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**BIOLOGICAL DISPERSAL -  
CONNECTIONS AT CONTINENTAL AND  
INTER-CONTINENTAL SCALES**



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## A synthesis of genetic structure across the Antarctic

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The genetic structure of populations crucially reflects their capacity to adapt or disperse in response to ongoing environmental change. There is now a substantial body of work addressing the genetic diversity and connectivity of Antarctic taxa, yet no systematic, quantitative synthesis of this data to inform future research or conservation priorities. In response, we have developed a comprehensive database of intraspecific genetic research on Antarctic and sub-Antarctic flora and fauna. Preliminary review of these studies reveals numerous emerging patterns regarding the scope, focus and findings of Antarctic connectivity research, including clear biases in sampling effort. A meta-analysis of these studies will help identify the most genetically vulnerable Antarctic populations, based on taxa, biogeographic region, dispersal mode and habitat. The database will be made openly accessible to provide researchers context and comparison for any future work regarding the connectivity and genetic diversity of Antarctic biota.

## Midway upon the journey of life: the importance of local and regional hydrography on population connectivity in Antarctic fish

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As Dante observed, the fate of individuals rests upon the whims of their environment. In the diverse array of notothenioid species, that environment is characterized by the prevailing current systems to which they are exposed throughout their life history. Many Notothenioids filling pelagic as well as demersal niches have evolved energy-conserving life strategies to reserve resources in the polar environment. This, coupled with their protracted life histories that combine extended early pelagic stages of more than a year with lifespans that extend into the multi-decadal range, disposes Notothenioids to complex connectivity scenarios over their life history. The occupation of different water masses by different life stages, coupled with circulation related to bathymetric features like glacial troughs and sea mounts, can serve to close the life cycle, informing the distribution of fish throughout their life history and the structure of their populations. Nevertheless, on the circumpolar scale, the Antarctic Circumpolar Current and the anticlockwise Antarctic Slope Current represent transport pathways that promote zonal movement within and across regions. The Antarctic Coastal Current, fed by glacial run off and hugging the coastline, connects inshore habitats on a more local scale. Temporal variability in these otherwise consistent hydrographic features has been shown to impact connectivity over time on seasonal and interannual scales. This presentation will explore the latest evidence for the integral role of hydrography and its influence on advective loss and supply to habitats downstream, when, as Dante's protagonist found, "the straightforward pathway had been lost".

## Revisiting the bipolarity of *Roaldia revoluta* (Mitt.) P.E.A.S. Câmara & M. Carvalho-Silva (Bryophyta, Pylaisiaceae)

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*Roaldia revoluta* (Bryophyta, Pylaisiaceae) is a strict bipolar moss, with an arctic-boreal-montane range, and in the southern hemisphere it is present in Antarctica (South Orkney, South Shetlands and Peninsula), Patagonia and New Zealand. Three main theories have arisen to explain the bipolarity: (1) American pathway with dispersal to the neotropics via mountain ranges to maritime Antarctica via Patagonia, (2) African pathway by means of east Africa mountains to sub Antarctic islands such as Kerguelen and (3) Indomalayan-Malesian Pathway, from Southeast Asia to Southeast Australia, New Zealand and associated islands. In this study we used a molecular approach to investigate the genetic evolution and relationships among representatives of *R. revoluta* from different parts of the globe. Nuclear (ITS + 26S) and Chloroplast marker (*rpl16*) were selected; total DNA was extracted from fresh and herbaria material. The results of our molecular analyses have shown very low genetic diversity among populations of *R. revoluta* across the globe. Both DNA regions has shown the existence of four haplotypes; the specimens from Antarctica all belong into Haplotype 1, the most widespread one. Although it was not possible to trace the species' precise dispersal route, we can assume that the American pathway hypothesis would be more appropriate since the populations with the highest number of haplotypes (for both types of markers) appear to follow the Europe – North America – Antarctica route.

