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Topic: Marine biology and ecology



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ABSTRACT Subject :

Virus-prokaryote interactions in the sea ice and underlying water of the Ross Sea

Abstract 14/02/2023 11:16:24



The Ross Sea (Southern Ocean, Antarctica) is one of the globally most important area for the production of sea ice and represents an important CO₂ sink. Antarctic sea ice hosts diversified biological assemblages comprising microeukaryotes (e.g. algae), prokaryotes, and viruses. Generally, in marine ecosystems, viruses are the most important cause of mortality of prokaryotic and eukaryotic organisms and can control biodiversity and ecosystem functioning with cascade effects on the carbon cycle and nutrient regeneration. However, information on virus-host interactions in Antarctic sea ice is limited. In the present study, we investigated the distribution of viruses and prokaryotes in the platelet and brown ice, as well as in the seawater collected below sea ice, in two different stations nearby the "Mario Zucchelli Station" (MZS) of the Ross Sea. We also assessed the interactions between viruses and their hosts, and the potential influence on the structure of the prokaryotic assemblages. We found that prokaryotic biomass and abundance followed similar patterns in the two investigated stations, with higher values in seawater than in the brown ice. Conversely, viral abundance and infection showed opposite patterns. Prokaryotic assemblages showed a lower diversity in the samples with a higher viral pressure suggesting a potential top-down viral control. We also found differences in the structure of prokaryotic assemblages in the two typologies of sea ice and in the underlying water. In particular, in the brown ice, Colwelliaceae (ca. 40%) represented the most relevant bacterial family while Pseudomonadaceae were mainly represented in the platelet ice (16%). Pseudomonadaceae were also the dominant taxa in seawater. However, we also observed that Colwelliaceae, Pseudoalteromonadaceae and Flavobacteriaceae, among the others, were shared among the different Antarctic matrices suggesting a stable core of bacterial members unaffected by the variability of environmental and biological conditions (including the viral pressure) in the different Antarctic matrices. Overall, this study provides new insights on viral-prokaryotic interactions and factors potentially influencing microbial diversity in one of the most extreme and dynamic ecosystems on Earth.

