot spots along the Antarctic Peninsula continental shelf: future status and current climate trends	Andrea Piñones	CEAZA	andrea.pinones@yale.edu	AnT-ERA	Observations from several multidisciplinary research programs over the last four decades identified a number of localized regions around the northern Antarctic Peninsula characterized by high biological production that is in excess of average conditions (e.g. biological hot spots). Associated with these regions are enhanced abundances of marine mammals and other top predators. These regions typically are persistent over several years and appear to be a common feature of the Antarctic shelf environment, in particular in parts of the Southern Ocean where the Antarctic Circumpolar Current (ACC) impinges the shelf break bringing nutrient rich Circumpolar Deep Water (CDW) onto the continental shelf. The advection of CDW not only brings nutrients to the continental shelf but may also transport krill larvae from upstream regions; advection and the subsequent retention along the shelf can facilitate the growth of the local populations of Antarctic krill and therefore the maintenance of these highly productive hot spots areas. Ocean circulation and the dynamical processes controlling the CDW intrusions exert a strong influence in the formation of the hot spots regions; however, these processes are not well understood and may not be the same for all the continental shelf regions. Accordingly, the goal of this proposal is to identify the physical mechanisms that establish and maintain biological hot spots in the northern Antarctic Peninsula and Bransfield Strait region. To that end, the project will include three inherently related components: (i) determining the dominant pathways of intrusions of CDW to the hot spots using a coupled sea ice/ice shelf/ocean circulation model (ii) examining the temporal evolution of these regions, spatial changes of sources/sinks of particles (e.g. nutrients and planktonic larvae) in the system, (iii) testing the sensitivity of the system to projected environmental changes by forcing the model with the boundary conditions obtained from greenhouse-warming simulations of global climate models. Identifying the mechanisms that control the formation and maintenance of biological hot spots has broad implications for the crucial components of the food web, from krill to the higher trophic predators. In the past four decades the Antarctic Peninsula has experienced a rapid increase in mean annual temperatures, a loss of ice shelves, a retreat of glaciers and a significant reduction in both the area and seasonal duration of sea ice cover. All these changes are rapidly shaping the Antarctic habitat, therefore, improving our understanding of the mechanisms controlling these hot spots is important for understanding food web dynamics, with major implications for the spatial

FP_02-14	Effect of warming and increased CO2 concentration on thermal acclimation of leaf respiration of Antarctic plants	Carolina Sanhueza	UdeC	csanhuez@gmail.com	CFCT	Leaf respiration plays a key role in determining growth and plant tolerance to adverse environmental and has a strong influence on net ecosystem exchange. Due to the predicted global warming produced by the greenhouse effect, the plant responses have become a major area of concern. Respect on the direct effect of rising atmospheric CO2 concentration on respiration it remains a matter of debate. Recent reviews have shown that the increase in CO2 effects on plant vary under different temperatures and functional groups and it is on respiration has been poorly studied. Currently is widely accepted that warming will be more pronounced at night, when respiration is the dominant physiological process. However, there is no consensus on the effect of warming on leaf respiration. The current consensus among ecophysiologics is that plant respiration will acclimate to long-term temperature change. However, the mechanisms underlying these responses are yet unclear. Measurements of leaf Rd have generally been performed at night (Rn) or during daytime after darkness (Rd). However, the status of metabolites in darkness may not be similar to those at night for which is essential to examine thermal acclimation of leaf respiration separately by Rn and Rd. Although, global warming will affect all the ecosystems on the planet, Antarctic ecosystems are experiencing on the highest rate of change in temperature. Deschampsia antarctica and Colobanthus have succeeded colonized the Antarctic. The acclimation ability of Antarctic vascular plants is unknown. Few studies have evaluated how both processes may be affected under warming conditions, and how these changes could alter the carbon balance of the two vascular species inhabit in the Antarctica. As far as we are aware, does not exists studies evaluating short and long term sensitivity responses of respiration under conditions of warming and CO2 enrichment in Antarctic plants. On this basis it is hypothesized that: Rd of Antarctic plants acclimates to warming and CO2 enrichment. This acclimation will be reflected in an adjustment such that foliar R/A ratio will be maintained under increased temperature and/or CO2 concentration, contributing to maintain a positive carbon balance under global change scenarios. The main objective correspond to examine the extent of respiratory acclimation, and the mechanisms underlying acclimation of Rd in C. quitensis and D. antarctica from the Antarctic peninsula under warming and elevated CO2 conditions. The specific objectives include 1) To evaluate gas exchange in individuals growing for long-term under warming in field, 2) To study the effect of elevated day- and night-time temperature on foliar Rd and carbohydrates
FP_03-14	Ozone variability influence on the coupled atmosphere-ocean system	Pedro Llanillo	USACH	pedroquechua@hotmail.co	CCA	Recent studies based on observational and model data have reported that the loss of stratospheric ozone (that occurs over the Antarctica in spring) has a great influence on the observed poleward migration of the Southern Hemisphere mid-latitude westerly jet during austral summers. The poleward migration of this jet has several impacts, such as a poleward displacement of the band of extratropical storms traveling within this jet, the warming of the Antarctic Peninsula and the cooling the continental interior of Antarctica. However, because of the oceanic linkage (i.e. the atmosphere-ocean coupling), the effects of atmospheric anomalies are not constrained to high latitudes. Changes in the atmospheric forcing, such as a strengthening and poleward migration of the westerly jet, may lead to variations in the formation areas of Antarctic and subantarctic water masses. Indeed, these variations may in turn lead to changes in the heat and salt content (which ultimately determine the pathways that Antarctic and subantarctic water masses will follow in the ventilation of the ocean interior), as well as changes in the amount of anthropogenic CO2 and O2 (that Antarctic and subantarctic water masses can uptake and carry into the dark ocean). In this context, my hypothesis is that there is a significant correlation between the changes in the highlatitude ozone column, and the changes in the O2 supply to the mid latitude ocean. Accordingly, the main goal of this proposal is to relate the strengthening and poleward migration of the westerly jet (shown to be linked with the stratospheric ozone loss), to the ocean ventilation (i.e. the supply of O2). This project will require exploiting observational and model datasets, paying attention to different ozone hole phases (increasing ozone hole in the early 90s versus relatively-stable ozone hole in the late 2000s). I will take into account the characteristic lag of the ocean circulation with respect to the atmospheric forcing. This lag is about 15 years for the ventilation of the central and intermediate depths (about 120-900 m) of the water column (Poole and Tomczak, 1999). In particular, I plan to a) Examine the historical hydrological data of the Southern Ocean and the Eastern South Pacific (ESP) by comparing vertical sections of key oceanographic properties. The goal is to find out relevant hydrographic changes by comparing different ozone hole phases. b) Analyze the key oceanographic properties in the modeled hydrological data of the
FO_01-14	Enzyme of Antarctic origin with beta-galactosidase activity, highly efficient at low temperature to delactose milk	Renato Chávez	USACH	renato.chavez@usach.cl	MBBA	Unavailable
FE_01-14	Multichannel espectroradiometer to monitor ozone and solar radiation in Antarctica	Raul Cordero	USACH	raul.cordero@usach.cl	CFCT	Unavailable

RT_06-14	Thermal evolution of the Antarctic Peninsula and the South Shetland Islands by thermochronology: implications to climate change	Francisco Hervé	UNAB	fherve@ing.uchile.cl	CFCT	The Antarctic Peninsula (AP), the South Shetland Islands (SSI) and the Ellsworth Mountain (EM) present rocks that hold the thermal evolution of this region of Antarctica since Paleozoic times. Suitable minerals can record the thermal histories of the rocks and therefore the thermal, deformational, and erosion processes can also be achieve by thermochronology. Thermal histories can be accurately obtained by analyzing accessory minerals hosted in rocks of diverse origin. The range of the temperature history varies by the closure temperatures of every mineral. Apatite is usually analyzed to obtain low temperature thermochronology (in the range of 40°–125°C), while titanite and rutile is used to obtain high temperature thermochronology (in the range of 350°–650°C). The research team has gathered a widespread sample collection in AP, SSI and EM, most of them from past INACH expeditions. They are attempted to be analyze in the facilities of the worldwide recognized Isotope Gechemistry, Geochronology and Thermochronology Group of the Earth and Environmental Sciences Section of the Université de Genève. The technical support of the researchers from this institution will provide analyzes not possible to perform in any laboratory of Chile. Low and Smith islands are part of the SSI and are composed of outcrops that represent a central role in the thermal and geological evolution of the area of interest. Therefore, a fieldwork in this area is very relevant in order to rescue this valued information, by collecting the samples necessary to carry out the thermochronological analyzes that would provide a novel information regarding thermal and tectonic events. These thermochronological analyzes allow to evaluate the cooling histories of the rock samples and will provide accurate insights of the rate of deformational, thermal and erosional processes at various spatial and temporal scales integrated over millions of years, with the objective of evaluating the influence of climatic and tectonic change in the region. This project will be a novel research study carried out in the Antarctic region, and thus will represent the achievement of high impact knowledge for Antarctic and non-Antarctic researchers.
RT_12-14	Microevolution of penguins in Antarctica: genomic-wide SNP analysis to understand adaptation	Juliana Vianna	PUC	jvianna@uc.cl	AntEco	The unique Antarctic biota represents the best models to comprehend adaptation and to explore the link between organisms and environment. Antarctic biodiversity has evolved under geographical isolation and extreme environmental conditions such as very low temperatures and intense seasonality, combined with a period of the year with complete or near darkness. Moreover, in face of climate change, increase of UV radiation and other anthropogenic pressures, it is important to understand how species and populations adapt to local environmental conditions. In despite of its relevance, just a few studies have evaluated organisms' genome to understand adaptation in Antarctica. The recent technical advances of the Next Generation Sequencing (NGS) and in the understanding of the genome have significantly contributed to understand Single Nucleotide Polymorphism (SNPs) or genes under selection. NGS made possible to obtain a large number of data, sequencing species entire genomes with reduced time and cost. The architecture of the adaptive SNP on the genome varies according to species evolutionary history and population genetic structure. Species with high population gene flow may show "genomic islands" of differentiation, while species with divergent lineages show a wide genomic divergence. Moreover, alleles involved in adaptation to an environmental variable in one location may not be the same to another population, lineage or species with the same environmental condition. Thus, we will evaluate signatures of natural selection and adaptation of populations across latitudes and local environmental conditions for each of the penguin species of the genus Pygoscelis with different levels of gene flow and isolation among populations. We will compare the SNPs under selection detected within each of three Pyscocelis species, but also compare between the three closely related species, Pygoscelis papua, P. adeliae and P. antarctica. The Pygoscelis penguins are adapted to colder temperatures around Antarctica and subantarctic islands. Historically, among the three living species, P. papua has the most northern distribution along the Antarctic Peninsula and subantarctic islands. While P. antarctica has a southern distribution, almost exclusively around the Antarctic peninsula, and P. adeliae, is the most dependent of the ice and its range reaches higher latitudes and a circumpolar distribution. In areas where the three species occur sympatrically, Its ecological segregation are caused by adaptation to their preferred habitats with specific differences in foraging and migratory behaviour, life history tactics

