

Algal microbial interactions: beyond bacteria

van der Loos Luna

Department of Biology, Faculty of Sciences, Ghent University, Krijgslaan 281-S8, 9000 Gent, Belgium
E-mail: Luna.vanderLoos@UGent.be

The marine world is a microbial one. Unseen, but present in vast numbers in seawater, microbes associate with all eukaryotic organisms. It is becoming increasingly clear that these microbes, which include archaea, bacteria, fungi, microalgae, protists and viruses, have a huge impact on the functioning of eukaryotic hosts. Marine macroalgae (seaweeds) are no exception in this. Many microbes play a crucial role in macroalgal health, functioning and development during the host's various life cycle stages.

The majority of algal-microbial studies, however, only focused on bacteria, while other components of the microbiome received little to no attention. Completely overlooked are viruses which have a large potential effect, as they are very abundant in seawater and can not only infect the algal host, but also other microbial players, thus adding an extra complex interaction to the whole community. This way, viruses may spread diseases among species or may be part of the host immune system and can thus have both positive and negative impacts on the host.

The number of studies focusing on macroalgal-associated viromes can be counted on the fingers of one hand. Double-stranded and single-stranded DNA viruses were found to be associated with several kelp species and the first characterization of a full viral community was completed on a red alga, *Delisea pulchra*. These studies demonstrated that macroalgae harbor a wide diversity of viruses, and that the occurrence of infection rates can be linked to the environment, thereby emphasizing the importance of viruses in the physiology of the host.

In my PhD project, I focus on the functional consequences of the macroalgae-microbiome association and how this is influenced by environmental change, using the green macroalgal species *Ulva* (Sea lettuce) as study organism. Growth of *Ulva* is influenced by many environmental factors, including incident light, nutrient concentrations, salinity and temperature. Likewise, these factors influence the microbiome composition associated with *Ulva*. Previous studies on sponges and corals demonstrate an immediate response of the virome composition to thermal stress, with an increased abundance of viruses that are known to infect the host. For macroalgae, such vital information is lacking, and comprises a great knowledge gap.

With the VLIZ Brilliant Marine Research Idea funding, I am currently working on a pioneering experiment: extending beyond the bacteriome and entering the virome of *Ulva* (unfortunately, due to the current pandemic, I cannot present my results as of yet). The objectives are twofold, namely: 1) To characterise the virome associated with a natural *Ulva* population, thus analysing for the first time ever the complete virome of a green macroalga. And 2) To assess the short-term response of the associated viral community to thermal stress using a metaviromic approach.

These experiments will be the first step towards unravelling the impact of viruses on macroalgae during thermal stress. If we want to understand the response of macroalgae to environmental change, we should not be limited to the bacterial communities: it is time to focus on viruses.