Shifts in microbe-mediated organic matter degradation patterns in relation to sea-ice dynamics in a coastal Ross Sea area

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The Ross Sea is one of the most productive areas of the Southern Ocean and plays an important role in the global ocean biogeochemistry. Changes in the Ross Sea biogeochemical features have been observed for decades and are expected to continue in the light of the ongoing and future global climate changes. Significant yet variable changes in sea-ice cover extent have been observed in the recent past; however, research on the trophic consequences of sea-ice dynamics has been focused so far on phytoplankton with cross-food web links from krill to large vertebrates, while neglecting the microbial components.

Aiming to fill this gap in the framework of a multidisciplinary investigation targeting microbial regime shifts in response to sea-ice melting, we measured microbially mediated hydrolysis rates of carbohydrates, lipids, sulphate esters and proteins, along a three-stations coast-offshore transect in Tethys Bay (Terra Nova Bay) from early November 2022 to late January 2023. Sampling was carried out on a quasi-weekly basis, aiming to cover a wide array of physical-chemical, as well as trophic, conditions dictated by sea-ice dynamics.

In early November, at the beginning of the sampling period, all the three stations were covered by sea-ice and characterized by generally low carbohydrates, lipids and proteins hydrolysis rates (<2 nM h^{-1}, <20 nM h^{-1} and <15 nM h^{-1}, respectively). Following sea-ice fragmentation, lipase and aminopeptidase activities abruptly increased (>200 nM h^{-1} and >70 nM h^{-1}, respectively), while carbohydrates degradation rates remained relatively slower, suggesting that carbon mobilization following sea-ice melting happened through lipids rather than polysaccharides degradation processes. By late January, lipase activity was comparable to values measured during sea-ice cover, while carbohydrates degradation rates remained relatively higher. This pattern may be explained by the development of a massive *Phaeocystis sp.* bloom in late December representing a source of freshly produced carbohydrates for the heterotrophic microbial community. Sulphatase activity was a notable exception to the general pattern observed for the other exoenzymes, with higher rates under sea-ice cover and a barely detectable signal during and after sea-ice fragmentation and algal bloom development. While data on sulphate esters degradation assayed through fluorogenic substrate analogues are scarce in pelagic ecosystems, there is evidence of the inducibility of this enzyme under low sulphur concentrations. Considering that *Phaeocystis sp.* copiously produces sulphated molecules under bloom conditions, it is plausible that sulphatase expression may have been reduced in response to this readily available sulphur source.

These preliminary data shine a light on organic matter degradation dynamics under different regimes of sea-ice cover, providing new insights on the functioning of microbial food webs during the transition between sea-ice fragmentation and algal bloom development.