RT_20-14	An assessment of the impacts of Antarctic bases on the aquatic ecosystems of the Fildes Peninsula	Roberto Urrutia	UdeC	rurrutia@udec.cl	MA	Since the discovery of Antarctica in the early 19th Century, the number of humans arriving to the continent has progressively increased. From the early explorers to hunters and whalers, scientists, and later tourists, all human visitors have left evidence on Antarctic landscapes of their passage. The increasing human footprint has begun to strain sensitive polar ecosystems, and there is growing concern about the threats posed to the continent's natural systems, including pollution, the modification of animal behaviour and the introduction of non-indigenous species. The Fildes Peninsula (King George Island, South Shetland Islands) has been the site of year-round human presence since the construction of Bellingshausen Station in 1968. There are now six permanent bases on the peninsula, implying one of the densest concentrations of humans in Antarctica, with a permanent population of ~125 and a summer peak of ~300 people. Substantial infrastructure has been installed to support these bases, including an airport, roads, pipelines, and diesel generators. The construction and operation of these facilities has caused considerable disturbance to the Antarctic environment, although the precise nature of the effects on most ecosystems is still poorly understood. Lakes are a pervasive feature of Fildes Peninsula landscapes, with a large number in close proximity to the permanent stations including those used as sources of potable water. Although it is logical that these water bodies have been affected in some way by the presence of the bases, apart from several studies determining baseline limnological characteristics very little research has been done to investigate their chemical processes and biological communities. We propose to study a series of lakes of the Fildes Peninsula using a combined paleolimnological-limnological approach in order to assess the degree to which they have been impacted by anthropogenic activities during the past century. We will determine conditions in Fildes Peninsula lakes by measuring key limnological characteristics in water samples, including basic parameters such as temperature, pH and specific conductivity as well as nutrients and metals, both below the winter ice and during the open water period. We will combine our data with that available from earlier studies to evaluate changes over time as well as intra-annual variation. We will then take sediment cores to determine the conditions in these lakes prior to human presence on the Fildes Peninsula, and to develop records of how anthropogenic
RT_22-14	A missing Component of Biodiversity: Evaluation the Biodiversity on parasite fauna in Antartic Fishes	Isabel Valdivia	UACH	isabel.valdiviarojas@gmail	AntEco	Parasitism is one of the most common life style among eukaryotes, at least 50% of known animal species can be considered as parasites. These organisms would be an essential part of any comprehensive study of biodiversity, as they provide a vision of both history and biogeography of other organisms (hosts), and the structure of ecosystems and the processes that are behind the diversification of life. Today has been indicated that parasitic organisms influence both the structure and functioning of terrestrial and aquatic ecosystems, because these are able to facilitate trophic link because the parasites make hosts more susceptible to predation and them less competitive. For these reasons, it is important the study of parasitic organisms as a whole, as well as the knowledge of the biodiversity of parasitic species to generate news ecological base line to understand our ecosystems. As we indicated above the level of knowledge of the biodiversity of parasites worldwide is scarce and even more unknown is in the Antartica: a place so unique and pristine and one of the less explored area world wide. The Antarctica is considered one of the most isolated ecosystems on the planet. Millions of years of isolation have allowed the evolution of a diverse and abundant wildlife that is highly endemic and adapted to a cold environment. Antarctica offers a good opportunity to study the parasite-host relationships and the evolution of hidden biodiversity present in the assembly of species that inhabit the benthic coastal area. The study of parasite biodiversity in Antarctica allow us to contribute to the knowledge of the state of the Antarctic ecosystem, since they are fundamental part in both the structure and the functioning of any ecosystem, besides the parasites can become good markers for global climate change, because if any of these hosts were susceptible to global warming, then the parasite would be also affected in a way not easy to understand. Thus the parasite biodiversity data could be an useful baseline to assess future global climate changes. To date, taxonomy of parasite fauna of Antarctic species has been developed using traditional morphometric and meristic techniques that could be not the adequate methods to determine the existence of sibling and cryptic species, leading to an error in the identification and quantification of species that have already been registered. Here molecular systematics technics and a DNA barcoding approach offer a good perspective to explore the biodiversity of parasites in the area. In this proposal we aim

RT_27-14	Applying evolutionary principles to infer climate adaptation in marine species: using a genomic approach	Juan Gaitán	UACH	juadiegaitan@gmail.com	AnT-ERA	This proposal addresses classic questions in environmental physiology using modern functional genomic approaches in invertebrate species (Nacella) inhabiting Antarctic and Subantarctic regions. The results of this research will provide answers for the practical problems of how and whether species will respond to climate change in the near future. We will address the challenges organisms face with rapidly changing environmental conditions, considering the four ways organisms could respond to such changes: (1) they can disperse to more hospitable environments (i.e., “migration”); (2) they can respond to this selection pressure, displacing their performance curve (i.e., “adaptation”); (3) they could benefit by the change, without needing any compensatory responses (i.e., “proliferation”); and/or (4) they can exhibit acclimatory (reversible) responses to short-term changes in environmental conditions (i.e. “phenotypic flexibility”). The recent advances in functional genomics allow for the study of molecular mechanisms at a whole-genome scale, linked to the levels at which individuals can alter their phenotypes to maintain performance in a shifting environment. Moreover, a growing collection of evidence supports the utility of functional genomics for comparative physiology, particularly to decipher the physiological responses to stress derived from acute environmental changes. Physiological and molecular mechanisms for cold adaptation in Polar Regions have received a detailed description for fish, particularly for Nothotheniоids. Invertebrate research on the topic is less advanced, but cold adaptations include modification at the level of life-history strategies, accumulation of secondary metabolites, energy budgets and aging. Antarctic intertidal zones are extremely harsh environments, and the endemic limpet Nacella concinna (Strebel, 1908) is one of the most conspicuous and dominant benthic invertebrate, colonizing such areas. These animals are exposed to strong fluctuations of water temperature along the vertical gradient in which they migrate. Here we propose to study the thermal reaction norms of N. concinna, including tenacity and performance measurements across temperatures. In addition, we intend to analyze the transcriptomic response using RNA-seq methods to reveal broad-based gene expression patterns underlying thermal tolerance across populations. To accomplish this, we will (1) construct thermal performance curves for individual limpets in eight populations from which the optimal temperature, amplitude and thermal limits will be estimated; (2) characterize their warming tolerances and
RG_03-14	A xylanase from an Antarctic filamentous fungus as model for the study of cold-active enzymes	Renato Chávez	USACH	renato.chavez@usach.cl	MBBA	Temperature is one of the most important factors affecting living organisms. Among other aspects, temperature affects the rate of the enzymatic reactions into the cell. The relationship between temperature and enzymatic activity has been broadly studied in thermophilic organisms. However, in comparative terms, very few studies have been performed in psychrophilic or cold-adapted enzymes. Remarkably, the surface on the Earth submitted to cold conditions (i.e. cold seas, Polar regions, glaciers, mountains, etc.) could be nearly 90%, so it is striking our poor knowledge about cold-adapted enzymes and the microorganisms that contain them. While the details underlying the adaptation of the enzymes to cold environments are not so clear, it is known that this adaptation involves the improvement of the catalytic efficiency of the enzymes. The improvement of the catalytic efficiency in cold-adapted enzymes has been associated to subtle changes in the sequence and structure of the proteins, leading to a higher flexibility in the enzyme, specifically in regions around the active site. However, this change in enzyme flexibility has another consequence: cold-active enzymes have a low thermal stability. Therefore, both facts (high activity at low temperatures and low thermal stability) are the main characteristics of cold-active enzymes. Supported by a previous Inach Project, we isolated an Antarctic filamentous fungus named Cladosporium sp. This fungus produces extracellular xylanases active at low temperatures. Also, this activity shows low thermal stability. To date, few cold-active xylanases have been studied and strikingly, only 3 of them have Antarctic origin. None of them has been purified from an Antarctic fungus. In this Project, using biochemical, bioinformatics, and DNA recombinant techniques, we propose to use a xylanase from the Antarctic fungus Cladosporium sp. as model for the study of the properties of cold-active enzymes. We also propose to characterize aminoacids putatively involved in the activity at low temperature and/or in the low thermal stability of this enzyme. For these purposes the native xylanase from Cladosporium sp. will be heterologously produced and biochemically characterized. In parallel, by comparative analysis of sequences and structures of xylanases active at different temperatures, aminoacids putatively involved in the adaptation of the xylanase from Cladosporium sp. to the cold environment will be identified. Finally, by site-directed mutagenesis, one of these aminoacids will be changed, and the effect of this change in activity at low temperature and thermostability will be measured.

RG_09-14	Assessment of heavy metals and persistent organic pollutants on Antarctic fauna from several locations of the Antarctic Peninsula	José Celis	UdeC	jcelis@udec.cl	MA	Antarctica is a remote, polar region surrounded by oceans, and seems far away from the influence of industries and other high impact anthropogenic activities. However, recent studies have shown certain degree of pollution that is affecting Antarctic fauna, which could be linked to a raising tourist activity, research activities or some local human activities and environmental accidents. Even though concentrations of most chemical elements in Antarctic ecosystems appear to be very low as compared to other world's areas, their increasing time trends, as a consequence of the strong population growth and industrial development in countries of the Southern Hemisphere, could be affecting some vulnerable endemic species such as penguins. This growth has been accompanied by the release of large amounts of heavy metals such as mercury (Hg) or cadmium (Cd), as well as persistent organic pollutants (POPs) such as organochlorine pesticides (DDT, HCB or endosulphan), polychlorinated biphenyls (PCBs) or polybrominated diphenyl ethers (PBDEs) into the atmosphere and waters. Heavy metals and POPs are toxic for mammals and birds, and can cause severe damage to different organs. Animals are excellent sentinels of environmental changes in ecosystems. Biomaterials such as blood, feathers and excreta can be used as bioindicators of pollution. Nevertheless, research about heavy metals and POPs in Antarctic fauna is still scarce. We believe that the Antarctic Peninsula is a place which is experiencing a continuous increasing pressure caused by different anthropogenic activities. The Antarctic Peninsula concentrates most of the human presence in Antarctica. Moreover, these pollutants can reach the Antarctica by sea and air. As a consequence, the concentrations of trace metals or POPs are affecting biologically some of the Antarctic fauna. The main goal is to assess the spatial and temporal variations of the levels of trace metals (Hg, Cd, Pb, Cu, As, Zn, Al, Cr, Fe, Ni, Mo and Mn), organochlorine pesticides (DDT, HCBs, endosulphan and others congeners) and PCBs in different biotic matrices collected from penguins (Pygoscelis papua, P. antarctica, P. adeliae), sea wolfs (Otaria flavescens), elephant seals (Mirounga leonina), Weddell seals (Leptonychotes weddellii) and leopard seals (Hydrurga leptonyx), inhabiting along the Antarctic Peninsula. Also, to determine the biological effects in those polar animals as a consequence of the contamination with the trace metals or POPs investigated here. The biotic samples
RG_14-14	Bacterial diversity in soils of different animal settlements from Cape Shirreff, Antarctica	Julieta Orlando	UChile	jorlando@u.uchile.cl	MBBA	Ice-free areas of the Antarctic continent represent a minor percentage of the total land area with a wide range of different soil types, chemistries and microenvironments. Here, low nutrient status, very low temperatures and relatively short periods when the microbial communities are metabolically active, have contribute to the misconception of minimal support of microbial biogeochemical activity. Conversely, these microbial communities may be particularly relevant in those areas concentrating colonies of sea-animals like birds and mammals, which transfer nutrients from marine to terrestrial environment through mainly their depositions as urea or uric acid. Then, due to the increase in the content of organic matter, and the high amounts of ammonium and nitrate, microorganisms associated to soils of animal settlements actually play important roles in the nutrient cycling in these extreme ecosystems. Besides, the deposition of marine birds and mammals strongly influences the physical and chemical properties of soils, leading in turn to changes in the structure and function of edaphic microbial communities, whose diversity and redundancy could improve the resilience to disturbances of these ecosystems. Although the broad importance of bacterial communities in different Antarctic environments, the number of microbial diversity studies is still relatively small and it is difficult to have a full understanding of the pattern of microbial diversity and composition under the extreme conditions of this continent. The current limitations in our understanding of the controls on the activity of the terrestrial microorganisms, and our even poorer understanding of the interactions between species in complex microbial communities, means that we are not able to predict exactly how such communities will respond to changes. In this project, we will follow a comprehensively strategy to look into the ecosystem functioning in one of the Antarctic Specially Protected Areas, starting from microbial structure and community composition to go deeply into key nitrogen biogeochemical cycling genes. The Antarctic Specially Protected Area No. 149 comprises the Cape Shirreff (Livingston Island), an important hotspot of faunal diversity, in which sea birds and mammals play an important role in the nutrient cycling. Our working hypothesis state that "Since in maritime Antarctica the coastal ice-free areas concentrate marine animal colonies, both birds and mammals, which produce a transfer of nutrients from the marine to the terrestrial environment, then, these nutrients, rather than other edaphic physicochemical parameter of those settlements, will shape the associated bacterial

