

Microbial community composition in the Canadian Arctic Archipelago marine system

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The Canadian Arctic Archipelago (CAA) is a marine region containing over 300 tidewater glaciers, where the seasonal input of large amounts of fresh glacial meltwater directly to the ocean is a defining characteristic. Recent work has shown that seasonal inputs of fresh glacial meltwater in the CAA, and Jones Sound (NU) specifically, make it an important site of water modification en route from the Pacific Ocean to the Labrador Sea and broader North Atlantic Ocean. Importantly, this meltwater may augment composition and productivity of the marine microbial communities that form the base of the regional marine food web. Yet, despite this, information is lacking on the marine microbial community composition in the Jones Sound region specifically, and is only sparsely available across the CAA.

To fill this gap in our knowledge, we undertook a 2-year sampling campaign spanning two major waterways in the CAA: Nares Strait and Jones Sound, NU. Here we compared regions with tidewater glaciers to those without, conducting transects from within 1-km of the glacier terminus (glacierized sites) or the shore (unglacierized sites) out to the open coastal ocean at the height of the summer melt season. Additionally, samples were collected in the spring from underneath the sea ice, before the onset of glacial melt, to explore seasonal dynamics in microbial community composition and structure. Seawater was collected down the water column at the surface (5 m), subsurface chlorophyll maximum (20–50 m), and in deeper (below the nutricline, >100 m) water at each station to assess community changes with respect to depth. Samples were analyzed for 16S and 18S rRNA amplicon sequencing to identify the bacterial and eukaryotic members of the microbial community, respectively, with a specific interest in describing the phytoplankton and heterotrophic community members. Results from this study will help to describe the CAA microbial community composition and better constrain the importance of seasonality and glacial inputs in shaping the marine microbial community in an under-studied high-latitude region.

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