## Spatial population genetic patterns and seed dispersal syndromes in plants on sub-Antarctic Marion Island

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Seed dispersal in plants comes in many forms, including by gravity, wind, water, ingestion by animals, and attachment to animals, and is expected to influence population genetic and biogeographic patterns. Sub-Antarctic islands represent ideal model systems for the study of evolutionary and ecological processes because of their simple and bounded yet well-developed terrestrial ecosystems and the presence of a diversity of biological and physical features in different species and different islands. Sub-Antarctic islands also feature unique environments with distinct species assemblages that are expected to be highly impacted by rapid environmental change, including climate change and the spread of alien invasive species. Understanding ecological and evolutionary processes, like dispersal and gene flow, can help predict species' responses to such changes. In this study, we focus on two plant species on sub-Antarctic Marion Island in the South Indian Ocean, the gravity-dispersed *Azorella selago* (Apiaceae) and epizoochoric *Acaena magellanica* (Rosaceae). We collected genome-level SNP data using Restriction site-Associated DNA Sequencing from populations across Marion Island, and compare spatial patterns in genetic diversity, genetic structure, and gene flow. We found a strong geographic gradient in genetic diversity in *Azorella selago* corresponding with the prevailing wind direction and the hypothesised location of a glacial refugium. In *Acaena magellanica*, we found no clear spatial patterns in genetic attributes, which may be indicative of greater dispersal distances and greater genetic connectivity across the island in this animal-dispersed species.

## Large scale connectivity of the marbled rockcod *Notothenia rossii* revealed through population genomics and modelling

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Ecological and evolutionary connectivity between population patches has important implications with respect to species distribution, population viability and local adaptation. The marbled rockcod *Notothenia rossii* was historically overharvested in the Southern Ocean and only recently shows signs of recovery. The species' distribution is fragmented between continental shelf, oceanic island plateaus and seamount regions. We applied a combination of species distribution modelling, individual-based dispersal modelling and population genomics to investigate genetic structure and connectivity of this ecologically important species. High resolution genomic data reveals apparent panmixia with virtually no genetic differentiation over vast distances. Individual-based modelling, however, indicates that large scale connectivity can only be achieved via stepping-stone transport. Species distribution models furthermore suggest that *N. rossii* may rely on previously unrecognized stepping-stone habitats for example at Bouvet Island and the Ob and Lena banks. We speculate that these results can partly explain the long recovery time of this species. Current conservation plans in the Southern Ocean can benefit from such multi-method assessments, especially in view of global change.

## Bacterial hitchhikers tell tales of Antarctic krill dispersal

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Antarctic krill (*Euphausia superba*) are amongst the most abundant animals on Earth, with a circumpolar distribution in the Southern Ocean. Krill are also the focus of an expanding fishery that is managed using regional catch limits, but it is unclear whether there is a single krill stock throughout these regions or if demographically distinct populations inhabit some regions. We show that Antarctic krill-associated bacterial communities exhibit spatial structuring, with some differentiation even at scales of a few kilometres. Linear mixed effects modelling showed this differentiation is almost entirely driven by spatial rather than environmental factors, especially for strongly krill-associated bacteria. Estimating the ecological processes driving bacterial community turnover showed this was driven by increasing dispersal limitation (rather than natural selection) with increasing geographic distance. Furthermore, divergent bacterial communities were generated from a single krill swarm split between aquarium tanks under near identical conditions, suggesting that physical isolation rather than environmental factors can cause krill-associated bacterial communities to diverge. Our results suggest bacterial hitchhikers provide unique insights into krill population subdivision and illustrate the broad potential for host-associated bacteria to inform studies of animal population structure.

## Opportunistic fungal assemblages present on fairy rings spread on different moss species in Antarctic Peninsula

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In recent years reports have been reported in several places of Antarctica, about mosses seem to be attacked by an uncertain organism. In these phenomena, the formation of a concentric ring characterizes the attack that ultimate result is the moss death. Moss samples with fairy rings were obtained in different sites across the South Shetlands. Only the sick part of the mosses was collected and stored in sterile plastic bags at 10 °C until the processing at the Laboratory of Polar Microbiology and Tropical Connections, Brazil. Small pieces of the mosses were inoculated on the Potato Dextrose Agar supplemented with 200 µg mL<sup>-1</sup> of chloramphenicol and incubated at 10 °C for 60 days. All sampled mosses were identified according to its macro- and micromorphological characteristics and using keys and literature. From the different mosses species with fairy rings, we isolated 40 fungal taxa. We provide an update on the host species identification with novel mosses with fairy ring effect. *Sanionia uncinata* shelter the highest fungal richness. *Mortierella* detected in all the mosses surveyed and represented the fungi most abundant recovered. However, others taxa present in the fairy ring mosses were already reported as opportunistic plant pathogens agents such as *Cladosporium* sp. and *Phoma herbarum*. We hypothesized that the some fungi recovered from fairy rings mosses might represent opportunistic secondary pathogens occurring after the first attack of known fungus *Psychonectria hyperantarctica* and, contributing to decreasing of natural defense of the sick mosses and accelerating its dissemination in Antarctica Peninsula.



