

Impacts of Arctic Ocean warming on phytoplankton–virus ecology and ocean biogeochemistry

Context: The Arctic Ocean plays a key role in Earth's climate contributing to 10% of the global carbon pump. This extraordinary capacity to absorb CO₂ from the atmosphere is due to the high solubility of gases in cold water and the highly productive continental shelves where phytoplankton convert dissolved CO₂ into organic carbon and, from sinking of organic matter, contribute to its sequestration into the deep ocean. This export of carbon (C) mediated by microbial communities is known as the biological carbon pump (BCP). The microbial communities in the Arctic Ocean are subject to unprecedented pressure due to ocean warming, as there is a four-times faster temperature increase in the Arctic than the global annual average¹. 2015 to 2022 have been the warmest years on record in the Arctic, with a dramatic average increase of 5°C in January since 1900², which critically modifies the hydrology and water circulation. These climate-driven changes have major consequences on ecological dynamics, ecosystem productivity, and species interactions^{3,4}. Characterizing and quantifying these ecological changes is essential, as they have cascading effects on the functioning of Arctic ecosystems, which add to the direct effects of rapid environmental changes.

The overarching objective of this PhD project is to quantify the impacts of Arctic warming on a key, yet understudied process in microbial ecosystems: the infection of phytoplankton by viruses. Likely all phytoplankton lineages are infected by viruses with known phytoplankton viruses being highly diverse. Viral infection is prominent in temperate and sub-tropical systems, representing 1 to more than 50% of phytoplankton mortality^{5,6,7}. By lysing cells, viruses bypass the BCP by releasing biotic C back into the pool of dissolved organic matter (DOM). This “viral shunt” is considered one of the largest C fluxes in the ocean⁸. Phytoplankton viruses have also been reported in Arctic waters and shown to be active⁹, however, virus-induced mortality remains to be quantified. Importantly, little is known about the impact of temperature on phytoplankton–virus interactions. Our previous studies in temperate species, combining experimental and theoretical approaches, showed a pronounced influence of temperature on viral infectivity and lysis, with dramatic predicted effects on microbial composition in future ocean^{10,11}. Responses to warming likely differ between phytoplankton and virus lineages. Therefore, **it is essential to characterize the thermal response of key phytoplankton-virus pairs implicated in the regulation of the BCP**, especially of cold-adapted Arctic species, which may be more temperature sensitive.

Hypothesis, objectives, and scientific strategy: In this project, **we will test the hypotheses that temperature alters the dynamics and interactions of Arctic phytoplankton and their viruses (H1) and the ecological and biogeochemical fate of infected cells (H2).** The proposed activities are designed to obtain a detailed mechanistic understanding of how Arctic warming impacts phytoplankton–virus interactions and incorporate this information at the ecosystem scale. To this end, a multidisciplinary strategy, combining biology, physiology, biogeochemistry, and mathematical modeling, will be used to quantify the consequences of Arctic warming on (i) infection patterns of dominant phytoplankton species (*in situ*), (ii) temperature-driven virus and phytoplankton traits and physiology (*in vitro*) and (iii) the cascading effects of these temperature-driven changes on phytoplankton-virus dynamics and mediated processes (*in silico*). The candidate will more specifically focus on phytoplankton and virus communities of the Lincoln Sea. This ecosystem is characterized by multiyear sea ice cover and is considered one of the last Arctic refuges from change. As a natural *in situ* “laboratory,” the Lincoln Sea is at the forefront of understanding how microbial dynamics and interactions will evolve in a changing Arctic environment. The work plan will be organized into three tasks addressing the three objectives:

Task 1: *In situ* observations – Characterization of the virus-phytoplankton communities and quantification of phytoplankton infection in natural environments of the Arctic Ocean. This task will be built on the REFUGE Arctic cruise from July to September 2024 to the Lincoln Sea. The project will utilize culture-dependent and culture-independent measurements of phytoplankton and virus diversity and abundance will include flow cytometry populations profiles, and cell/virus counts. A sensitive tracking of phytoplankton infection in the studied area will be assessed using a combination of bulk and innovative single-cell approaches (FISH, single-cell sorting) currently in development in the host laboratories. The diversity of phytoplankton–virus communities will be further established by metagenomic and metatranscriptomic sequencing in association with the biodiversity team of the REFUGE-Arctic project. Phytoplankton and virus isolation will be performed aboard and on land.

Task 2: *In vitro* experiments – Determination of the thermal response of three major phytoplankton-virus pairs of the Arctic Ocean community. We will monitor how temperature affects phytoplankton and virus dynamics characterizing the Lincoln Sea during onboard and in-laboratory experiments. We will focus on Arctic species *Micromonas polaris*, *Chaetoceros neogracilis*, and *Pyraminomonas sp.*, which are dominant in the Arctic Ocean. Abundances, infection patterns, and host–virus dynamics will be determined experimentally *via* flow cytometry and molecular approaches under different temperature conditions. Host and viral traits as a function of temperature will be estimated by integrating dynamical models of host–virus interactions with our experimental data using bayesian inference.

Task 3: *In silico* simulations – Evaluation of the impact of warming on phytoplankton–virus dynamics and ecosystem functions. Using results from tasks 1 and 2 we will develop community models of phytoplankton-virus interactions to quantify the impact of warming on ecosystem functions like diversity and C export potential. Specifically, we will investigate the impact of temperature fluctuations on the maintenance of the Arctic population's coexistence and quantify the ability of temperate phytoplankton-virus populations to invade and coexist with native warmer Arctic communities. Finally, by extending our ecological models to introduce simple biogeochemical formalism, we will estimate the impact of phytoplankton-virus diversity gains and losses on key ecosystem functions driving the BCP. These theoretical results will be compared to *in situ* biogeochemical measurements realized by the REFUGE-Arctic team.