RG_15-14	Identification of new fungal species from Antarctic marine sponges	Inmaculada Vaca	UChile	inmavaca@uchile.cl	AntEco	To date, over 1 000 non-lichenized fungal species have been recorded by collection or isolation from Antarctica. This high variety of species suggests that the fungi may be the most diverse biota in Antarctica. On the other hand, the continuos addition of new species identified by molecular surveys to this record suggests that the true diversity may be greater than is currently estimated. Although the majority of species described from the Antarctic region have been identified as members of broadly cosmopolitan groups, there is some evidence for both, endemic and indigenous strains. In particular, the high number of isolates belonging to genus Geomyces in many different Antarctic environments has suggested to several authors that these fungi could be Antarctic indigenous. The confirmation of this hypothesis requires a comprehensive taxonomic knowledge of these isolates. However, the confusing taxonomic classification of fungi belongs to genus Geomyces and related genera have even prevented their classification at species level. In this proyect, the formal taxonomic descripction of 66 fungal isolates from Antarctic marine sponges phylogenetically related to genus Geomyces is proposed. For that, both morphological and molecular characterization techniques (phylogenetic analysis of five molecular markers and RAPDs) will be employed. As result of this research, it is expected the formal description of these isolates as new species, contributing in this way to the knowledge of the Antarctic fungal biodiversity. Additionally, the description of a new species will provide new data to clarify the
DG_01-14	Role of mercury resistance mechanisms in tellurite cross-resistance in psychrotolerant bacteria isolated from Antartic Chilean territory	Fernanda Rodríguez	USACH	fernandarodriguez27@gma	MBBA	Low concentrations of some heavy metals and metalloids can be very toxic for most microorganisms. Among them, mercury (II) and tellurite, have the lowest minimal inhibitory concentrations in E. coli. Both of them exert cell damage by thiol depletion, enzyme inactivation and oxidative stress. Mercury bacterial resistance is given by mer operon which aims the transformation of toxic cationic mercury by the flavoenzyme MerA, to elemental mercury which is volatile and less toxic. On the other hand, the mechanisms of tellurite detoxification are not well understood. However, it has been demonstrated that some metabolic flavoenzymes are able to reduce tellurite to its less-toxic form elemental tellurium, and also that an enhanced response against oxidative stress can confer tellurite resistance in some bacteria. The Antarctic continent is constantly exposed to diverse abiotic stresses like low temperature, high salinity, UV radiation, among others, which cause oxidative stress. Recently, it has been show a dramatic increase of heavy metals in Antarctica, mostly due the grasshopper effect. In this sense, the Antarctic continent has become an interesting place for sampling and isolation of bacterial strains resistant to multiple stresses, which include that produced by heavy metals. The understanding of molecular mechanisms of mercury and tellurite resistance, and also the oxidative damage associated to these psychrotolerant bacteria, could allow for the design of new bioremediation strategies of polluted sites of low temperature environments. In this context, we have isolated psychrotolerant bacteria from Antarctica that are resistant to mercury and tellurite. However, these strains are resistant to tellurite only in the presence of mercury, suggesting that Hg could somehow trigger a molecular response that confers cross-resistance to tellurite, as well as for mercury. The aim of this project is to determine if tellurite resistance of psychrotolerant Antarctic bacteria exposed to tellurite is due an activation of molecular mechanisms against oxidative stress and tellurite reduction mediated by MerA enzyme. The specific aims are: 1) To characterize bacteria isolated from Antarctica resistant to mercury and tellurite, and to demonstrate the cross-resistance phenomena. 2) To determine damage and resistance parameters of oxidative stress in these strains exposed to mercury, tellurite or both toxics. 3) To identify genes of mercury resistance involved in the cross-resistance to tellurite in these strains. 4) To determine if the mercuric reductase, MerA, is able to reduce tellurite in vitro. In objective n°1 we will perform a microbiological characterization of the strains, identification by 16S rDNA sequencing

DG_06-14	Biochemical Mechanisms of desiccation tolerance in the Antarctic moss *Sanionia uncinata*	Marisol Pizarro	USACH	marisol.pizarro@gmail.com	MBBA	Desiccation tolerance is defined as the ability of a plant to revive after drying event (5-10% moisture). It has been postulated that tolerance mechanisms are primitive, because it is a common feature in the early lineages of plants such as mosses whose origin was 504 million years ago during the Ordovician period. This period was characterized by numerous events drought and low humidity. One of the most extreme environments is the maritime Antarctic Territory, due to strong winds, high levels of ultraviolet radiation and low temperatures, which has restricted the development of only two vascular plants and many bryophytes. The moss Sanionia uncinata (Amblystegiaceae) is the main colonizer of the maritime Antarctic, but have not been described the mechanisms that allows it tolerate to this environment. Dehydration tolerant mosses show increased levels of compatible osmolytes and also increased expression of dehydrins and other LEA mediated by Abscisic acid accumulation, but, these mechanisms have not been described for Sanionia however recent studies at the Laboratory of Plant Physiology and Biotechnology USACH have shown that under dehydration S.uncinata accumulates high levels of raffinose family oligosaccharides, such as raffinose and stachyose. Given this antecedents we postulate that desiccation tolerance in the Antarctic moss S. uncinata is mediated by an increase in the expression of genes dehydrins and increased levels of raffinose family oligosaccharides and that these changes are modulated by ABA levels. To test this hypothesis the moss was incubated in a culture chamber with calcium chloride as desiccation agent and cell viability, photosynthetic efficiency, reactive oxygen species levels, membranes lipid peroxidation and antioxidant enzymatic activity of CAT, POD, APX, GR was determined as parameters of oxidative stress, in addition, the levels of dehydrins was assessed by Western blotting and the transcript levels of dehydrins and galactinol synthase was assessed by RT-PCR.
DG_08-14	Study of the extracelular reduction of tellurite and copper in bacteria isolated from the Chilean Antarctic territory	Mauricio Valdivia	USACH	maur.valdivia@gmail.com	MBBA	Stress is an inevitable condition for life of all organisms. This especially applies to microorganisms (MO) residing or located in all kinds of environments, including some extreme as Antarctic. The most common environmental factors affecting MO are temperature, pH, nutrient limitation, pressure, radiation, and metals, among others. However, MO display the ability to quickly adapt to changes in their environments. Recently, compounds of tellurium (Te) have been widely used in oil refinery, solar panels, and optical sensors. However, its use has increased environmental pollution. Copper, on the other hand, is required for growth in all living organisms, but toxic at high concentrations. Chile is a copper producer country and it results in highly polluted rivers, lakes and soils with this and other metals. Environmental bacterium that has emerged in recent years corresponds to Shewanella. Its main feature is the ability to use a wide range of electron acceptors for anaerobic respiration including fumarate, nitrate, nitrite, thiosulfate, sulfide, Fe (III), Mn (III), Cr (VI), U (VI), As (V), V (V) and others. As a result of this property has attracted attention in bioremedación, biogeochemistry and bioelectricity. Shewanella oneidensis reduced tellurite with intracellular and extracellular accumulation of tellurium nanocrystals. Furthermore, exposure to the toxic lead to changes in the components of the lipid membrane. Furthermore, in S. oneidensis were found to homologous proteins CopA and CusA of E. coli. The expression of the structural genes (copA and cusA) of both proteins is increased in response to copper stress under aerobic and anaerobic conditions. However, the literature regarding copper and tellurite in Shewanella is scarce to date without having identified reduction mechanisms. During an expedition to Antarctica in 2012, a bacterium belonging to the genus Shewanella was isolated. This reduces tellurite at concentrations 1 mM (250 times the minimal inhibitory concentration of E. coli -both Gram-negative). In this context, the copper that is added as divalent cation (Cu+2) is reduced to elemental copper (Cu0). This reduction is observed phenotypically in forming a metallic film on the liquid-air interface of the culture medium. This metal biofilm has not been described to date in literature and is presented as the first bacterium that has this particular phenotype. Shewanella bacteria of the same genus, such as S. oneidensis not exhibit this phenotype reduction. The idea of this project seeks to obtain other Antarctic marine bacteria that have

DT_09-14	Nutraceutical metabolites and photosynthesis activity in Antarctic snow microalgae: Effects of temperature and UV radiation	Claudio Rivas	UACH	claudio.rivas@postgrado.u	MBBA	Globally, there is an exponential increase in the human population, while the capacity of fishery and to supply the production of nutraceutics from the marine and fresh water organisms, e.g. of Long Chain Polyunsaturated Fatty Acids Ω3, and Astaxanthin, is limited (FAO, 2010). Although the microalgae cultures are emerging as an alternative for sustainable source of Long Chain Polyunsaturated Fatty Acids Ω3, and Astaxanthin production, in Chile, commercial freshwater microalgae culture is strongly concentrated in the northern part of the country, due to that commercial species such as Haematococcus pluvialis show optimal growing temperatures close to 25ºC and require constant solar radiation, two factors that allows to stimulate the biomass growth and astaxanthin production. While these temperature and light conditions are abundantly available in the Northern Chile, fresh water is limiting, competing with the needs of water for human consumption (Valdes-pineda et al 2014). Therefore, it is necessary to search for new fresh water microalgae strains, which can efficiently grow at low temperatures and produce nutraceutical metabolites at high rates. Snow algae are abundant in the Antarctic and are known to produce nutraceutical metabolites at temperatures close to 0°C, however, their physiology, ecology y molecular biology of these organisms is not well studied and hence, we dont know how these metabolites vary in their composition when are subject to changes in temperature and solar radiation, i.e. other conditions than the Antarctic environment. Thus, it is relevant to assess the variation in Long Chain Polyunsaturated Fatty Acids Ω3, and Astaxanthin production in Antarctic snow algae, subjected to different temperature levels and UV radiation exposure in order to understand the acclimation mechanisms and the changes in the lipid profiles. Based on this information, we can contrast its performance against two widely studied fresh water microalgae species: Chlamydomonas reinhardtii y Haematococcus pluvialis and thus, to gain insights into the potential use of cold-temperate strains replacing the actual use of warm-temperate microalgal species. The knowledge of responses of these microorganisms to different experimental conditions not only have implications for the ecology and physiology of Antarctic flora but also it should be regarded as a topic with important biotechnological potential. The
MT_01-14	Study of the active layer of frozen soils within the area of Düse Bay, Antarctic Peninsula	Sebastián Ruiz	UMAG	sruizp@outlook.com	AnT-ERA	The Antarctic Peninsula geographic area is the key to study the extent to which temperature variations are gradually modulating the climate. This zone has different regions in which the influence of such variation affects differently. The mean annual air temperatures (MAAT) are lower in East Antarctic Peninsula (EPA) when compared to the West Antarctic Peninsula (WAP) at equivalent latitudes, between 63 ° S and 64 ° 50'S. However, since most research focuses on the west side of the peninsula, there is an information gap regarding the soil in the Eastern area, where is located the Düse Bay. The perennially frozen soils are a sensitive indicator of such effects, been also a significant part of the cryosphere. The active layer, formed by the thawing of the upper boundary of such soil, varies its thickness due to the surface energy exchange. The properties of such soils regulate how these energy flows occur, determining its evolution and degradation. The analysis of the composition of these soils allows determining how they will respond to future changes. Therefore, we attempt to assess how certain soils in EPA respond to temperature variations, considering their specific compositions and the effect of altitudinal lapse rate on the distribution of its continuity as cryo-soils. To do this, we have to perform different perforations covering different levels of altitude, and then measure the depth of active layer, collect soil samples from different locations and finally, measure soil and air temperature. A drill is used to bore a hole of at least 2 m in the rocky soil. Soil samples will be analyzed in water content, particle size, porosity and thermal conductivity. These values will allow determining apparent thermal diffusivities of such soils and estimating a measure of response to temperature variations. For a period of at least 2 weeks differences in air temperature and soil temperature should be recorded in order to have an on-site recording of these variables for comparison between these records and forecasts. It is expected lower active layer thicknesses than in WAP, and also a continuous permafrost occurrence at a lower bound of altitude than these recorded in South Shetland Islands (SSI). The thermal diffusivities obtained help to establish if these cryo-

