



Review

Pelagic and benthic communities of the Antarctic ecosystem of Potter Cove: Genomics and ecological implications



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ABSTRACT

Molecular technologies are more frequently applied in Antarctic ecosystem research and the growing amount of sequence-based information available in databases adds a new dimension to understanding the response of Antarctic organisms and communities to environmental change. We apply molecular techniques, including fingerprinting, and amplicon and metagenome sequencing, to understand biodiversity and phylogeography to resolve adaptive processes in an Antarctic coastal ecosystem from microbial to macrobenthic organisms and communities. Interpretation of the molecular data is not only achieved by their combination with classical methods (pigment analyses or microscopy), but furthermore by combining molecular with environmental data (e.g., sediment characteristics, biogeochemistry or oceanography) in space and over time. The studies form part of a long-term ecosystem investigation in Potter Cove on King-George Island, Antarctica, in which we follow the effects of rapid retreat of the local glacier on the cove ecosystem. We formulate and encourage new approaches to integrate molecular tools into Antarctic ecosystem research, environmental conservation actions, and polar ocean observatories.

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1. Introduction: Environmental change in the northern maritime peninsula region

One of the most dramatic consequences of anthropogenically induced climate warming is the vast retreat of coastal ice sheets and melting of the glacial ice caps currently observed in the Northern sector of the West Antarctic Peninsula (WAP) (Vaughan, 2006; Osmanoglu et al., 2013; Osmanoglu et al., 2015). Rapid deglaciation is opening shallow water coastal environments (defined here as down to ~150m) of highly fragmented bathymetry and substrate type (from rocks and bolder fields to sandy and muddy areas) to new colonization (Wölfel et al., 2014; Quartino et al., 2013). This includes growth of new coastal biomass from macroalgal beds with associated epiphytes to pioneering assemblages of migratory and sessile fauna with capacity for larval dispersal.

Physical and environmental change in WAP shallow marine areas is fast. As an example, sea surface temperature (SST) at our study site, the shallow Potter Cove on King George Island (South Shetlands), has increased by approximately 0.36 °C per decade [6, based on 20-year time series of SST data], accelerating microbial and heterotrophic turnover rates. As a consequence, benthic and pelagic species and communities are facing highly dynamic environmental conditions as they move inland and colonize newly uncovered areas. Summer meltwater waves released from climate sensitive coastal ice sheets (Osmanoglu et al., 2013) cause freshening of the shallow water bodies, which impact pelagic biodiversity. Scouring by drifting icebergs and ice growlers, and calving through the glacial fronting lines can interfere with rapid and sustained benthic colonization in glacial proximity. Melting ice masses and thawing of coastal permafrost areas further mobilize lithogenic particle transport with surface meltwater plumes effecting shading and constraining primary and secondary production in melt water impacted areas (Schloss et al., 2012; Khim et al., 2007; Yoo et al., 2015; Fuentes et al., 2016).

Species colonizing or transiently surviving (pelagic) in present day glacial cove and fjord environments have managed through Pliocene and Pleistocene glaciation cycles by shifting between habitable areas of polynyas or ice fracture zones under former or extant Antarctic ice shelves (Weihe & Abele, 2008; Azam et al., 1991). Hence, they are fit to deal with low light intensities, low temperatures, and extreme scarcity of food. Only few sessile (sponges, ascidians and bryozoans) or slowly moving species (e.g. limpets, echinoderms, polychaetes, isopods, amphipods and pygogonids), frugal enough to survive such conditions, colonize the areas in front of melting glaciers. As a consequence, macrobenthic species richness in present day melt impacted bays and coves in the West Antarctic is lower compared to ice free shelf areas or coastal sectors less influenced by glacial disturbance (Quartino et al., 2013; Thatje et al., 2008; Siciński et al., 2012; Dayton & Oliver, 1977).

Antarctic intertidal environments and rock pools show considerable daily variations of abiotic parameters such as temperature, salinity, and light climate, especially when low tides are around noon. Aerial exposure at freezing temperature is a natural stressor, that is tolerated by only few Antarctic macrofauna and algae species (Waller et al., 2006; Weihe & Abele, 2008), but it remains an open question whether this enhanced stress tolerance is generic to the majority of species in these coastal community.