## Evolutionary history of *Halicarcinus planatus*, first marine alien reaching Antarctica

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In 2010, a breeding female *Halicarcinus planatus* (Decapoda, Brachyura) was collected in Deception Island (South Shetlands), nevertheless its native distribution is circum-Subantarctic. *Halicarcinus planatus* has a low bathymetric range, a planktonic larval duration of 45-60 days, and may tolerate negative temperature because it is able to down-regulate the Magnesium concentration in the haemolymph that increases with the cold.

The appraisal of its presence along the West Antarctic Peninsula indicates that *Halicarcinus planatus* no longer occurs in Antarctica. The phylogenetic relationships among mitochondrial and nuclear haplotypes of *Halicarcinus* spp. display a basal position of *H. planatus* related to its congeners, as well as a clear separation between *H. planatus* samples from Auckland-Campbell Islands and the remaining group from Pacific coast of southern South-America, Falkland/Malvinas, Kerguelen. The levels of mitochondrial diversity of *Halicarcinus planatus* populations are the highest known so far in southern South America, but tend to decrease toward the north, whereas in Subantarctic islands they are significantly lower. The mitochondrial haplotype network is dense and strongly reticulated, showing sign of population-size reduction only in Kerguelen. Eight microsatellites loci helped to reveal a significant genetic differentiation among all samples, except among those from Kerguelen. Cluster analyses separates Kerguelen samples from the rest. Despite the long duration of the planktonic phase, it seems that the dispersal capacity of *Halicarcinus planatus* does not allow to homogenize populations across the Southern Ocean. The more recent but very limited gene flow that existed between Patagonia and Kerguelen would have more likely occurred by rafting.

## Hidden diversity in the periwinkle *Laevitorina caliginosa* across its distribution in the Southern Ocean.

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The origin of the Antarctic Circumpolar Current (ACC) around 30 Ma shaped past and present oceanographic patterns in the Southern Ocean (SO) and this oceanographic feature is also considered as a main biogeographic driver. Accordingly, a main paradigm of the SO biogeography is the high levels of endemism and the marked bioregionalization between the Antarctic and the sub-Antarctic biota. Nevertheless, there are several examples of broadly distributed SO organisms that challenge this view, including the periwinkle *Laevitorina caliginosa* distributed across Antarctic and sub-Antarctic provinces. Here we performed an integrative biogeographic study in *L. caliginosa* across its distribution in the SO. Through multi-locus phylogenetic analyses and divergence time estimates we analyzed evolutionary patterns in the species. Phylogenetic reconstructions based on mtDNA and nucDNA markers and morphological comparisons recorded the presence of seven evolutionary units within the nominal species *L. caliginosa*. Among them, a single lineage was effectively found in the Antarctic Peninsula but it expands its distribution towards geographically distant sub-Antarctic areas like Marion, Crozet and the Kerguelen islands. The rest of the lineages (six) are endemic to the Magellan province, three of them in the Strait of Magellan, two in Cape Horn and a single one in the Malvinas/Falklands islands. Divergence time estimates suggest that the origin and diversification of *Laevitorina* occurred long after the physical separation of the provinces where they are currently found. Moreover, molecular and morphological results suggest that the Magellan province represents an area of diversification for *Laevitorina*, as recorded in other SO marine mollusks.

## Contrasting biogeographical patterns in the vetigastropod genus *Margarella* across the Antarctic Polar Front.

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This study aims to understand phylogenetic relationships and diversification rates in the genus *Margarella* from South America, the Antarctic Peninsula, and sub-Antarctic islands. Through multi-locus phylogenies and time-calibrated analyses we resolved biogeographic signals in the group. Out of seven nominal species analyzed, species delimitation analyses recognized only four significant evolutionary units. *Margarella antarctica* occurs exclusively across the Antarctic Peninsula while two lineages were found in South Georgia (*M. achiles* and *M. steineni*). A fourth lineage included sub-Antarctic *Margarella* populations belonging to *M. expansa*, *M. porcellana*, *M. pruinosa*, and *M. violacea* collected between South America and the Kerguelen Islands. In spite of the clear morphological variation recorded in these sub-Antarctic specimens, they should be considered as *M. violacea*, following taxonomic description criteria. Mitochondrial divergence-time estimates suggest that the origin and diversification of these four evolutionary units occurred at the end of the Miocene, between 7 and 5 Ma. We recorded also contrasting biogeographical patterns in *Margarella* where the sub-Antarctic species, north of the Antarctic Polar Front (APF), is distributed across thousands of kilometers while *Margarella* species distributed south of the APF showed a much narrower geographical distribution and high levels of endemism. Such contrasting patterns may be the consequence of the presence/absence of buoyant kelps across the APF, which are potential long-distance vehicles for these vetigastropods. Accordingly, north of the APF, *Margarella* would maintain connectivity through rafting while inside this boundary the absence of buoyant kelps may preclude the admixture of lineages between the Antarctic Peninsula and South Georgia.

