

# Exploration of Arctic and Antarctic seaweed biodiversity in the context of polar climate change

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Polar regions are hotspots of climate change, inevitably affecting seaweed biodiversity by sea ice recession, increased iceberg scouring, and increased inputs of glacial melt water, all of which can have major impacts on phytobenthic communities. However, any studies in this context confront major challenges in terms of (1) scarce historic baseline datasets and (2) environmental and logistical constraints for scientific collections, and *in situ* observations by diving. This paper presents highlights from our expeditions to northern Baffin Island (Canadian Arctic, 2009) and Adelaide Island (Antarctica, 2010-2011) which assessed the biodiversity of seaweeds and associated eukaryotic pathogens at established study sites. Our dataset provides a baseline inventory for future work assessing impacts of the

currently ongoing changes in the Arctic and Antarctic marine environment. In both cases, diving surveys and collections of macroscopic algae were complemented by applying the Germling Emergence Method and DNA barcode sequencing of the live isolates obtained from substratum samples.- We present a baseline seaweed species checklist for both regions, reporting numerous new records of seaweed taxa and associated pathogens. The paper also discusses implications for establishing baseline inventories and managing safe and scientifically productive diving operations in remote polar locations.

# Tales of life & death in the plankton: Diatom dissolution & upper ocean silica-cycling

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Marine diatoms are a functionally diverse algal group capable of rapid growth rates, contributing to ~20% of global and ~40% of oceanic primary production. Diatoms often dominate phytoplankton blooms in marine environments in terms of biomass, primary production and fluxes of material to the deep-sea, fueling pelagic and benthic ecosystems. However, diatoms are paradoxically prone to rapid dissolution whereby the silica (Si) incorporated into diatom cells (bSiO<sub>2</sub>) during growth returns into the dissolved pool (Si(OH)<sub>4</sub>). Here, measurements of diatom productivity, biomass, species composition, dissolution and export are presented from three distinct oceanic regions (South Georgia spring bloom, Celtic Sea autumn bloom, and a filament from the Benguela Upwelling) to explore how diatom ecological traits and growth conditions directly influence Si-cycling in the upper ocean. Nutrient supply to diatoms in South Georgia and the Benguela Upwelling directly impact on diatom growth rates, whereas light is a strong limiting factor in the Celtic Sea in autumn. Nutrient depletion and

zooplankton grazing result in a transition from export to dissolution as the dominant loss term in South Georgia, while sub-optimal growth irradiance and high levels of non-living (detrital) bSiO<sub>2</sub> lead to dominance of dissolution in the Celtic Sea. In each case, the level and composition of detrital bSiO<sub>2</sub> is key to determining the dominant term in the upper ocean Si-cycle; net gain (population growth) or net loss (population decline). Ratios of living to non-living diatom biomass as indices of community dynamics are discussed in the wider context of implications for the biological carbon pump and ecosystem productivity.

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## Impact of infaunal ecosystem engineers on microbial communities

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The Extended Evolutionary Synthesis theory predicts that, through their niche construction, organisms greatly influence community structure, stability and productivity, and co-direct evolutionary responses to selection in ecosystems (Odling-Smee et al., 2003; Laland et al., 2015). The degree to which niche constructing activities are complementary or conflicting impacts the magnitude and stability of biochemical and physical gradients formed within sediment profiles. These gradients generated by the ecosystem engineers are selective pressures to microbial communities in sediment. The aim of this work was to test how complementary and conflicting ecosystem engineering impacts microbial community diversity and function and the consequences on sediment function such as surface stability, nutrient cycling and primary production.

A well-established microcosm system (Emmerson et al. 2001) of intertidal sediment with overlying brackish water with treatments containing neither, one, or both *Corophium volutator*, *Nereis diversicolor*, or manual turbation was incubated at 12 °C for 10 weeks. Functional outcomes of overlying water turbidity, sediment stability, extracellular polymeric substance and chlorophyll content were analysed. Dissolved oxygen and redox potential gradients were measured at 0, 5 and 10 weeks using microelectrodes. Microbial community composition at the sediment surface and at depths of 15, 30 and 45 mm was analysed using high throughput 16S rRNA (V3- V4 region) sequencing using 300 bp PE reads on an Illumina Miseq.

Different niche constructor combinations resulted in varying functional outcomes and different biochemical selective pressures. Turbidity was higher in manual turbation and *C. volutator* than other treatments.

Evidence for the cooperative alteration of dissolved oxygen and redox gradients compared to individual infauna treatments was observed. This ultimately resulted in shifts in microbial community composition. Surface communities were significantly different between infauna treatments, with manually turbated sediments exhibiting very different communities compared to other treatments. Communities were more similar as depth increased, regardless of treatment.

These results support the Extended Evolutionary Synthesis theory that niche construction is a powerful evolutionary force where organisms modify their own and others' selective environments, and predicts that 'Ecosystem stability, productivity and dynamics are critically dependent on niche construction.' Furthermore, the difference in microbial communities resulting from manual turbation compared to bioturbation hold significant inference for the impact of anthropogenic disturbance on biogeochemical cycling by microbial communities.

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