We summarize emerging knowledge of shallow water community composition and species specific functional responses to Antarctic coastal change obtained through genomic analyses of the major organismal groups. The work was done in Potter Cove on King-George Island (Isla 25 de Mayo, South Shetland Archipelago), a 10 km² shallow (maximum depth 80 m) fjord, strongly impacted by glacial melting. This review is structured according to the major organism groups for which we have obtained genomic data, starting with the prokaryotes (Archaea and Bacteria in water column and the marine sediments). In this section we include results from whole genome sequencing projects of three Antarctic bacterial strains with potential implications for

biotechnological application, coastal ecosystem management, and the mitigation of Antarctic coastal contaminations. We then present the results from molecular surveys of the most important groups of coastal microeukaryote plankton, and finally discuss two typical macrofauna keystone species for which we analyzed response to environmental change at the level of gene expression.

Work was conducted in the frames of a long-term ecosystem research program that was started 25 years ago as initiative between the Instituto Antártico Argentino (IAA) and the Alfred Wegener Institute Helmholtz Center for Polar and Marine Science, Germany (AWI). The project builds on various cooperative programs and EU supported networking projects. Supported by these affirmative actions, we established an Argentine-European research group collaborating at Dallmann Laboratory, an annex to the Argentine Carlini Station on King-George Island. Abiotic change and ecological shifts in this coastal ecosystem are continuously investigated by gathering multi-layered knowledge in different system compartments (glaciology, hydrography, bathymetry, geology, biogeochemistry and biology) in space and over time. A major aim within the biological studies in our current EU networking project IMCONet (EU FP7 IRSES, action no. 318718, www.imconet.eu) was, to understand how glacial melting affects the Antarctic coastal environment and its communities.

Our approach in Potter Cove was therefore dual and included

(A) **The characterization of community composition as a function of environmental variability.** We combine spatial and time series (eco)system observations (e.g. climatology, glacial retreat and fast ice dynamics, hydrography, biogeochemistry, a.o.) with seasonal samplings of pelagic and benthic microbiota communities, using molecular techniques such as fingerprinting, clone libraries and recently also amplicon and metagenome sequencing (work in progress and not included in this review). This produces new knowledge on local biodiversity and connectivity, and also on the functional response of the communities to abiotic and biotic changes.

(B) **Functional genomics/phenomics of polar species.** We combine analysis of genetic connectivity and geographical provenance with comparisons of population specific traits *in situ* and with controlled stress exposure experiments to understand evolutionary limits of species/population specific stress response. In these experiments we use ecologically important key species (e.g. macroalgae and molluscs) of known geographic habitat expansion. Individuals are exposed to defined stress levels and their physiological and genetic stress response investigated, either based on transcriptomic analysis or through a combined analysis of stress genes and physiological stress markers.

In this paper we summarize first results obtained and published with combinations of molecular and genomic techniques and discuss their implications for the investigation of environmental processes typical for the complex Potter Cove ecosystem. More extensive analyses are currently ongoing so that the limited amount of published knowledge will grow significantly in the near future. Hence, it appears timely to propose here and now prioritization of approaches that integrate extended use of molecular genomics in ecological research to fill existing knowledge gaps and to develop the best practice of ecosystem monitoring in the future. We are increasingly able to include targeted use of cost intensive molecular studies in the development of event driven ecosystem observation strategies.

2. Microbes: Archaea, bacteria and viruses in Potter Cove

It was only in 1991 that the importance of organic matter and nutrient cycling through the Antarctic microbial web has received full appreciation when Azam and coworkers published their seminal paper, describing the role of the microbial loop for Antarctic pelagic environments (Azam et al., 1991). In the absence of primary production during the Antarctic winter period, bacterial productivity, supported by the dissolved organic carbon (DOC) pool from the previous summer, becomes the pivotal food source for the heterotrophic grazer communities (Azam

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