## Passengers into the cold: Invasive marine species discovered on non-native kelp rafts in the warmest Antarctic island

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Antarctic shallow coastal marine communities were long thought to be isolated by hundreds of kilometres of deep ocean and the Antarctic Circumpolar Current. The discovery of non-native kelp washed up on Antarctic beaches led us to question the permeability of these barriers. Over 70 million kelp rafts are afloat in the Southern Ocean at any one time. These living, floating islands can play host to a range of passenger species including from their original coastal location and those collected en route. Driven by winds, currents and storms towards Antarctica, these rafts are often cited as theoretical vectors for the introduction of new species into continent and the sub-Antarctic islands. We found non-native kelp, with a range of “hitch-hiking” organisms, on an Antarctic beach inside the flooded caldera of an active volcanic island. This is the first evidence of non-native species reaching the Antarctic continent alive on kelp rafts. One passenger species, the bryozoan *Membranipora membranacea*, is an invasive and ecologically harmful species in some cold-water regions, and this is its first record from Antarctica. The caldera of Deception Island provides considerably milder conditions than the surrounding waters and it could be an ideal location for newly introduced species to become established. These findings help to explain many of the biogeographic patterns and connections we currently see across the Southern Ocean. However, with the impacts of climate change we may see an increase in the number of species capable of surviving the long journey and becoming successfully established in Antarctic waters.

## Monitoring change in East Antarctic vegetation communities over a decade using digital photography

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Climate change is affecting Antarctica and minimally destructive long-term monitoring of its unique ecosystems is vital to detect biodiversity trends, and to understand how change is affecting these communities.

We assessed moss health and species composition at seven time points between 2000 and 2014 at two East Antarctic sites. Semi-automatic object-based image analysis (OBIA) was used to classify digital photographs using a set of rules based on digital red, green, blue (RGB) and hue-saturation-intensity (HSI) value thresholds, assigning vegetation to categories of healthy, stressed or moribund moss and lichens. Microsamples of moss were identified to species level for analysis of species composition.

Overall moss health, as assessed using the mean percentages of healthy, stressed and moribund mosses within quadrats, changed over the period of study at both sites, as did species composition. A marked increase in stress and decline in health was observed across both sites in 2008, followed by recovery to baseline levels of health by 2014 at one site, but with significantly more stressed or moribund moss remaining at the other site. This was associated with a decrease in *Schistidium antarctici* and an increase in *Ceratodon purpureus* at both sites.

These results have informed a conceptual framework for monitoring the changing condition of Antarctic mosses. These communities are potentially important proxies for monitoring coastal climate change in Antarctica and further ongoing monitoring is required to ensure their appropriate management and protection.

## Biogeographic patterns in the mesopelagic realm from the Arctic to Antarctic: a case study of two panoceanic chaetognaths and one euphausiid with antitropical distribution

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Mesopelagic species with panoceanic distribution are traditionally considered as single-species taxa. However, recent molecular studies provided evidences for a presence of several cryptic or pseudocryptic species within each of these taxa. The cryptic speciation can heavily bias our perceptions of large-scale biogeographic patterns that calls for a retrieval of the true diversity within common and ecologically important groups. We present a case phylogeographic study of two mesopelagic chaetognaths (*Eukrohnia hamata* and *Pseudosagitta maxima*) and one euphausiid (*Nematoscelis megalops*), which show similar biogeographic patterns in distribution. Both chaetognath species are widespread, ranging from the Arctic to the Antarctic zone of the Southern Ocean and dominating in the Polar and Subpolar regions. The euphausiid *N. megalops* occurs in warm-temperate belts of the North and South Atlantic, Indian Ocean and South Pacific. We analyzed the molecular (mtCOI, H3 and additional ITS1 for *P. maxima*, 28S and 18S for *E. hamata*) diversity of these species throughout the Atlantic Ocean from 65° S to 85° N. Phylogenetic analyses retrieved several distinct mitochondrial clades within these species, most of which are geographically separated: two clades of *N. megalops*, three clades of *P. maxima*, and five clades of *E. hamata*. All three species encompass different clades in the Northern and the Southern Hemispheres, two clades of *E. hamata* are divided by the South Polar Front. In some cases genetic differences between clades are supported by morphology and/or size structure (the latter is for *E. hamata* population in the Southern Ocean).

