Modeling the impacts of marine virus-microbe interactions dynamics on the biological carbon pump

Context: The Biological Carbon Pump (BCP) is one of the main carbon export pathways in the global ocean and is driven by microorganisms[1]. In the surface layers, photosynthetic microorganisms transform dissolved inorganic CO_2 into organic carbon. This organic matter is then exported due to gravitation and sequestered in the deep ocean[1]. During the sedimentation of the particulate organic carbon (POC), particles get colonized by heterotrophic bacteria, who use up to half of this fixed carbon, this altering carbon fluxes and the BCP[2]. This matter can be used to produce new biomass that re-enters the system through the microbial loop[3], be respired to CO2, or be transformed into different dissolved organic matter (DOM) compounds. Ecological processes, like the growth and mortality of phytoplankton, are driving the BCP because by modifying the fate and composition of organic matter, they steer the different carbon export pathways. Both photosynthetic and heterotrophic microbes can be infected and lysed by marine viruses. Through this infection and lysis, viruses can control marine microbial dynamics and represent an important source of mortality, releasing organic matter to the extracellular medium[4]. **Yet, little is known about the net effect of viruses on the carbon export flow into the deep ocean**. To date, two main hypotheses have been proposed: (1) the **viral shunt**, where phytoplankton lysis releases highly available DOM, diverting up to 5 to 25% of the carbon export into the microbial loop[5]. (2) the **viral shuttle**, where phytoplankton lysis releases sticky compounds like transparent exopolymer particles (TEP), increasing particle aggregation (up to 40%) and thus carbon export[4]. This dichotomous view of the impact of viruses on carbon export is simplistic, and the role of viruses in the BCP is more complex. Indeed, viruses can initiate latent and/or chronic infections of their microbial hosts[6], modulating the dynamics of their hosts and affecting community dynamics and the BCP. **The main objective of this PhD is therefore to quantify the impacts of marine viruses on the BCP by linking microbe-virus dynamics and the fate of organic matter.**

Objectives, and scientific strategy: In this project, **we will quantify the impacts of marine viruses on the biological carbon pump using mathematical modeling**. The proposed activities are designed to obtain a detailed mechanistic understanding of how microbe-virus interactions impact carbon pathways in the BCP. To this end, **we will combine ecological population and community models coupled with biophysical models** to quantify the consequences of (i) phytoplankton infection on particle aggregation and the microbial loop, (ii) the infection state and different virus cycles (lytic, lysogenic, and chronic) in phytoplankton and heterotrophic bacteria on the viral shunt and shuttle, and (iii) marine virus infection on carbon export at the ecosystem level. The candidate will specifically focus on developing a set of models to quantify key ecological, biophysical, and biogeochemical processes of the BCP and use laboratory and environmental data to compare and validate their results. The work plan will be organized into three tasks addressing the three objectives:

Task 1: Quantifying the Impacts of Phytoplankton-Virus Interactions on Particle Aggregation and the Microbial Loop. We will develop a comprehensive suite of ecological, aggregation, and export models to quantify the effects of phytoplankton infection on particle aggregation and the microbial loop. The ecological model will describe the dynamics of phytoplankton-virus interactions[7], enabling us to quantify virus-induced lysis, mortality rates, and the number of infected cells. The aggregation model will characterize particle aggregation based on their size spectra and biophysical processes[8], allowing us to quantify particle aggregation and sedimentation rates. Additionally, the export model will outline a simplified carbon flux, considering the size spectra of POM and their sedimentation rate[9]. By integrating this set of models, we will directly link and quantify the impact of infection on particle aggregation. Concurrently, we will assess the influence of phytoplankton lysis on the microbial loop by incorporating heterotrophic bacteria ecology and dissolved organic matter dynamics into our models. Calibration of our models will be performed using roller tank experiments conducted within the framework of the ANR BONUS in collaboration with Anne-Claire Baudoux.

Task 2: Quantifying the Impacts of Infection State and Viral Cycles on the Viral Shunt and Shuttle. Building on task 1, we will modify the ecological models to describe the dynamics of phytoplankton-virus and bacteria-phage interactions. This model will account for the infection state and different virus life cycles, including lytic, lysogenic, and chronic. Lysogenic and chronic viruses exhibit different levels of lysis compared to lytic viruses, thereby modulating the mortality induced by lysis[4]. This approach will enable us to establish connections between key measurements, such as the percentage of infected cells, and processes involved in the viral shunt and shuttle (mortality, aggregation and DOC production), effectively linking Tasks 1 and 2. Furthermore, our model will facilitate the quantification of the role of phage infection in altering the viral shunt and shuttle.