MT_03-14	Depsides and depsidones from Antartic lichens: Antioxidant activity and their possible effect as tau aggregation inhibitor	Francisco Salgado	UChile	fsalgado@ug.uchile.cl	MBBA	Alzheimer's disease (AD) is a progressive neurodegenerative disorder (apparently irreversible). Clinically it is characterized by a selective degradation of neurons in the hippocampus and cortex. In AD brains, can be observed two main protein aggregates in the brain: senile plaques (SP) consisting of amyloid-β (Aß) peptide and neurofibrillary tangles (NFT), which is composed mainly of protein tau. Self tau aggregation is involved in the primary neurodegenerative process. Many authors have performed high-throughput assays to find inhibitors of tau aggregation proces. It has been suggested, that the polyphenolic compounds of natural origin, (specifically the hydroxyl groups of these) have the potential to prevent aggregation of tau and Aß proteins based on their anti-oxidant and anti-inflammatory. In this context, Antarctic lichens, exposed to low temperature conditions, high levels of ultraviolet radiation, and prolonged periods of darkness, increase the formation of ROS in them, which leads to believe, that these organisms may contain metabolites that achieve the antioxidant function so as to protect them from the damages produced by cause of the extreme conditions. Up to date, studies carried out in this field, have demonstrated the antioxidant activity of many extracts, mainly MeOH and Acetone. Isolated compounds deriving from these extracts have shown greater antioxidant effects and in lesser concentrations than that of the tropical lichens as well. However, the obtained data is still scarce in comparison to the abundant resources of lichens in the Antarctica. In addition, the reports regarding the relation between the antioxidant activity of samples and their purely phenol compounds are still limited. The topic of antioxidant depsides and depsidones is still a controversial one. According to scientific literature there are only reports of antioxidants or radical catchers from an experimental point of view, but not from a theoretical point of view. For this reason, this controversy is clarified considering the use of theoretical and experimental models. In turn, once the antioxidant activity is quantified, an attempt to investigate its effects will be made, along with the aggregation of the tau protein. The objectives of this work are: · Isolate and purify depsides and depsidones from antartic lichens. · Identify depsides and depsidones mainly by spectroscopic methods (NMR mono and bidimensional). · Evaluate the antioxidant activity of the isolated metabolites (DPPH and ORAC)
MG_04-14	Effect of lichen compounds on biofilm formation and quorum sensing type I system of *Vibrio anguillarum*	Claudia Torres	UdeC	ctorresb@udec.cl	MBBA	With the expansion of aquaculture industry in Chile, infectious diseases (produced by virus, fungi and bacteria) have emerged as disastrous economic consequences. In 2013 annual losses attributed to diseases were stated to be about U.S. $ 100 million. Vibrio anguillarum is an opportunist fish pathogen that cause hemorrhagic septicemia (vibriosis) on Salmon, which has been transformed in an emergent illness in Chilean aquaculture industry, causing between 7 to 10% of salmon mortality on marine hatchery centers. One of the causes that explain the unsatisfactory results of antibiotic on therapy or/and prophylaxis is also due to them are not very effective against the most important environmental pathogen reservoirs: the microbial biofilms. These are natural microbial community; living attached on live or artificial surfaces, and protected inside of an organic matrix synthesized by themselves. Here, many bacterial pathogens can be accumulated and periodically released to environment. A large amount of scientific evidence have shown that biofilms are 10 to 100 (even 1000) times more resistant or tolerant to antibiotics or biocides, the its free living (plancktonic) counterparts and even more, biofilms forming pathogens, express a gene repertory which increase its damage power (virulence). In fact, if microbial biofilms (waterlines, biofilters and ponds) are not taken in count inside the pathogen epidemiology model, it will be impossible to have control of bacterial infectious diseases in farming, particularly the intensive freshwater step of the salmon aquaculture. However, for V. anguillarum biofilms control, the disruption of Cell-Cell communication, based on cellular density (Quorum Sensing system, QS) has not been studied. In this microorganism, the QS regulates gene expression involved on biofilm formation. by means signals molecules as N-acyl-L-homoserine lactone (AHL, AI-1). The importance of QS in the pathogen bacteria virulence was evident, so the modification of this system is proposed like a new anti-infective strategy. Has been found that the lichens have a different biological activity related to their special ecological conditions, therefore, proposed that lichens metabolites which interfere with V. anguillarum cell communication (QS) can be a innovative solution for construct efficient for Vibrio anguillarum 3276 control, and it can became a model strategy for controlling biofilm formation of fish pathogens in environment and aquaculture facilities. We hypostatized that Vibrio anguillarum 3276 biofilm development is inhibited by

MG_05-14	Evaluation of the cytotoxic activity of extracts isolated from Antarctic and Subantarctic actinobacteria, *Candida* sp., and from human cancer cell lines	David Astudillo	UV	david.aab88@gmail.com	MBBA	Ecosystems generate a series of services and goods that are used by humans for their benefit and to meet their needs. Biodiversity from a biochemical point of view is extremely important, since in many cases metabolites or genes with interesting and useful biological activities have been isolated. In such cases, the metabolites end up being applied in pharmacology, biomedical or various industrial processes. Historically metabolites from terrestrial environments are the most abundant and most studied. However, in the past decades have shown a great interest in the study of metabolites of marine origin, since in many cases these are very active and also because being new chemical structures, these serve as models or as scaffolds to synthesize new drugs. Currently metabolites of microbial origin are the most abundant and the most used medically. The group of organisms responsible for synthesizing of these metabolites are actinomycetes and, in most cases, these metabolites are present characterized by a broad spectrum of action on gram-positive bacteria, gram-negative bacteria, fungi, human cell lines, virus, and antibiotic-resistant bacteria and fungi. Whereas described above, this study aims to assess the cytotoxic activity of extracts isolated from Antarctic and Sub-Antarctic actinomycetes bacteria, Candida sp and human cancer cell lines. To achieve this goal, we will work with extracts of strains of actinomycetes isolated from Antarctic terrestrial sediments, which are inventoried in the Chilean Antarctic Institute (INACH). Also, work with samples of marine sediments of the Antarctic and from Punta Arenas which isolate, cultivate and identify new strains. Once isolated strains, the anti-microbial effect will be evaluated in bacterial and fungal culture technique using double-layer agar. If there is activity shall cultivate the strain to increase biomass. Then extracts with water and ethyl acetate of compound excreted into the culture medium free of cells are made. Organic solvent extracts may be concentrated in a rotary evaporator under reduced pressure, while aqueous phases are then lyophilized. Subsequently, the cytotoxic effect on bacteria and Candida sp is evaluated. determining the minimum inhibitory concentration of each extract. In human cancer cell lines sulforhodamine B assay was used to assess the cytotoxicity of extracts. If the extracts are to be cytotoxic in human cells, the procedure to assess whether induced cell death by apoptosis. Then, first analyzed in human cells if the extracts cause morphological similar nuclear level changes observed in apoptosis using stain Hoechst
MG_06-14	Antibacterial effect of derivated compounds from Antarctic lichens against *Acinetobacter baumannii*	Xabier Villanueva	UdeC	xvillanuevamartinez@gmai	MBBA	Since the discovery of Penicillin by Alexander Flemming in 1929, Antibiotics have been a fundamental tool in the fight against bacterial infectious diseases. Nevertheless, its massive use has facilitated the selection of drug-resistant strains, which in addition of a declining antibiotic pipeline has generated a critical situation, in which for some bacterial strains only 1 or 2 therapeutic options are available. This phenomena, known as Multi-Drug Resistant (MDR) bacteria, has been of great impact in Healthcare Centers such as hospitals, in were a set of particularly resistant strains known as ESCAPE (Enterococcus spp., Staphylococcus aureus, Clostridium difficile, Acinetobacter baumannii, Pseudomonas aeruginosa y Enterobacteriaceae) has emerged. Of these, A. baumannii is remarkably important, because of its extraordinary antibiotic resistance and its great ability for surviving on non-living surfaces inside Healthcare centers. Of these features from A. baumannii, the first one is related with the expression of multidrug efflux pumps (mostly from the RND family, also with activity over disinfectants) and many classes of beta-lactamases, remarkably Ambler's D class beta-lactamases, for being OXA-51-like beta-lactamases intrinsically present in the specie; and the second one is related with the biofilm formation, playing a key role the bacterial surface proteins Bap-like and CsuA/BABCDE. In this scenario, there is a need for researching new compounds with antibacterial activity. Accordingly, extreme environments are a potential source of new agents, because of the need for the live beings of these habitats to answer to a high environmental stress. In this line, Antarctic lichens are a promising source of new drugs, because of their known ability for producing many molecules with biological activity. These organisms, resulting from the symbiosis between a photobiont (alga or cyanobacteria) and a mycobiont (fungus), have a low growth rate and must survive in highly stressing environments, for which they produce a series of secondary methabolites with diverse properties such as anti-UV and antimicrobial activity. Because of the above exposed and the great literature that demonstrates the antibiotic activity of lichen derivatives, it will be investigated the antibacterial effect of total extracts from Antarctic lichens against MDR-strains of A. baumannii isolated from Chilean hospitals. In addition, pure secondary metabolites obtained from total lichenic extracts that show antimicrobial activity will be assayed. In first place, for determining which metanolic total extracts from Antarctic lichens possess antimicrobial activity against clinical strains of A. baumannii, several assays
PC_01-14	Clustering of George VI Ice shelf tributary glacier types	Guido Staub	UdeC	gstaub@udec.cl	CFCT	Unavailable

PC_02-14	Shifts in marine Antarctic microbial community structure and function in response to deglaciation and sea ice meeting accelerated by climate change	Beatriz Diez	PUC	bdiez@bio.puc.cl	AnT-ERA	Microorganisms (both eukaryotic and prokaryotic) are key players in biogeochemical, cycles and establish complex trophic interactions that maintain the funtionality of marine polar systems. Yet the dynamics of microbial communities in response to major physical, chemical and biological changes induced by seasonal changes in coastal Antarctic regions has not been addressed even though these changes are predicted to accelerate and become stronger due to climate change. This imposes currently unpredictable consequences for the structure of biological communities and productivity in Antarctic coastal regions. During summer, increases in temperature induce sea-ice and glacial melting and this leads to input of nutrients, metals, particles and freshwater microbes associated with strong stratification of the upper water column. To predict and model the impact of such events, which have accelerated in the last decades, we need to better understand the shifts in biological sucessions, functions and interactions induced by continental freshwater and sea ice dischange. In the present project, microbial community structrure, funtion and interactions will be studied in marine coastal waters in Antarctica (Chile Bay, Greenwich Island). In the past two years, we have been studying the community composition during the austral summer in the Chile Bay Microbial Observatory (CBMO) in collaboration with Dr. Martin Polz (MIT), counterpart of this proposal. The new proposal will extend this previous sampling to include transects and manipulated experiments in microcosms. Using state of-the-art, culture independent molecular (metagenomic and metatranscriptomic) approaches, we will generate the first comprehensive data to explore the effect of input of (i) freshwater, (ii) macro and micronutrients and (iii) microbes into the coastal Antarctic system by ice meltwater. Taxonomic and functional molecular comparisons will be complemented with environmental metadata (e.g., temperature, salinity, O2, nutrients, trace metals and chlorophyll a), carbon and nitrogen organic particle, isotopic composition and uptake rates. Manipulated experiments will test the responses of microbial communities to different factors exerted by ice meltwater to the marine system. These will help to understand how ecological shifts in response to specific factors will affect the biological pump and the C and N cycles with the ultimate goal of informing models of how accelerating deglaciation and reduction of the ice-cover will influence coastal Antarctic waters.
FD_01-15	Research Center: High Latitude Marine Ecosystems Dynamic	Humberto González	UACH	humberto.gonzalez.estay@	CCA	
FR_01-15	Diversification of the spiny plunderfish *Harpagifer* in the Southern Ocean	Elie Poulin	UChile	epoulin@uchile.cl	AntEco	One of the most remarkable processes of diversification in the Antarctic realm is the evolution of the coldadapted notothenioid fishes. While most of the teleost groups were completely eradicated from Antarctica, this suborder dominates in diversity, abundance and biomass. The evolutionary success of the Notothenioidei at sub-zero ecosystems has been explained by the presence of antifreeze glycoproteins (AFGPs), a key innovation in this Antarctic group. In particular, recent molecular study indicated that the most species-rich lineages within the notothenioids diversified and evolved during the late Miocene (11.6 to 5.3 Ma), 10 Ma after the acquisition of AFPGs. However, most of these studies have been biased toward the relationships within the Antarctic Clade rather than in the association among phylogentetic closed taxa found inside and outside the Polar Front. Therefore, the evolutionary history of non-Antarctic notothenioids remains not well-established, even if AFGP genes in temperate-water notothenliids can be used to infer an Antarctic evolutionary origin. Among the Families of Antarctic notothenioids, determined by the presence of AFPG activity, the Harpagiferidae represents a particular model in relation to the biogeography of its representatives. This monogeneric Family includes a single Antarctic species, Harpagifer antarcticus, restricted to the western Antarctic Peninsula and a number of sub-Antarctic species geographically assigned to South America (H. bispini), Falkland Islands (H. palliolatus), South Georgia (H. georgianus), Marion Island (H. marionensis), Kerguelen plateau (H. kerguelensis and H spinosus) and Macquarie Island (H. macquariensis) among others. Through this proposal, we will determine the levels of genetic of molecular divergence among congeneric species of Harpagifer from different provinces in the SO. The information contained in their DNA sequences will permit us to estimate rhythms and trends in the diversification of genetic lineages of a marine benthic near-shore organism. At the same time, we will use phylogeographic approaches in different species to evaluate the impact of the Quaternary glacial cycles in each of the analyzed SO Provinces. We will contrast levels of genetic diversity to determine the patterns of genetic structure among these Provinces. It will be possible to determine the effects of the Quaternary glacial cycles over the distribution of genetic lineages in these species and it will be possible to estimate whether the Antarctic species remained in refugia along the Antarctic Peninsula during the last glacial event or re-colonized this area after the LGM from northern Antarctic Islands in the Scotia Arc. We will also perform