## Assessment of the capacity of *Halicarcinus planatus* to arrive and settle as a potential invader of Antarctic shallow ecosystems.

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*Halicarcinus planatus* is a small brachyuran crab distributed in shallow marine waters of southern South America and Sub-Antarctic islands. This species has a planktonic larval duration of 45-60 days and is also able to down-regulate the Magnesium concentration in the hemolymph that tends to increase with colder conditions. Due to this physiological characteristic, associated to the high dispersal potential, *H. planatus* has been historically considered as a potential invader of Antarctic shallow ecosystems. In 2010, a single ovigerous female of *H. planatus* was found in Deception Island. The aim of this study is to evaluate the invasive potential of *H. planatus* to settle in Antarctica. The results of lagrangian model of particle diffusion simulation showed that Patagonian larvae cannot reach the Antarctic Peninsula due to the Antarctic Circumpolar Current that forms a strong barrier. The assessment of genetic structure and connectivity through SNPs analyses among South Patagonia and Sub-Antarctic Islands identified 3 main groups: New Zealand, Kerguelen and South America. Overall, the dispersal capacity is low, but may reach a distance 1000km. Nevertheless, a single individual in Kerguelen was assigned to Patagonia, 8000 km away. The survival assessment in Antarctic conditions indicated that the crab died after 15 days at -1°C. Consequently, niche model show that the species cannot live in Antarctica before 2100 (RCP8.5). To conclude, in the present day, *Halicarcinus planatus* is neither able to reach Antarctica by dispersal way, nor to settle in Antarctic shallow ecosystems, yet. However, it will be a potential invader in 80 years.

## Contrasting dispersal patterns in Antarctic Cassidulinidae, benthic foraminifera

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Cassidulinidae, although distributed worldwide, are one of the most characteristic rotaliid benthic foraminifera inhabiting the Antarctic continental shelf. This study focuses on two genera, i.e. Cassidulinoides and Globocassidulina, that show strikingly different geographical ranges and genetic population structures, that are based on ~1000 bp fragment of the SSU rDNA. While different species of Antarctic Cassidulinoides show limited ranges and very simple, star-like shaped haplotype networks, two species of the genus Globocassidulina show wide, possibly circum-Antarctic distributions and complex haplotype network structures. For the representatives of the first genus, limited dispersal following a population bottle neck is suggested, while representatives of the second seemed to survive the last glaciation retaining genetically diverse populations either in multiple refugia or in deep-sea settings. This pronounced difference is probably due to varying dispersal potential of propagules, that are probably more persistent in the case of Globocassidulina. The Bayesian phylogenetic reconstruction suggests that the diversification of Antarctic Cassidulinidae occurred after their separation from sub-Antarctic lineages following the Middle Miocene, which was one of the main stages of progressive thermal isolation of the Antarctic.



## Assessing connectivity among moss populations in Antarctica and the Southern Hemisphere using targeted exon capture

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Antarctica has long been considered a biologically isolated continent, with this driving evolution of the region's unique biota. Though we know that many species have survived for millions of years on the continent, weathering Pleistocene (and earlier) glacial periods, we still know little about where glacial refugia were located. In addition, a range of new studies are suggesting that colonisation of Antarctica by terrestrial species has occurred over more recent timescales through natural incursions, but we lack knowledge of the extent of genetic connectivity for taxa within and beyond the Antarctic. With global environmental change leading to significant warming and increased habitability of parts of Antarctica, there is an urgent need to assess the extent to which Antarctica truly is biologically isolated. Fundamental to this is determination of the processes that drive evolution and structure spatial patterns of biodiversity, and a better understanding of the likelihood, mechanisms and consequences of future dispersal events, both natural and anthropogenic. Here, we apply genomic methodologies (targeted exon capture) to three widespread moss species collected from across the continent, throughout the sub-Antarctic, and from surrounding Southern Hemisphere landmasses. We use these data to infer refugial locations, assess dispersal and diversity patterns, and determine the source regions for past and recent moss colonisations of Antarctica. We hypothesise that some populations in Antarctica will show low diversity and close genetic affinities with other landmasses, reflecting recent arrival in Antarctica.