Relevance to Institut de l'Océan: The Arctic Ocean is rapidly moving into a new state due to global warming, impacting the microbial ecosystem which drives the carbon cycle. Viral infection of phytoplankton is a key process in controlling phytoplankton worldwide, yet little is known about the impacts of warming on phytoplankton-virus interactions, particularly in the Arctic ocean. This project will obtain a mechanistic understanding of phytoplankton–virus infection and outcomes under different thermal conditions enabling a better understanding of the resilience and future of the Arctic Ocean microbial ecosystem. In this respect, this project seamlessly integrates with the challenge “*Changements globaux, risques et adaptations*.” Also, this multi-partner collaborative PhD project will bring together members of two laboratories from Sorbonne University (50/50 gender ratio) with complementary expertise, (1) UMR 7232 team GENOPHY (DD, SY, GM), which studies the mechanisms of development and adaptation of phytoplankton-virus interactions through genomics and experimental evolutionary approaches and (2) UMR 7144 team ECOMAP (ACB), whose focus is characterizing marine microbial ecosystems, their dynamics and how they drive the functioning of the present and future ocean. Last, the integrative (from cell to ecosystem) and multidisciplinary strategy (**biology, ecology, physiology, and mathematical modeling**) aims to foster collaboration between (sub-)fields that are often too disconnected, namely *in situ* observations from the REFUGE Arctic campaign, *in vitro* cultivation from laboratory experiments, and *in silico* ecological dynamics from model simulations. Such a strategy is in line with the modern approaches to systems biology, which consist of studying different levels of information to understand the global functioning of an environmental system.

Supervision: The supervising team includes: **Gilles Mirambeau**, a senior Ass. Prof. (HDR) at SU based in UMR7232. GM is a specialist in molecular and cellular mechanisms of viral infection and published 36 publications. **Sheree Yau** is a young CNRS researcher (UMR7232) whose research focus is the evolution and ecology of viruses of phytoplankton using molecular omics approaches (26 publications). **David Demory** is a young CNRS researcher (UMR7232) in theoretical ecology and oceanography. He combines experimental and mathematical models to study the virus-microbe eco-evolutionary dynamics in the ocean (12 publications). **Anne-Claire Baudoux** is a senior CNRS researcher (UMR7144) with long-standing expertise in virus ecology and ocean biogeochemistry (45 publications).

SY and **ACB** will pass their HDR during the Ph.D. project. This Ph.D. project is proposed in the framework of the project REFUGE-Arctic campaign involving an interdisciplinary International consortium. Besides the supervising team, the Ph.D. candidate will benefit from the intellectual, technical, and methodological support of REFUGE-Arctic partners, as well as current supervision team collaborators: Eva Ortega (biogeochemist) and Bart Haegmann (Ecological theorist) from UMR 7621 (LOMIC) and Samuel Shaffron (bioinformatician) from UMR 6241. The PhD research will be funded by the BNP Paribas REFUGE ARCTIC program and active project grants in the host labs (ANR PRCI: ELVIRA 2022–2024, ANR PRC BONUS: 2023–2027). The host labs also have pending grant submissions (ERC starting grant, Emergence, ANR JCJC 2023 calls) and will apply for travel funding.

Relevant publications by the supervising team:

GM: de Vargas et al. 2022 ([doi:10.3389/fmars.2022.936972](https://doi.org/10.3389/fmars.2022.936972)).

SY: Yau et al. 2019 ([doi: 10.3390/v11020189](https://doi.org/10.3390/v11020189)), Yau et al. 2020 ([doi:10.1126/sciadv.aay2587](https://doi.org/10.1126/sciadv.aay2587))

DD: Demory et al. 2017 ([doi:10.1038/ismej.2016.160](https://doi.org/10.1038/ismej.2016.160)), Demory et al. 2021 ([doi:10.1111/ele.13722](https://doi.org/10.1111/ele.13722))

ACB: Dinasquet et al. 2022 ([doi:10.5194/bg-19-1303-2022](https://doi.org/10.5194/bg-19-1303-2022)), Jacquet et al. 2023

([doi:10.35690/978-2-7592-3527-8](https://doi.org/10.35690/978-2-7592-3527-8))

References:

- ¹Rantanen and Mika et al., 2022 ([doi:10.1038/s43247-022-00498-3](https://doi.org/10.1038/s43247-022-00498-3)), ²Masson-Delmotte et al., IPCC 2021 report, ³Garcoa et al., 2018 ([doi:10.1073/pnas.1805518115](https://doi.org/10.1073/pnas.1805518115)), ⁴Malhi et al., 2020 ([doi:10.1098/rstb.2019.0104](https://doi.org/10.1098/rstb.2019.0104)), ⁵Bratbak et al., 1993 (<https://www.jstor.org/stable/24832806>), ⁶Baudoux et al., 2006 ([doi:10.3354/ame044207](https://doi.org/10.3354/ame044207)), ⁷Carlson et al. 2022 ([doi:10.1038/s41564-022-01088-x](https://doi.org/10.1038/s41564-022-01088-x)), ⁸Fuhrman 1999 ([doi:10.1038/21119](https://doi.org/10.1038/21119)), ⁹Gregory et al., 2019 ([doi:10.1016/j.cell.2019.03.040](https://doi.org/10.1016/j.cell.2019.03.040)), ¹⁰Demory et al. 2017 ([doi:10.1038/ismej.2016.160](https://doi.org/10.1038/ismej.2016.160)), ¹¹Demory et al. 2021 ([doi:10.1111/ele.13722](https://doi.org/10.1111/ele.13722))