FR_02-15	How would experimental warming affect freezing tolerance of antarctic vascular plants?	León Bravo	UFRO	leon.bravo@ufrontera.cl	AnT-ERA	Regional warming in the Antarctic Peninsula has been reported widely in the literature. In fact, a significant expansion of Deschampsia antarctica Desv. and Colobanthus quitensis Kunth (Bartl.) population all over the South Shetland Island has been reported. These plant species have reached as south as 69° Lat S in Alejandro I, Islands close to the base of Antarctic Peninsula. Several publications have described the effects of regional climate change on Antarctic plant populations, and several articles also describe the physiological mechanisms of freezing tolerance, such as accumulation of cryoprotectants, antifreeze and cryoprotective proteins. However, there is limited information on how warmer environment would affect freezing tolerance and cold acclimation/deacclimation responses of these two Antarctic vascular plants. In this proposal we would like to address the question whether experimental warming would induce plant cold-deacclimation, we will study its kinetic and temperature threshold. To follow the deacclimation process we will study how cryoprotective biochemical and physiological mechanisms will be affected by in situ and laboratory experimental warming. Hypothesis: Experimental warming will decrease freezing tolerance of Antarctic vascular plants causing an early deacclimation. Therefore low temperature induced mechanism will be disrupted by warming, consequently plants will not reach their potential freezing tolerance after warming exposure. If this hypothesis is correct it is predicted that: 1. Experimental warming will decrease accumulation of cryoprotectant solutes and proteins, but will not necessarily modify the specific activity of each protein. 2. Experimental warming will decrease apoplastic antifreeze activity in D. antarctica by changing the antifreeze protein profile (amount or diversity of polypeptides) but individual proteins would preserve their specific activity. Therefore, in molar basis, they will be equally effective cryopreserving cells or macromolecules in vitro. General Objective: Study the effect of experimental warming on freezing tolerance traits of Antarctic vascular plants. Specific Objectives 1. Characterize freezing tolerance and cold acclimation/deacclimation capacity of two species of vascular plants subjected to simulation of the current regional warming in the Maritime Antarctica
FR_03-15	Reflectivity of Antarctica	Raúl Cordero	USACH	raul.cordero@usach.cl	CFCT	Antarctica significantly affects Earth's climate and it is also notably affected by climate change. The ongoing rise in greenhouse gas emissions as well as ozone depletion contribute to changes in temperature, surface reflectivity (i.e. the albedo), sea ice cover, and ice sheet instability. In particular, changes in the albedo may shift the radiative balance of the Earth's atmosphere and further accelerate climate change. Since it may play an important role in the Earth's climate warming pattern, we aim to further describe the reflectivity of Antarctica by using both ground-based measurements and satellite-derived estimates. Our objectives are as follows. 1) Examine how the near-surface air temperature affects the reflectivity of snow-covered surfaces. The reflectivity will be characterized by measuring under weather different conditions (a) the albedo and (b) the hemispherical conical reflectance factor (HCRF). Changes in albedo over the course of the day will be used to assess the sensitivity of the snow to changes in the temperature. We expect that the assessment of the temperature-dependent albedo will facilitate estimations of the radiative forcing due to climate change-related changes in the reflectivity of Antarctica. Moreover, ground-based measurements of the HCRF will be used to test satellite data (such as Moderate Resolution Imaging Spectroradiometer (MODIS), Medium-spectral resolution, imaging spectrometer (MERIS) and Polarization and Directionality of the Earth's Reflectance (POLDER-PARASOL)). We expect that validated satellite data will allow deriving a distribution of the reflectivity for large areas in Antarctica. Our experimental activities will be predominantly concentrated around Union Glacier Camp (located in the southern Ellsworth Mountains on the broad expanse of Union Glacier, 79º 46' S; 82º 52'W) and the Escudero Station (located on King George Island, 62º 12' S; 58º 57' W, Antarctic Peninsula). 2) Discern between the cloud cover and the sea ice influences on changes and trends in the Lambertian equivalent reflectivity (LER). LER data are satellite products that account for the combined cloud, aerosol and surface reflectivity as observed from space. Since the area surrounding the Antarctica is largely unpolluted, we will focus on assessing the effects of the cloud cover and the sea ice on LER data. Accordingly, we will compare satellite-derived estimates of the cloud cover and of the sea ice concentration, with a multi-satellite-based LER dataset (referred to as MEaSUREs: Reflectivity data for Earth's Surface Clouds and Aerosols) for October-March over the period 1979-2012. The MEaSUREs data have been already facilitated by the

FR_04-15	Paleogeographic patterns v/s climate change in South America and the Antarctic Peninsula during the latest Cretaceous: a possible explanation for the origin of the Austral biota?	Marcelo Leppe	INACH	mleppe@inach.cl	AntEco	It has always been difficult to explain the origin of the biota southern South America. There are many models and continental configurations; however, despite many advances in molecular phylogeny and paleogeographic reconstructions, there is still no consensus in the scientific community. After the break-up of the Gondwana continent, the southern Patagonian-Antarctic area occupied a key position for further geological and biological development in the Southern Hemisphere. At the end of the Cretaceous the world was under a greenhouse event, but recently new evidence suggest that at least locally (probably globally), in the Patagonian-Antarctic zone, a drastic fall in the mean temperature could have originated ice formation in Polar Regions. This cold short lapse was followed by a sudden warming, condition that persisted until the end of the Cretaceous. The moment was also very likely the last terrestrial connection between South America and the Antarctic Peninsula because the glaciostatic fall in the sea level, producing the exchange of terrestrial organisms such as Nothofagus dominated floras from Antarctica into Patagonia and vertebrates as hadrosaurs and sauropods from Patagonia to the Antarctic Peninsula. The extensive record of the Campanian-Maastrichtian deposits in Patagonia (Las Chinas-Cerro Guido Complex, Dorotea, Laguna Parrillar and Dumestre localities) and Antarctica (King George, Nelson, Seymour, James Ross and Adelaide Islands) will allow us to assess the importance of climate change during the Late Cretaceous as a driving force in the evolution of the southern biota, as well as understanding the role of the connectiondisconnection of both land masses. The most modern techniques in stratigraphy, palaeontology (micro and megafossils), palaeoclimatology (CLAMP and Climate Analysis with the Coexistence Approach), geochemistry (isotopic and zircon analyses), paleobiogeography and morphodynamic mineralogy (presence of micro-glendonite) will be used to answer the question about the determinants of the composition of the austral biotas during the Campanian-Maastrichtian interval: the
CI_01-15	Melting Claims: Antarctica as a challenge for theories of territorial and resource rights, and as a conceptual locus for rethinking the normative grounds of sovereignty claims over natural resources	Alejandra Mancilla	INACH	amancilla@inach.cl	MA	In this two-year research project, my aim is to show that certain unique features of Antarctica – among them, being 'the world's last store house of natural resources' (Suter 1980, p. 22), the last continent with no permanent population, and the last place on the planet where claims by individual countries remain frozen – make it not just a sui generis case to be treated in an ad hoc way by theories of territorial and resource rights. Rather, Antarctica should be seen as a point of departure to rethink and reassess the latter. I thus take the White Continent to be a privileged physical and conceptual locus from where to critically examine the adequacy of current theories of territorial and resource rights, and from where to build a novel framework that better deals with the Antarctic case, but also with other relevantly similar places – like natural world heritage sites and international ecosystems. The project has two parts. A first, critical part engages with the current literature on territorial rights and normative justifications of sovereignty over land and natural resources. The objective here is to examine the main statist and cosmopolitan theories and show why they are inadequate to justify Antarctic claims. A second, positive part seeks to construct a novel normative framework to justify claims over land and natural resources in Antarctica. This is especially timely when what has been called as the 'new Holy Trinity of Antarctic values', i.e. environmental protection, peace and science (Hemmings 2012, p. 145), are under pressure both by new international actors and by ecological and environmental challenges such as climate change. The methodology will consist mainly in revising the relevant literature on the topics of territorial and resource rights and sovereignty claims over Antarctica. Moreover, I will engage in discussion with some of the world experts in these topics at specialized conferences and workshops, and get critical feedback from dissemination talks directed at academic and non-academic audiences in Chile and abroad.

RG_31-15	Diversity and inter-annual variability of eukaryote microbial communities in Antarctic coastal waters	Juan Ugalde	UMayor	juan@ecogenomica.cl	AntEco	Marine microbial eukaryotes are a group of microorganisms that, even when they are critical for energy transfer and ecosystem function, has been less studied that other groups of microorganisms, like bacteria and archaea. This microbial group is conformed for a vast diversity of different taxa and has been recently subjected to multiple revision on its phylogenetically relationships. Besides having a tremendous phylogenetic diversity, microbial eukaryotes also spans a wide range of cellular size. This variations in cellular side strongly influences the energy transfer through the food web due to the inherent difference on modes of nutrition, cell cycles, metabolic strategies and ecological interactions. Thus, variations on the size structure of microbial eukaryotes will have an effect over the ecosystem function of marine systems. Microbial eukaryotes have an enormous contribution to Antarctic ecosystems, in one side because they are the primary food source of the entire Antarctic fauna due to photosynthesis and in the other, the main contributors to energy fluxes into the microbial food webs trough heterotrophy. Antarctica is one of the fastest warming region on earth due to Global Change, and then is imperative to in improve our knowledge of this microbial group in order to better understand the ongoing changes and to improve predictive models with biological in situ observations. Also, the strong seasonal variability of Antarctica, characterized by a long winter and a short summer, gives a good scenario for understand how this microbial group respond to environmental changes. In this proposal, size-fractionated samples of microbial eukaryotes collected at a fixed station at Fildes Bay, King George Island, Western Antarctic Peninsula, will be analyzed in terms of its taxonomic diversity. Diversity of microbial eukaryotes will be analyzed during five consecutive summers, in order to analyze the central patterns of summer inter-annual microbial eukaryote community variation, and the differences between size fractions. The integrated use of high throughput amplicon sequencing, multivariate statistical analysis and network analysis will be used to link the taxonomic information with the environmental information, to determine the amount of variability explained by physico-chemical variables measured. The results of this proposal will contribute to the global understanding and knowledge of microbial eukaryotes diversity in Antarctica, its temporal variability and the main environmental factors that explain summer inter-annual variability of microbial
RT_02-15	DNA barcoding as tool to described the Antarctic parasite biodiversity in marine invertebrates species.	Leyla Cárdenas	UACH	leylacardenas1@gmail.com	AntEco	Biodiversity is defined as "the variability among organisms from all sources, including terrestrial, marine and other aquatic ecosystems and ecological complex that they are part: this includes diversity within species, between species and of ecosystems". Parasites would be an essential part of any comprehensive study of biodiversity, as they provide a vision of both history and biogeography of other organisms (hosts), and the structure of ecosystems and the processes that are behind the diversification of life. In the Antarctica millions of years of isolation have allowed the evolution of a diverse and abundant wildlife that is highly endemic and adapted to cold. This region is a natural laboratory for study the life cycle adaptations in parasites associated to benthic fauna. To the date, the total taxonomy of parasite fauna of Antarctica has been developed using mainly classical taxonomy, that could be not the adequate method to determine the existence of sibling or cryptic species, leading to an error in the identification and quantification of the actual biodiversity in the area. Here, molecular systematic approach and DNA barcoding are widely used tools for specimen identification to species level and offers an opportunity to explore the parasite biodiversity in the area. Digenea and Cestoda are among the most species-rich groups of parasitic metazoans and have been also reported in species occurring in subtidal coastal Antarctic waters. Because many parasites have complex life cycles, they require multiple hosts, often from different trophic levels, to complete its development. Thus, the trophic interaction and the host species distribution could be the main factors that determine the presence of a given parasite in a particular environment. In addition, parasites in different developmental stages can be morphologically distinct from one other, here molecular analysis are very useful for confirm their life cycles. In this proposal we aim to describe the digenean diversity in marine invertebrates through molecular systematic and DNA barcoding. For this we will (1) to characterize the parasite fauna in marine invertebrate species; (2) to generate population descriptors (intensity and mean abundance and prevalence); and (3) to describe the life cycle of the most abundant and widely spread parasites in the system. We hope to generate the information for future studies of both the ecology of parasite-host systems and foundational data to study the of marine parasite fauna in the area.