## Molecular divergence in *Adenocystis utricularis* (Bory) Skottsberg 1907 co-distributed through the Magallanes Region, Subantarctic island and the Antarctic Peninsula

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The distribution of the biota of the Southern Ocean is the result of great geological, oceanographic and climatic changes during the last 50 million years (Ma). However, several groups of benthic marine organisms exhibit marked taxonomic similarities between the Antarctic Peninsula and the southern coast of South America where families, genera, and even species are currently co-distributed in these continents. Macroalgae, such as *Gigartina skottsbergii* and *Iridaea cordata*, are located on both sides of the Drake Pass. Advances in molecular techniques have allowed us to determine phylogenetic relationships and levels of molecular divergence between populations of both continents to estimate whether they constitute separate evolutionary units. In this study it was determined through the use of molecular markers, COI5P and *rbcl* if the nominal species *Adenocystis utricularis* represents the same evolutionary unit in Antarctic and sub-Antarctic populations. According to the results, *Adenocystis* showed the presence of five different evolutionary units between the Antarctic Peninsula, the Sub-Antarctic Islands and the Magellan region, for both markers. Interestingly, a high affinity was found between haplotypes of subantarctic islands such as Kerguelen and Yerbas Buenas with Antarctic Peninsula. Such results are similar to those recorded among populations of *G. skottsbergii* on both sides of the Drake Pass. In this way, *Adenocystis* populations on both sides of the Drake Passage, is presented as a cryptic species. In this context, cryptic speciation plays an important role in the evolution of the Southern Ocean and therefore, the systematic, biogeography and biodiversity of the region require major revisions.

## Future challenges for notothenioid population genetics and connectivity studies

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Insights gained from genetic studies of Antarctic notothenioids over the past 25 years within the context of the Southern Ocean system emphasize the complex ways, at different life stages and along multiple pathways, in which habitat, ocean circulation and life history can interact to structure populations and their connectivity. These studies also suggest how multidisciplinary approaches incorporating hydrography can inform understanding of genetic structuring and gene flow around the Antarctic. From this background, this contribution will begin synthesizing biophysical hypotheses that can help explain gene flow in a range of species. The identification of gaps of knowledge and related open questions will help to guide future multidisciplinary and disciplinary-specific tests. Given the current documented threats to the Antarctic biodiversity, it appears timely to adopt a wider view on population connectivity in Antarctic notothenioid fish, to develop a systemic perspective and integrated approaches capable of addressing the new challenges for future genetic investigations. Such integrated studies are relevant not only to enhance our understanding of the ecology and evolutionary trajectories of Antarctic fish, but also to support important conservation measures. Ultimately, decisions governing the choice of size, number, spacing and location of protected areas should reflect species-specific patterns of population connectivity and dispersal, gene flow and genetic structuring.

## Species, hybrids and populations of *Chionodraco* spp. icefishes in Weddell Sea

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Once considered an occasional event across animal species, hybridization is now seen as a widespread phenomenon. Hybridization can promote genetic diversity and help the rescue of inbred populations, but it can also decrease the reproductive success of individuals by the production of unfit hybrid offspring and lead to genetic homogenization disrupting local adaptations. Here, we analyse the extent of hybridization among three species of icefish belonging to the genus *Chionodraco* (order Perciformes, suborder Notothenioidei, family Channichthyidae). Notothenioid are extensively studied in evolutionary biology since they represent an important example of adaptive radiation, one of the most relevant in the marine realm. By means of a panel of 18 microsatellite loci, we investigated the species boundaries, population genetics and phylogeographic patterns of the species *Chionodraco hamatus*, *Chionodraco myersi* and *Chionodraco rastrospinosus*. These species are morphologically very similar and difficult to distinguish. *C. hamatus* and *C. myersi* are sympatric while *C. rastrospinosus* is allopatric compared to the other two species. We discovered that *C. rastrospinosus* has a larger distribution than previously known, coming in contact with the two other species in Weddell Sea and hybridizing with them. In order to understand the possible routes of dispersion, a Lagrangian particle model of the regional oceanic currents was also implemented. Understanding the population dynamics of species, especially the factors modulating demography and gene flow among populations, is crucial for future predictions of species evolutionary trajectories and for a clear description of biodiversity.