Task 3: Quantifying the Large-Scale Impacts of Marine Viruses on Carbon Export and the BCP. Expanding on the modeling efforts in Tasks 1 and 2, we will construct a comprehensive community model elucidating microbe-virus dynamics and its implications for the BCP. This model will seamlessly integrate the ecological dynamics of phytoplankton, bacteria and their viruses and incorporate aggregation and export quantifications. This model will be developed in collaboration with researchers at MIT and the University of Maryland who maintain the large-scale ocean ecosystem model DARWIN. Finally we will use environmental and field data obtained during the ANR APERO campaign in the North Atlantic Ocean to compare our quantitative estimation to in situ measurements.

Relevance to *Institut de l'Océan*: The global ocean is rapidly moving into a new state due to global warming, impacting the microbial ecosystem that drives the carbon cycle. Viral infection of phytoplankton and bacteria is a key process controlling microbes worldwide, yet little is known about the resulting impact of microbe-virus interactions on ecosystem functioning. This project will obtain a mechanistic understanding of how microbe–virus dynamics affect the biological carbon pump. Specifically, the student will provide quantitative estimations of the impacts of marine viruses on key processes like the viral shunt and the viral shuttle. 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 with complementary expertise, (1) UMR7621 (FJ and BH) which studies ocean biogeochemistry and microbial ecology and (2) USR3579 team GENOPHY (DD), which studies the ecological and evolutionary phytoplankton-virus dynamics. Last**,** the integrative (from cell-virus interactions to large-scale ecosystem processes) and multidisciplinary strategy (**biophysics, ecology, biogeochemistry, and mathematical modeling)** will foster collaborations between fields that are too often disconnected, namely virus-microbe interactions and oceanography. **Such a strategy is in line with the modern approaches to systems biology, which consist of simultaneously studying different levels of organization to understand the overall functioning of an environmental system.**

Supervision: The supervising team is composed of: **Fabien Joux**, professor at Sorbonne University and director of UMR7621. He is a specialist in marine microbial ecology and ocean carbon fluxes (65 publications). **David Demory** is a young CNRS researcher (USR3579) in theoretical ecology and microbial oceanography. He combines experiments and mathematical models to study the virus-microbe eco-evolutionary dynamics in the ocean (12 publications). **Bart Haegeman** is a CNRS researcher (UMR7621) in theoretical ecology. with a particular experience in modeling the impact of biodiversity on ecosystem functioning (60 publications). **BH** will pass his HdR during the PhD. This PhD project will take place in close interaction with several national and international projects: The ANR BONUS, the vDarwin project (MIT and University of Maryland) and the ANR APERO. Besides the supervising team, the PhD candidate will benefit from the support of Anne-Claire Baudoux (ocean virologist) from UMR7144 and Joshua Weitz (quantitative virologist) from the University of Maryland. Research equipment (computer needs) and travel expenses will be covered by on-going projects in the labs.

Relevant publications by the supervising team:
FJ: Tisserand et al. 2020 (https://doi.org/10.1098/rsta.2019.0356), Dadaglio et al. 2018 (https://doi.org/10.3354/ame01883)
DD: Demory *et al.* 2021 (https://doi.org/10.1111/ele.13722), Beckett and Demory *et al.* (*in press*, bioRxiv version: https://doi.org/10.1101/2021.06.15.448546)
BH: Bestion *et al.* 2021 (https://doi.org/10.1073/pnas.201959111), Synodinos *et al*. 2021 (https://doi.org/10.1111/ele.13780)

References:

[1]Boyd et al. 2019 (https://doi.org/10.1038/s41586-019-1098-2)
[2]Buchan et. al. 2014 (https://doi:10.1038/nrmicro3326)
[3]Azam *et al.* 1983 (https://doi.org/10.3354/meps010257)
[4]Zimmerman et al. 2020 (https://doi.org/10.1038/s41579-019-0270-x)
[5]Wilhelm and Suttle 1999 (https://doi.org/10.2307/1313569)
[6]Correa *et al.* 2021 (https://doi.org/10.1038/s41579-021-00530-x)
[7]Weitz 2016 (https://doi.org/10.1515/9781400873968)
[8]Jackson 2015 (https://doi.org/10.1002/lom3.10018)
[9]Guidi *et al.* 2016 (https://doi.org/10.1038/nature16942)