RT_09-15	Environmental levels of xenobiotics in the Shetlands southern islands, Antarctica.	Mónica Montory	UDEC	mmontory@udec.cl	MA	Rapid growth worldwide has led to an increase in the synthesis of chemicals, most of these are xenobiotics, compounds nonexistent in nature and they are synthesized by man. Within this type of contaminants are the organohalogens compounds, like PCBs (polychlorinated biphenyls) and PBDEs (Polychlorinated biphenyl ether) among others. Antibiotics, anti-inflammatories, hormones and PFOs (perfluorinated) belong to a new xenobiotics group called Emerging Pollutants. The xenobiotics have high toxicity and can be transported over long distances, which are distributed globally and can reach Antarctica, where due to the weather conditions, are slowly degraded (Corsolini et al., 2006), and are incorporated into the food chain, bioaccumulate and / or biomagnified (Corsolini & Focardi, 2000). Most studies of pollutants realized in Antarctica are linked matrices biotic as: Feathers, penguins, algae, etc (Wolschke et al, 2015; Cheney et al, 2014, van den Brink et al, 2011; Gupta et al . 1996). In these studies, the dynamics and the ability of xenobiotics for staying in abiotic matrices of Antarctica have not yet been studied correctly. In Antarctica, the South Shetland islands are an interesting study area, because they are a tourist attraction and have many research stations, generating an increase in human activity. The aim of this study is to evaluate the environmental levels of xenobiotics in abiotic matrices as: soil, water, snow and air, in the South Shetlands. The methodology will be to take samples of water, soil, snow and air and to concentrate the xenobiotics from the samples. From these extracts, the xenobiotics will be quantified by using chromatographic techniques (ECD, MS-MS, NICI). The xenobiotics to be analyzed will be PCBs, PBDE, hormones, antibiotics, anti-inflammatory and PFOs. The islands under study will be King George, Livingstone and Deception. A control island without anthropogenic activity is considered also (Lagotellerie island). With the information gathered will be possible assess the negative effects of the xenobiotics and its presence near tourist sites and scientific bases. The project will be important to assess vulnerability of Antarctica due to human activity, to propose management tools to improve the quality of the Antarctic environment, ensuring the conservation of native resources. Finally, it will contribute to the evaluation of international treaties relating to Antarctica.
RT_14-15	Characterization of methane cycling in Antarctic and sub-Antarctic lakes	Ma. Soledad Astorga	UMAG	msoledad.astorga@umag.c	MA	Freshwater ecosystems represent only 3% of Earth surface, but are responsible for 6-16% of global CH4 emissions to the atmosphere. Despite their importance in the greenhouse gas budget, the magnitude and the mechanisms involved in CH4 cycling still remain partially unknown and need to be further constrained. This is particularly the case of Antarctic and sub-Antarctic regions, where no report on CH4 cycling have been done before. In the worrying context of climate change, a better knowledge of CH4 cycling in these permanently cold environments is of crucial importance in order to better understand and predict global changes. CH4 cycling and emission in aquatic ecosystems are controlled mainly by two opposite biological processes; methanogenesis (anaerobic CH4 production) and methanotrophy (aerobic CH4 oxidation), which reduces substantially the amount of CH4 produced, that is emitted to the atmosphere. The whole lake CH4 budget can be solved by measuring the emission of CH4 and the methanotrophic activity, giving by difference, the methanogenic rate. In addition to measuring the aforementioned processes, the identification and quantification of the microbes involved are also of foremost importance. In particular, the role of methane oxidizing bacteria (MOB) is of prime interest since they are directly involved in the “in-situ” control of greenhouse gas emissions. In this context, our team has recently developed new methods based on a single technological platform (Off-Axis Integrated Cavity Output Spectrometry), which allow for the determination of; (i) CH4 emission (ii) dissolved CH4 concentration in the water column, and (iii) methanotrophic activity, with a data acquisition frequency and a sensitivity unreported before. Our team is also well prepared to study the phylogenetic and metabolic diversity of MOB. With our interdisciplinary experience, we have the required background to study, in details, the processes involved in CH4 cycling and the microbes involved. Our team has recently and successfully characterized sub-Antarctic lakes of the Magallanes region (-53° lat.) and has previously studied the methane production activity and identified key methanogenic archaea from the Antarctic soils and sediments, during an INACH field project (RT09-12). We are now willing to expand our previous survey, through a detailed study of two lakes from the Cape Horn region (-55° lat.) and two lakes from the King George Island (-62° lat.). We plan our study over two contrasting seasons (summer and winter), to be able to understand the annual CH4 cycling. This approach would allow understanding the seasonal, spatial and latitudinal variation of CH4 cycling, for the first time in that region of the world.

RT_28-15	Effects of Antarctic environment on vitamin D status and health risk biomarkers of its inhabitants	Arturo Borzutzky	PUC	drarturo@gmail.com	MA	Vitamin D (VD) is a hormone that is synthesised in the skin upon exposure to solar ultraviolet B (UVB) radiation. VD deficiency predisposes humans to bone loss and increased fracture risk, and possibly to other health problems, including cancer, cardiovascular risk, autoimmunity, respiratory infections and allergies. Chilean Antarctic territory has receives the lowest solar UVB exposure compared to rest of the country. Its cold temperatures and harsh climatic conditions, oblige its population to spend most of their time indoors and to use warm clothing covering most of their body when outdoors, further reducing their skin exposure to solar UVB. This extreme Antarctic environment places the population, both children and adults, of the Chilean Antarctic territories at highest risk of severe VD deficiency. The Scientific Committee on Antarctic Research has determined that among the research priorities for the next two decades is the question of how humans will adapt and mitigate the risks of frequent and long stays in the extreme Antarctic environment. We plan to evaluate how this environment affects VD status of its inhabitants and associated consequences on their health by measuring serum 25-hydroxyvitamin D (25OHD) of the Antarctic population, together with biomarkers of bone metabolism, immune status, and cardiovascular risk known to be associated with VD deficiency. An initial cross-sectional study of blood samples obtained from residents of Chilean Antarctica will be performed. We then will transition to a clinical trial of oral supplementation with vitamin D3 to raise 25OHD levels. The U.S. Institute of Medicine has recommended supplementation with VD 600 IU daily in populations at risk of VD deficiency. However, several lines of evidence have suggested higher doses in population living at high latitudes. To provide an answer to this clinical uncertainty, we propose to randomize the adult population of Chilean Antarctica to one of two different regimens: one arm will receive 600 IU daily and the second arm 25.000 IU once weekly. The primary outcome of this study will be the increase in 25OHD serum levels to sufficient levels (≥30 ng/ml). To assess this increase, blood will be drawn from study subjects quarterly during one year or during the length of stay of each subject. We will also evaluate change in parameters of bone metabolism, immunity, and cardiovascular risk, adherence to supplementation and safety. All children will be given VD3 600 IU daily during the study and will be evaluated with blood samples only before and after supplementation. The study of two different doses and regimens will eventually provide highly relevant information to develop policies regarding optimal VD supplementation specifically designed for this high-risk
RT_32-15	Ground-based Measurements of the Radiance Distribution in the Antarctic Peninsula	Raúl Cordero	USACH	raul.cordero@usach.cl	CFCT	The better understanding of changes in major climate parameters (such as reflectivity/albedo and clouds) is essential in the Antarctic Peninsula (AP), a region strongly affected by climate change. The AP has seen in recent decades a significant increase in total cloud extent, while changes in sea ice concentration (SIC) have led to major changes in the reflectivity over the Southern Ocean (SO) off the AP. Therefore, the surface radiation doses (significantly modulated by clouds and reflectivity) are likely changing. The prediction of further changes requires the proper assessment of the radiation climatology (i.e. the characterization of the effects of major climate parameters on the surface radiation). In this proposal, we aim to characterize the downwelling and upwelling radiance distributions on King George Island (at AP/SO) by using ground-based measurements. Accordingly, we will develop a novel non-scanning motionless multidirectional system suitable for long-term measurements of the radiance distribution. This new instrument will allow the fast sampling of the radiance spectrum (from the UV to the IR), enabling in turn ground-based measurements on King George Island at least during a year. We expect that we will be able to assess the effects on the radiance of the local cloud variability and the seasonal changes in the albedo. Since in nature surfaces are not horizontally flat, the dose of solar radiation affecting the biosphere depends on the angular distribution of the radiance. Therefore, special attention will be paid to the UV range of the spectrum. These measurements should allow improving the estimations of biologically effective radiation doses in the Antarctic Peninsula. The project will be carried out by a multidisciplinary group with a proven scientific productivity and a record of effective partnership. Our group successfully led several “FONDECYT” projects and also the “Antarctic Team Research Project (Anillo)” (funded by CONICYT, Grant ACT-98). Indeed, our efforts investigating the radiance distribution have strong synergies with planned ground-based measurements of spectral albedo at Escudero Station and at Union Glacier Camp over the next four years (as part of a Chilean CONICYT-funded project led by R.R. Cordero). Furthermore, this proposal will be carried out in close cooperation with Institute of Meteorology and Climatology of the University of Hannover (Germany). Finally, we expect a positive impact on both graduate and undergraduate programs. Indeed, two Chilean PhD students will be directly involved in the proposal. Assessment of Antarctic climate and processes requires a better understanding of the influence of major climate factors (such as cloud and albedo) on the surface radiation. This

DT_02-15	Foraging Ecology in extreme environments. The role of climate variability and mother-offspring dependence on the foraging strategies of the Antarctic fur seal (Arctocephalus gazella)	Renato Borrás Chávez	PUC	rborras@gmail.com	AntEco	Studying foraging behavior in nature is crucial to comprehend the relationship between energy acquisition and the reproductive success of a species, which has a direct effect at a population scale. For instance, short-term decisions such as habitat selection of a marine predator will have long-term consequences on growth and survival of their offspring. This, highlights how important it is to comprehend finer scales of foraging ecology since those decisions will directly affect fitness. One of the main variables shaping the foraging strategies used by individual is environmental variability. The intensification of such variability is currently represented by global change. To date, many climate change studies have focused on understanding its effects on physiological aspects and it has only been recently that studies have begun to focus and comprehend its effect on behavior. This focus needs to be strengthen since populations with a higher behavioral plasticity may have better options to cope with climate change. The Antarctic fur seal, Arctocephalus gazella (from now on AFS) is a good example. Previous studies have shown strong association between environmental variability, prey distribution and the diversification of foraging strategies used by AFS. However, strategies may change in places with high environmental variability such as the southern limits of the species distribution and the edge of its physiological tolerance (i.e. the Western Antarctic Peninsula) were the rise of ocean temperature and the accelerated climate change make this particular area very important since is a current representation of future scenarios of environmental variability. Additionally, AFS are “central place foragers” and the energy acquired on each strategy will have a direct effect on the offspring, which are direct representatives of the species fitness. For this, some studies infer that the degree of mother-offspring dependence throughout the breeding season may play a major role on shaping foraging decisions and prey selection. By the use of GPS “temperature depth recorders” the objectives of this study are: To fully describe the foraging strategies utilized by AFS at the southern limit of the species distribution and evaluate how important two main variables are at shaping those strategies; the mother-offspring dependence degree (hypothesis 1: This variable will determine how foraging strategies change throughout the breeding season) and the environmental variability expressed in oceanic surface temperature and climate conditions (hypothesis 2: If there are differences between years, this variable will modify prey distribution and therefore the
DT_05-15	PROSPECTION AND CHARACTERIZATION OF BIOSURFACTANTS PRODUCED BY ANTARCTIC BACTERIA	Claudio Lamilla Mardones	UFRO	claudiolamilla@gmail.com	MBBA	The biosurfactants are amphipathic molecules composed of two regions, a hydrophilic or hydrophobic and other polar or nonpolar, hydrocarbon chain consisting of a variable length can be anionic, cationic or nonionic. They are generated in the stationary phase of microbial growth, and are excreted extracellularly in the form of secondary metabolites by various microorganisms, such as bacteria, fungi and yeasts. The biosurfactants have a high economic interest given the wide variety of applications in the food, cosmetic, pharmaceutical and environmental protection. Within the latter, highlighting the bioremediation of contaminated sites metals and hydrocarbons, in which oil and its derivatives are the main source of environmental pollution. Recent studies have shown that from sediments, soil and water (salt or fresh) of contaminated sites have been isolated fungi and bacteria can synthesize biosurfactants and also that bacterial strains isolated from Antarctic pristine places, have the capacity to produce them. Given the above, the aim of this project is to characterize Antarctic biosurfactants produced by bacteria capable of biodegrading petroleum hydrocarbons. For this, microorganisms are isolated in samples of marine sediment, freshwater and soil samples obtained in different environments of the Antarctic, in pristine places, as with human occupation, they exhibit the capacity to produce biosurfactants, which may facilitate biodegradation hydrocarbon. To this end, various tests were conducted to evaluate the production of these secondary metabolites using the Bushnell Haas medium enriched with different hydrocarbons such as diesel oil and hexadecane. Biosurfactants producing strains are identified by the 16S rRNA gene using universal primers 27F and 1492R. From the identified bacteria, it proceeds to the purification of biosurfactant and subsequent structural characterization trough proteomic and spectroscopic methods such as MALDI TOF-TOF, TF-IR, HPLC-GC and NMR. This research project aims to contribute to the isolation and characterization of Antarctic bacterial strains producing biosurfactants which are useful in bioremediation of hydrocarbon contaminated sites and also to the identification and characterization of these bioactive metabolites. Finally, given the wide variety of biological activities attributed to these molecules, we hope to contribute to their use in the biotechnology industry in any of the different areas of application of biosurfactants.

