Title: Microbial genomics-informed environmental monitoring in Arctic waters

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Introduction

Microbes form the base of marine food webs, and microbial communities collectively support and perform diverse essential ecosystem functions, including metabolizing, or biodegrading pollution such as hydrocarbon spills. Genomics, specifically metagenomics, involves the study of genetic material from environmental samples, and enables the assembly of the genomes, or full DNA sequences of microbes in the sample. This reveals both which microbes are present and information on their individual and collective functional characteristics – who is there and what can they do?

As the most sensitive living response system, monitoring changes in the makeup and functioning of microbial communities can give early warning of environmental impacts and changes, such as from a spill, that may reverberate up trophic levels and affect ecosystem, animal, and human health. Further, microbial monitoring is important to understand the impact of perturbations on microbial communities themselves, as short and long-term changes in microbial communities have implications for ecosystem functioning and for microbial responses to future perturbations. Genomics techniques enable monitoring that is logistically simpler and less expensive than traditional marine environmental monitoring techniques, thus making it possible, with appropriate capacity development, for local people and organizations to directly participate in year-round monitoring, which is necessary to understand local and seasonal natural variations in microbial communities and activity.

In the Arctic, genomics-informed monitoring can help to meet observational needs around hydrocarbon detection and spill remediation. Due to the lack of response capacity for anything beyond minor marine spills and the limited effectiveness of containment and mechanical recovery (especially in ice infested waters), which is the only spill response currently permitted in the Canadian Arctic, the bulk of spilled hydrocarbons are left to be remediated by natural processes. However, the lack of observing assets and a monitoring mandate means that the effectiveness of this natural attenuation and the ultimate impact of particular spills remain largely unknown. We argue that Monitored Natural Attenuation should be the baseline response to Arctic spills, i.e. applying genomics-informed microbial environmental monitoring in the specific context of hydrocarbon spills, in addition to remote sensing to detect and track spills and direct monitoring of hydrocarbons in the marine environment when possible. This approach would provide a more complete picture of the fate and consequences of spills, and also support decisions regarding when more active response measures are appropriate and necessary.

Recent work (Murphy et al, 2021; Cramm et al, 2020; Ferguson et al, 2020; Vergeynst et al, 2019) confirms the presence of cold-water-adapted microbial hydrocarbon degraders in Arctic waters, and that they are capable of biodegrading components of spilled hydrocarbons. Monitoring these microbial communities in the context of a spill can provide a proxy measure of the microbial bioremediation process, showing when hydrocarbon degrading microbes are most prominent and active and when biodegradation processes are no longer significant. As microbial communities reorganize following response to a spill, monitoring can help determine if and how the functioning of microbial communities in the ecosystem has changed, which is important to understanding the nature of recovery from the spill and could provide vital information regarding the consequences of future spills in the area.

Combined monitoring of this type is optimally effective in identifying change only when dynamic microbial baselines have been established, and where microbial monitoring can be ongoing, over time and space, and under various marine conditions, including when ice is present. Baseline information can also help to identify areas and/or seasons where the nature of microbial communities would leave the marine environment especially vulnerable to damage from spills. Such knowledge could be used to better plan shipping routes and to inform spill response planning and equipment placement. As part of the GENICE project, a large baseline microbial community dataset is being established with samples collected from the Beaufort Sea, the Canadian Arctic Archipelago, Hudson Bay, Baffin Bay and the Labrador Sea, (Figure 1).



Figure 1. Sampling locations of baseline samples collected from 2013 to 2019. The shape of the symbols indicate the type of sample collected: sediments (squares), surface seawater (circles), bottom seawater (triangles), surface sea ice (hexagons), and water column (diamonds). The color represents the year of sampling: 2013 (red), 2014 (orange), 2015 (magenta), 2016 (yellow), 2017 (green), 2018 (white), and 2019 (pink) (unpublished results, University of Calgary, Geomicrobiology group).

While research confirms the potential of microbial-based environmental monitoring for understanding the microbial bioremediation of spilled hydrocarbons, some key questions remain unanswered, e.g., How accurate is the resulting proxy measure of bioremediation? Do microbial communities return to baseline after a spill or are there long-term changes? What hydrocarbon components remain after bioremediation has 'completed' and are they toxic? How do other factors like photo-oxidation and ice impact microbial biodegradation? However, these questions can be most effectively addressed by actually beginning to use genomics to monitor changes in microbial communities, which serves environmental monitoring and research needs via deliberate feedback mechanisms such that both are enhanced simultaneously.

We suggest developing a microbial community monitoring program, using genomic approaches, that targets sample collection to areas where marine spills are most likely

to occur and/or where resulting harms would be most consequential, e.g. areas along primary shipping routes, in areas of importance to Inuit for cultural, food security or other reasons, in protected areas, areas of sensitive habitat, and areas subject to offshore, onshore or nearshore development. Such a genomics-informed environmental monitoring program would set the stage for optimally implementing Monitored Natural Attenuation in the event of a spill. Promising contexts for implementing this include the Impact Assessment of developments with shipping implications (i.e. as part of preproject baselines and ongoing environmental monitoring), the establishment of Marine Protected Areas and shipping corridors, and spill planning and preparation surrounding community harbours and oil handling facilities.

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