## Pathogenic potential of thermophilic isolate *Aspergillus fumigatus* isolated from ornithogenic soil of Antarctica

Vívian Gonçalves<sup>1</sup>, Soraya Amorim<sup>1</sup>, Marliete Costa<sup>1</sup>, Daniel Santos<sup>1</sup>, Luiz Rosa<sup>1</sup>

<sup>1</sup>*Federal University Of Minas Gerais, Belo Horizonte, Brazil*

*Aspergillus fumigatus* is the most commonly involved in cases of aspergillosis in immunocompromised patients. We recovered a strain of *A. fumigatus* from ornithogenic soil of Antarctica, which displayed potential in vitro virulence such as the capability to grow at 37° C, different pH, produce spores  $\leq 1 \mu\text{m}$ , and resistance against antifungal drugs. Due the increase incidence of aspergillosis caused by *A. fumigatus* in immunocompromised patients, we performed in vivo assays inoculating different concentrations of *A. fumigatus* spores in healthy Balb C mice. When fungal spores were inoculated at  $1 \times 10^8$  spores/mL in immunocompromised Balb C mice, fungus was lethal. Our results indicated the fungi as *A. fumigatus* living in Antarctica should be monitored and studied to avoid health risks of dispersion to out of Antarctica.

## In vitro virulence of Antarctic *Pseudogymnoascus* fungi of Antarctica

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*Pseudogymnoascus destructans* is reported in different substrates of Antarctica and considered a psychrophilic pathogenic species and responsible for the reduction of the bat population in North America and Eurasia through the White Nose Syndrome (WNS). Despite the importance, there is no information on the virulent potential in vitro of *Pseudogymnoascus* in Antarctica. Eleven isolates of the genus *Pseudogymnoascus* obtained from different substrates of Antarctica were selected to assess its pathogenic potential in the present study. Six isolates were able to grow at temperatures of 5 to 28 °C, pH ranges 4, 7, and 9, and showed phospholipid, esterase, and hemolytic activities. Their spore sizes ranged from 2.1 µm ± 0.5 µm to 3.4 µm ± 0.5 µm, indicating the potential for penetration into the pulmonary alveoli. Four isolates were resistant to fluconazole. The MIC values ranged from 0.25 to 0.5 µg in assays performed with itraconazole and 0.5 µg with amphotericin B. The results obtained in vitro indicate that virulence factors presented by *Pseudogymnoascus* isolates of Antarctica are relevance, raising concern regarding its possible spreading in the face of global warming.

## Global warming and the emergence of pathogens trapped in Antarctic permafrost

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In the present study, we aimed to identify and characterize virulence potential fungi present in the Antarctic permafrost the King George and Deception islands. Permafrost samples were processed in different culture media and incubated at 37 °C for 60 days. After the selective temperature growth, different isolates of *Aspergillus hiratsukae*, *Aspergillus thermomutatus*, and *Rhodotorula mucilaginosa* were obtained. These isolates were assayed about their growth resistance at temperatures up to 50 °C, growth in different pH ranges, hemolytic activities, and the production of hydrolytic enzymes. *Aspergillus* isolates were able to grow at 45 °C and *R. mucilaginosa* at 50 °C. All isolates were able to grow in all tested pH ranges, produce proteinase enzymes and create a halo of hemolysis in blood agar. All taxa tested here are already reported as human pathogens in immunocompromise patients. The in vitro results indicated that these permafrost Antarctic fungi display virulence factors and may represent a concern as to their possible dispersion in the face of global warming.

## Taxonomic Studies of the *Syntrichia* Brid. in Antarctica

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Antarctica has a unique biodiversity, adapted to extreme conditions such as intense cold, high ultraviolet radiation and low humidity. In this continent, mosses are the predominant vegetation. Among the most diverse moss families in Antarctica is Pottiaceae, with 10 described genera, the most diverse being *Syntrichia* Brid. with five species (*Syntrichia caninervis* Mitt., *S. filaris* (Müll. Hal.) R.H. Zander, *S. magellanica* (Mont.) R.H. Zander, *S. sarconeurum* (Hook. F. & Wilson) Ochyra & RH Zander and *S. saxicola* (Cardot) R.H. Zander). It is a taxonomically complex group, due to its morphological variability and close proximity to other genera of the family like, leaving a gap on the understanding of relationships between taxa, especially due to the scarcity studies involving DNA. Seeking a better knowledge of the Antarctic species of *Syntrichia* and their relationships within the genus, a phylogenetic study was carried out using nuclear DNA sequences (ITS2 region). DNA was obtained from collections made in different parts of Antarctica and Subantarctica, as well as from herbarium specimens. Between one to five DNA sequences were obtained for each target species and analyzed under Maximum Parsimony, Maximum Likelihood and Bayesian Inference. Our results show that three of these species correspond to *Syntrichia filaris*, *S. magellanica*, and *S. saxicola*. *Syntrichia sarconeurum* has a different distribution than presented in the literature, excluding the samples cited for Princess Elizabeth Land, which correspond to an unknown group. As for *Syntrichia caninervis*, the studied samples correspond with another species, also belonging to the genus. All species exhibited monophyletism.