DT_10-15	Diversity and activity of nitrous oxide-reducing bacteria in Antarctic soils influenced by marine animal settlements	Lía Ramírez Fernández	UCHILE	liaramirez88@gmail.com	MBBA	Antarctic coastal ice-free areas concentrate colonies of different marine animals, where their depositions affect the soil physicochemical properties, forming Antarctic terrestrial ecosystems enriched in organic carbon, total nitrogen and phosphorus, which allow high microbial activity. In these soils, high emissions of greenhouse gases have been recorded, including nitrous oxide (N2O). N2O is a potent and a predominant ozone-depleting substance in the atmosphere. As a consequence, in Antarctic Peninsula and the surrounded islands, in particular, a high destruction of the ozone layer, a high heating rate and a noticeable thaw of ice zones are recorded. In this scenario it is necessary to determine the different sources emitting N2O and, more importantly, microorganisms involved in the process of consumption of N2O in these soils, which could play a key role in mitigating emissions of this greenhouse gas. Although there are many microbial metabolic pathways involved in N2O emissions, there is only one known pathway for its consumption: the enzymatic reduction by the nitrous oxide reductase (N2OR). This enzyme is encoded by nosZ gene, which has two phylogenetically different versions, clade I or "typical" and a recently discovered clade, clade II or "atypical". Organisms which potentially would possess the nosZ clade II gene would be abundant in polar soils and would have higher ability to reduce N2O; therefore they would be keys in mitigating N2O emissions in these soils. This microbial consumption of N2O may be affected by soil physicochemical factors; in particular, low pH has been described as a limiting factor for N2O reducing. In this project it is proposed that, in Antarctic soils influenced by marine animal settlements, would exist a high abundance of N2O reducing bacteria belonging to nosZ clade II gene, and therefore they would possess a high N2O consumption ability; however, soil physicochemical factors altered by animal colonies, would affect the N2O reduction, contributing to high emissions of this greenhouse gas. Using massive sequencing strategies, qPCR and metabolic assays, the diversity of N2O reducing bacteria, their N2O consumption ability, and the effect of edaphic physicochemical factors on these ones, will be determined in Antarctic soils influenced by settlements of marine animals. According to our best knowledge, studies have not been made on Antarctic ecosystem soils, in which the composition of bacterial communities involved in N2O reduction has been determined, thus this research will be a contribution to the understanding of nitrogen recycling in these soils
MG_03-15	Purification and Characterization of a new Laccase isolated from the antarctic thermophile Geobacillus sp. ID17	Joaquín Atalah Zúñiga	UCHILE	akhin.dw@gmail.com	MBBA	Laccases are enzymes from the Multi-Copper Oxidase family, which have aroused interest because of their wide substrate range, the high variability of biochemical properties between species, and their still elusive mechanism of action. The presence of four copper atoms in their active site, each of which exhibits distinct chemical coordination number make them an interesting model for the study of the structure-function relationship of proteins. This copper atoms are also responsible of the catalytic properties of Laccases, and they show redox and spectroscopic features that are unique to this class of enzymes. They can be found in fungi, plants and prokaryotes. Bacterial Laccases show a many advantages in biotechnological potential over fungal ones , which to this day remain better studied. In general, they posses a better thermostability, and a different pH activity profile, which makes them better suited for some applications. Their properties make them great candidates for divers applications such as textile dyes degradation, compound processing in the food industry, Catalysts for organic synthesis, bioremediation, etc. The aim of this thesis is to characterize a Laccase recently identified in the thermophilic bacteria Geobacillus sp. ID17 isolated from an enviromental sample taken from Desolation Island in the Antarctic territory, which would be the first antarctic Laccase to be properly characterized, and the firs intracellular laccase reported from the Geobacillus genus, which is why it may present interesting features that could open the doors to new uses for the bacterial multi-copper oxidases. It's biochemical properties are going to be testes, as well as it's substrate range. The properties of it's active site will also be assesed using spectroscopic techniques. It is expected that this work yields new knowledge that contribute to the comprehension of the biochemical properties of this class of enzymes, to their use as biotechnological tools and to a better understanding of the mechanisms through which the Antarctic microorganisms relate to their environmental conditions.

MT_08-15	Development and optimization of an analytical methodology for determination of PAHs by solid phase microextraction using stir bar sorptive extraction (SBSE) for snow samples collected from the glacier La Paloma, Antarctic Peninsula	Carmen Sánchez Baeza	UTFSM	carmengloriasanchezb@gr	MA	One of the main objectives of the Center for Environmental Technologies and the Laboratory of Environmental Chemistry (CETAM-LQA) of the Technical University Federico Santa María (UTFSM) to assess temporal changes in chemical components of different environmental matrices (water, air, soil) subject to alterations by human activities. This research aims to improve understanding of this and other phenomena associated with the deposition of aerosols in the snow of Antarctica and its impact on the greenhouse effect, which is critical to better understand global climate change, particularly the enormous importance of Antarctica as reflecting surface, essential in the radiative balance of the planet. This will complement a longitudinal database of the phenomenon of aerosol deposition on snow and its impact on white surfaces of our country (glaciers), so the origin of these, either anthropogenic (combustion processes from mobile sources or still originating in the cities) and / or natural (volcanic eruptions, forest fires, etc.). The glacier La Paloma (63º21'20 "S, 57º48'21"W, 409.msnm) located in the Trinity Peninsula at the northern tip of the Antarctic Peninsula, is a particularly appropriate area for this type of studies, weather conditions that ensure a good quality preservation of records nivológica annual accumulation. Another feature is its easy access from the Base Bernardo O'Higgins, simplifying logistics support for the campaign and, finally, its glaciological potential. The hypothesis of this research is that "There is global atmospheric transport of Polycyclic Aromatic Hydrocarbons (PAHs) to the northern tip of the Antarctic Peninsula". The general objective of this research is: • Develop and optimize an appropriate analytical methodology for determination of PAHs in samples of snow in the area of the glacier La Paloma, and their links with the global transport of these contaminants to remote sites. Analytical methodologies are used for HPLC-FL HAPs and / or GC-MS with application microextraction absorption in stirbar (SBSE), method that allows the use of this in-situ in the snow bar, to retain and concentrate organic compounds of interest, even directly in the sampling site, to further develop analysis of contaminants in the aqueous matrix (snow) by desorption extraction technique, this in order to reduce costs, waste, time per sample amount of sample to collect and transport to the laboratory as well as costly and complex maintenance of the cold chain of snow samples intended for organic chemical
PR_01-15	Determining the presence of drug residues in waters of the Southern Ocean	Maccarena Marcotti Murúa	UST	maccarena.marcotti.m@ho	MA	Unavailable
PR_02-15	Stratigraphy and palaeoenvironment of the lower strata of Fildes Peninsula Group	Fernanda Carvajal Hermosilla	UNAB	fer.carvajal.h@gmail.com	CFCT	Unavailable
PR_03-15	Rhodobacter sp response to stress induced by UV radiation: Plateau vs. Antarctic	Lenka Kurte Palma	UCN	lenka.kurte@live.cl	MBBA	Unavailable
FP_01-15	Assessing the role of rhizosphere's bacterial communities in the physiological performance of Colobanthus quitensis under salt stress	Jorge Gallardo	UBio-Bio	jgallardoc@inach.cl	MBBA	Unavailable

FP_02-15	Anthropogenic pressure over the Antarctic microbial world: Stability of soil communities facing hydrocarbon pollution disturbance	Sebastián Fuentes	PUC	sebastian.fuentes.a@gmai	MA	Abiotic limitations are prevalent on most Antarctic soils, with scarce or absent vegetation, and a general lack of insects or herbivores. In this scenario, microorganisms are particularly relevant, as they are the drivers of most ecological processes. In this simplified food web, nutrients cycling are dominated by the microbial world. Because of this relative simplicity, Antarctic soils are ecosystems especially vulnerable to disturbances. Human activities and settlements in the Antarctic continent generates a major environmental risk due to pollution by waste management, liquid effluents, air pollutants and fuel leaks. Hydrocarbon (HC) pollution is an anthropogenic disturbance of major concern since abiotic limitations such as low temperatures and nutrient limitation slow down the natural microbial attenuation of HC. Environmental disturbances, either natural or anthropogenic, alter microbial communities (MC), affecting their stability and, eventually, their ecological functions. Therefore it is crucial to assess to what extent anthropogenic disturbances can impair Antarctic MC stability and ecological functions. Stability depends on the nature of the disturbance, the environmental physicochemical properties and the MC structure. Nonetheless, the actual impact of each factor is poorly understood and remains as a major challenge in microbial ecology. In any particular niche, the MC structure is influenced by its disturbance history, since every new disturbance introduces the selective pressure in which some traits (i.e. functions) become advantageous. The increasing pressure over Antarctica generates a continuous disturbance history to which MC has to adapt. Thus, we hypothesize that, under comparable environmental conditions, MC stability facing a disturbance relies on the trait selection by the disturbance history. To test the hypothesis, HC pollution (the disturbance model) over Antarctic soil MC (the system model) will be studied. This proposal considers a combination of a sampling strategy to obtain relevant in situ information, and microcosm experiments to study the effects of HC disturbance under controlled conditions. Three main activities are proposed: i) Establish a baseline of MC structure and its relationship with environmental metadata, achieved by sampling ice-free soils along Antarctic Peninsula and South Shetland Islands, including sites with and without HC pollution history. ii) Assess the influence of the HC pollution history over the MC dynamics and stability facing increasing HC levels, performed in microcosm experiments. iii) Generate
FI_01-15	Assessing the utility of Antarctic sponges for studying global climate change: individual to community level responses	César Cárdenas	INACH	ccardenas.biosub@gmail.c	AnT-ERA	The Antarctic Peninsula has undergone drastic changes in air and water temperature over the last fifty years and continues to experiences some of the most rapid climatic warming on the planet. The projected changes in temperature constitute major threats to ecosystem functioning, services and integrity, as they can affect key functional species, thus affecting their associated ecosystem processes. Because ecophysiological responses to climate change can be species-specific, biological interactions such as competition and predation may also be altered, hence cascading throughout the entire benthic community. Sponges are important members in Antarctic rocky reefs where they play important roles in community dynamics, as microhabitat providers and also positively influencing diversity and composition of Antarctic benthic communities. Because of their dominance they are also expected to play other important roles described for other latitudes (e.g. bentho-pelagic coupling), however, they remain unstudied in Antarctic habitats. Existing literature clearly shows that our understanding of how increasing temperature will affect Antarctic sponges, and the functional roles they play in Antarctic ecosystems is incomplete. However, research into how tropical and temperate sponges respond to temperature change is more advanced and suggests that if we are able to address this knowledge gap for Antarctic sponges and their associated microbial communities they may become important indicators alerting us to temperature stress in Antarctic benthic communities. Because a negative effect on the symbiotic performance of Antarctic sponges and their associated microbial communities can potentially alter the ecological roles of sponges, addressing this information gap is also vital in improving our understanding of how the functioning of Antarctic benthic communities is likely to be affected by temperature stress. To achieve this requires increasing our understanding of the dynamics of Antarctic sponges from a molecular to community level. The physiological tolerances of Antarctic marine species are thought to be tightly coupled to the extreme environments within which they live. Therefore, their responses to increasing temperature can be expected to differ substantially from species at other latitudes. This has led to the hypothesis that Antarctic marine species have a limited ability to acclimate to warmer temperatures, resulting in the loss of critical biological functions. I will conduct research to determine if Antarctic sponges can be used to alert us to

FI_02-15	Assessing the role of iron and light on phytoplankton production and air-sea CO2 fluxes in a changing western Antarctic Peninsula	Ernesto Molina	USACH	emolina@bio.puc.cl	CCA	Our understanding of biophysical processes in the ocean, and in particular in the changing western Antarctic Peninsula, has been limited by a lack of observations, and an earlier generation of idealized numerical models. This project will use an intense 3-year period of shipboard, combined with sophisticated data assimilating ocean models, to analyse and simulate physical, optical and biological processes in the Bransfield Strait region. This will significantly advance our understanding of the physical forcing of biological processes such as primary production at the scale of the Bransfield Strait, and comes at a time when the scientific and broader community is urgently seeking quantification of the regional impacts of a warming ocean.
PC_01-15	A multi-disciplinary approach to understand the impact of ice loss and deglaciation on Antarctic coastal benthic ecosystems	Antonio Brante	UCSC	abrante@ucsc.cl	AnT-ERA	West Antarctic Peninsula is experiencing a recent and rapid increase of temperatures due to climate change. Some of the effects of this warming trend can be observed in the retreating glaciers, collapse of ice shelves and lengthening of the sea-ice melting season. In spite of these findings there are a limited number of studies evaluating the effect of these environmental changes on coastal Antarctic ecosystems. This project is a collaborative work between the Universidad Catolica de la Ssma. Concepcion, Bangor University and the British Antarctic Survey to study the effects of ice loss and deglaciation on the benthic ecosystems on the West Antarctic Peninsula. We use a multidisciplinary approach to evaluate genetic, physiological, population, community and ecosystem impacts.
PC_02-15	Evolutionary history of Colobanthus quitensis and its associated microorganisms: implications for understanding present biogeographic patterns, adaptation to environmental change and interactions with glacial cycles	Marco Molina	UTALCA	marco.molina@ceaza.cl	AnT-ERA	The main goals of this proposal are to assess the evolutionary history of C. quitensis in Antarctica and southern South America by evaluating: (i) how its genetic diversity is distributed within and among populations, (ii) how historical processes have influenced the contemporary distribution of C. quitensis across its southern range of distribution, and (iii) To determine whether geographical patterns of genetic variation are consistent with the diversity of microflora and its symbiotic effects. These predictions will be tested using experimental approaches as well as population genetic and phylogeographic analyses. This research proposal will shed fundamental new light on the evolutionary history of the flora between South America and the Antarctica.
FR_01-16	Characterization of Low Clouds over the Antarctic Peninsula and the West Antarctic Ice Sheet (WAIS)	Penny Rowe	USACH	prowe@harbornet.com	CFCT	The West Antarctic Ice Sheet (WAIS) and the Antarctic Peninsula (AP) are found to be among the most rapidly warming regions on Earth. Clouds have a strong impact on the surface radiation budget, but the role of clouds in the WAIS and the Antarctic Peninsula warming is not well understood. Supercooled liquid clouds, in particular, are common along the coast of Antarctica, with important radiative consequences, but the amount of supercooled liquid water in polar clouds is typically underestimated by GCMs. Furthermore, in the Southern Ocean (SO) climate models and reanalyses have biases in absorbed shortwave radiation attributed to biases in clouds and albedo. Despite the need for a detailed understanding of Antarctic clouds, in situ measurements are limited. Goals: • Measure low-cloud properties in situ over the AP, SO, and WAIS. • Validate satellite-based measurements and compare results with reanalysis data and surface-based measurements made elsewhere in Antarctica. • Investigate the influence of sea ice concentration on cloudiness in the SO, using these measurements and satellite-based measurements. • Validate and improve the representation of clouds and radiation in forecast modeling. Impact: This research will give Chile an opportunity to significantly contribute to global efforts aimed at the better understanding of the Antarctic climate, in particular, at the assessment of the impact of clouds on the surface radiation budget. Methodology: In Situ Measurements: We will purchase an unmanned aerial vehicle and a radiosonde-borne cloud property measurement package (the Universal Cloud and Aerosol Sonde System, or UCASS), which will be field-tested, revised as needed, and deployed at King George Island in the AP/SO (years 1 and 3) and Union Glacier int he WAIS (year 2). We will deploy the instrument when low level clouds are present. As possible, we will time flights with satellite overpasses, and will attempt to make measurements in two conditions: 1) when only a single layer of low-level clouds are present, and 2) when multiple cloud layers are present. Continuous pyrgeometer and pyranometer measurements will also be made. Validation and comparison to other datasets: To validate satellite-based measurements, in situ measurements made near-in-time will be identified and relevant

FR_02-16	Equilibrium and non-equilibrium processes in space plasmas and the solar-wind-magnetosphere-ionosphere interactions	Marina Stepanova	USACH	marina.stepanova@usach.	CFCT	One of the most challenging problems in Space Physics is understanding of physical mechanisms responsible for the development of geomagnetic storms and substorms, the nature of which remains a subject of strong debates. During the past four decades the solar wind-magnetosphere-ionosphere interactions have been studied from various vantage points by combining satellite and ground-based measurements. For example, the recently launched Van Allen probes and Magnetospheric Multiscale (MMS) missions (NASA), together with THEMIS/ARTEMIS mission, produce accurate and simultaneous multipoint measurements of magnetospheric parameters with an excellent resolution. These measurements are complemented by observations made on extensive networks of ground-based instruments such as all-sky cameras, radars, and magnetometers. In particular, the South-American B-field Array deployed in Chile and Chilean and North American bases in Antarctica have provided important data about the fast variations of the geomagnetic field over a range of geomagnetic latitudes. The magnetosphere of the Earth is a complex multi-scale self-organized system. It is formed as a result of the interaction between the solar wind supersonic and superalfvenic turbulent plasma flow and the geomagnetic field. In ordinary fluids, interaction between a supersonic fluid and an obstacle leads to the development of a turbulent wake behind the obstacle. The magnetosphere of the Earth has a much more complicated structure. Some regions of the magnetosphere, including the plasma sheet and the magnetosheath, are turbulent, while other regions are characterized by almost laminar flow. The total pressure balance generally holds for all magnetospheric regions, and the inner magnetosphere is generally in a magnetostatic equilibrium. In this context, the geomagnetic storms and substorms are a consequence of equilibrium and non-equilibrium processes, forming a chain of solar wind-magnetosphere-ionosphere interactions. Equilibrium and non-equilibrium processes are not independent, and ideally should be studied self-consistently. The main goal of this proposal is to contribute to the understanding of the role of equilibrium and nonequilibrium processes in dynamics of the magnetosphere. Special attention will be paid to the processes of turbulent transport, magnetostatic equilibrium in the inner magnetosphere, turbulent solar windmagnetosphere interactions, and processes in the auroral ionosphere. We will focus especially on the transition region between the dipole-like and the tail-like geomagnetic configuration, in which, according
FR_03-16	Ecophysiology of Antarctic snow algae: adaptation mechanisms to a changing polar environment	Iván Gómez	UACH	igomezo@uach.cl	AnT-ERA	The vast extensions of snowfields in polar regions host highly diverse and abundant communities of cold adapted microorganisms. A group of photoautotrophs is especially important: the snow algae, which are represented by members of all major algal divisions including Chlorophyta, Bacillariophyta, Cryptophyta and Cyanobacteria. In various species of Chlorophya, the life cycle phases are recognizable by their characteristic green or red pigmentation. In coastal areas of the maritime Antarctica, an ecoregion that comprises the West Antarctic Peninsula and adjacent islands, the snow ecosystems are in close interaction with the marine realm, and thus, the snow algae play important subsidiary roles, through the melting runoff, food web and degradation products in the biogeochemical cycles of the whole coastal system. Due to global climate change, regional warming is altering the melting/freezing regimes, and hence, the seasonal duration of the snow packs, with poorly understood consequences for the biological processes, especially those driven by highly adapted Antarctic extremophiles. Hitherto many aspects related with physiological performance and environmental stress tolerance of snow algae are practically unknown and require urgent attention in order to predict the responses of the Antarctic biota to new scenarios, characterized by elevated temperature and UV radiation (Clarke et al. 2012). The present proposal will examine three main aspects: a) development, physiological performance and productivity of snow algae in the context of the life cycle; b) stress tolerance mechanisms of snow algae; and iii) diversity and ecological role of the associated microbial community. Based on physiological and molecular approaches the project attempts to identify the adaptive and acclimative strategies that snow algae exhibit in response to environmental factors beyond their tolerance threshold. A primary aspect will be the examination of photosynthetic acclimation of the different life-cycle phases (green and red snow) of some dominant chlorophyta (e.g. Chlamydomonas, Chloromonas, Chloroccocum), including light requirements, photosynthetic efficiency and pigment photoacclimation and bio-optical characteristics. These are essential traits that determine the light use efficiency and consequently, the primary production. Stress tolerance will be assessed through three types of responses to elevated temperature and solar UV radiation: a) photochemical adjustments; b) synthesis and activity of anti-stress substances; and c) functional gene expression (transcriptomics). The genomic analysis

FR_04-16	Phylogeography, population genetic structure and connectivity of the Subantarctic crab *Halicarcinus planatus*, the first alien marine invertebrate discovered in Antarctica	Karin Gerard	UMAG	gerardkarin@yahoo.fr	AntEco	Climate change directly impacts and shapes the biodiversity. In this context, biological invasions are a crucial component of global change, but also a threat to native biodiversity. Antarctica remains the most pristine continent on the planet and the most isolated surrounded by oceanographic, bathymetric, climatic and geographic barriers. The West Antarctic Peninsula has been described as one of the areas most affected by global warming thus enhancing the probabilities of introduction of alien species, their subsequent ecological adaptation and proliferation. The Antarctic marine fauna includes more than 4000 species and comprises a significant percentage of Earth's biodiversity. Shallow marine benthic communities around Antarctica are well known and exhibit high levels of endemism, gigantism, slow growth, longevity and late maturity. Several families of durophagous (shellbreaking) predators that are highly abundant and diverse in subantarctic shallow waters such as decapods, teleosts and chondrichthyens are almost completely absent in the Southern Ocean. Nevertheless, many records of non-Antarctic decapods, mainly lithodid crab have been reported during the last decades, thus indicating an ongoing invasion. So far, there are no evidence of expansion in geographic or bathymetric range for any lithodid species in the Southern Ocean. Deep Antarctic lithodids are relatively rich endemic species, with a distinct assemblage south of the ACC boundary. This family may have existed around Antarctica for long enough to have speciated, remained in situ and is rather constituted by native species extending their range due to environmental change. This year, a fully mature and breeding female Halicarcinus planatus was reported in Deception Island. This species is a small brachyuran crab with a subantarctic distribution and closely associated to the Antarctic Circumpolar Current. Halicarcinus planatus has a low bathymetric range, two spawning event per year and a planktonic larval duration of 45-60 days. This subantarctic species exhibits a tolerance to temperatures lower than 0°C and is also one the few decapods able to down regulate the [Mg2+] in the haemolymph. This carb is therefore able to physiologically cope with the cold. Larvae transportation through the Antarctic Convergence may occur by means of natural dispersal or transportation in ballast waters. The increasing maritime traffic associated to touristic and scientific activities in southern summer occurs during the period of planktonic larval occurrence. In parallel, the West Antarctic Peninsula are

Project codes		Clave línea investigación	
R	INACH REGULAR	AntEco	
T	INACH REGULAR FIELDWORK	AnT-ERA	
G	INACH REGULAR NO FIELD	CCA	Climate Change in Antarctica
D	PHD PROJECT	CFCT	physical sciences
M	MASTER PROJECT	MBBA	Microbiology, biochemestry and molecular biology
PR	DEGREE PROJECT	MA	Enviromental sciences
MA	ENVIRONMENT		
INT	INTERNATIONAL COLLABORATION		
FI	FONDECYT EARLY CAREER		
FP	FONDECYT POSTDOC		
FR	FONDECYT REGULAR		
FO	FONDEF-Fund to Promote Scientific and Technological Development		
FE	FONDEQUIP-Fund for scientific equipment		
AN	BICENTENIAL RINGS		
FD	FONDAP- Fund for prioritary areas		
PC	SPECIAL INT COOPER PROJECTS		
CI	NEW SCIENTIST INSERTION		
CO	CORFO-INNOVATION FUND		