## Ecological processes influencing the bacterial and microbial eukaryote assemblages within the Southern Kerguelen Axis region

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Biologically productive Southern Ocean (SO) waters are an important site for nutrient recirculation, support primary production of global oceans, and drive significant carbon dioxide sequestration via physicochemical processes and the biological pump. Biological pump processes are microbially driven with substantial contributions from bacteria and microbial eukaryotes, and the biological pump's efficiency is highly dependent on the microbial community present. Ecological processes generating commonly observed biogeographic patterns (selection, dispersal, drift and speciation) are central to understanding microbial biogeography but remains poorly investigated in the SO. Based on 16S and 18S rRNA sequences generated from 36 surface samples within the Kerguelen Axis region, we quantified the ecological processes and spatial, environmental and biological interactions shaping bacterial and eukaryote communities. Our null-modelling approach results inferred that selection was a much more important determinant of bacterial community composition variations, whereas dispersal limitation, at the same scale, was 2 to 9-fold more important for eukaryote communities compared to bacteria. Besides environmental conditions, seasonal variation and spatial distance, biological interactions amongst microbes may also structure microbial communities. Spatial and commonly measured environmental factors explained 50% or less of variation among bacterial and eukaryote communities, suggesting potentially important roles of biotic interactions. Among the significant biotic interactions detected, 27% were inter-domain bacterial-eukaryote interactions extensively involving copiotrophic Flavobacteriales and parasitic Syndiniales that were over-represented compared to their relative abundance. Validating these microbial interactions and quantifying their relative importance in structuring SO microbial communities compared to abiotic factors, will help understand the response of SO ecosystems to environmental change.

## The COPE project: Conservation management of polar ecosystems using genomic approaches to study connectivity across spatial and functional scales

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Recently the second of several planned large Marine Protected Areas (MPA) has been set up in the Southern Ocean. MPAs are most effective if implemented as a network that considers functional diversity within and between species, relying on scale-dependent connections between MPAs. Three key features of connectivity are important in this context: 1) geographic or landscape connectivity, 2) environmental or habitat connectivity, and 3) genetic connectivity. While knowledge on geographic bio-regionalisation is fairly well-advanced, in-depth estimates of environmental and genetic connectivity require further development. In the COPE project, ecological niche models and population genomic approaches complement each other to advance the understanding of spatial connectivity in key benthic and pelagic Antarctic organisms (crustaceans and actinopterygian fishes). Connectivity is investigated at ecological (contemporary) and evolutionary (heritable/adaptive) scales. Thousands of genomic variants, obtained by reduced representation sequencing or shallow whole genome re-sequencing, will provide estimates of neutral and adaptive genetic variation at several trophic levels. In COPE, these estimates are used to characterize the ecological and evolutionary components of connectivity across space. The genomic information will be integrated in ecological niche modelling at the habitat and population level. COPE's results are expected to considerably advance our understanding of the spatial and functional distribution of biological variation in the SO. These insights will contribute to the Marine Ecosystem Assessment of the SO (MEASO) and will be directly applied at the political level to develop suitable management and conservation strategies through the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR).

## Otolith chemistry provides powerful natural markers to test hypotheses concerning bio-physical interactions in the Southern Ocean: with some case studies as examples

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In the natural world no organism exists in isolation, and every organism must interact with the environment and other organisms. Such interactions are fundamental to survival and biological processes at the population and ecosystem levels. The inherent complexity of the marine environment often requires the overlap of disciplines which are more traditionally separated. The manner by which various marine life forms are influenced by their surrounding physical environment represents an interface between biology and physics that is an often overlooked area of research, but one which can be rich in cross-disciplinary information incorporating currents, frontal dynamics, and eddy activity. Biochemical approaches are used widely to examine the life history processes of marine animals, and chemistry deposited in fish otoliths offers several biochemical markers to understand bio-physical interactions in marine fish species. In this talk, we will focus on investigating coupled biophysical processes in the Antarctic fish *Electrona antarctica*, *Electrona carlsbergi*, *Pagothenia borchgrevinki* and *Dissostichus mawsoni*, which occupy different habitats in the Southern Ocean. In particular, results from *E. antarctica* suggest the potential for otolith chemistry as a powerful natural tag to help understand the bio-physical interactions shaping population structure and dispersal across different habitats in the Southern Ocean.

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