Extended abstract

Brilliant Marine Research Idea 2020

1. General information

Title of the idea	Algal microbial interactions: beyond bacteria, let's go viral
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2. Brilliant Marine Research Idea

Extended abstract

The marine world is a microbial one. Unseen, but nevertheless present in vast numbers in seawater, microbes (including archaea, bacteria, fungi, microalgae, protists and viruses) associate with all eukaryotic organisms. It is becoming increasingly clear that these microbes have a huge impact on the functioning of eukaryotic hosts. Marine macroalgae (seaweeds) are no exception in this. Interactions between macroalgae and the microbiota are extremely diverse, ranging from mutualistic to parasitic. Many of the microbes play a crucial role in macroalgal health, functioning and development during the host's various life cycle stages. Viruses in particular 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. The majority of previous studies on algal-microbial interactions, however, only focused on bacteria, and other components of the microbiome received very little to no attention. The number of studies relating to macroalgae associated viruses can be counted on the fingers of one hand, and the full virome of green macroalgae has never been characterized. The objectives of this research proposal were to develop a protocol to extract viruses associated with a natural *Ulva* population and to characterize the virome, thus analyzing for the first time ever the complete virome of a green macroalga. We tested several different protocols to extract both DNA and RNA viruses from *Ulva* samples, using different preservation methods, different amounts of algal tissue weight, different concentration methods, and different sample types (bleached, unhealthy tissue and non-bleached, healthy tissue). Our results show that using low weight input material yielded higher viral nucleic acid concentrations, likely due to more efficient homogenization. Using a PEG concentration protocol on the contrary yielded lower concentrations. Samples preserved in Zymo DNA buffer yielded higher DNA concentrations, but samples stored at -80˚C yielded higher RNA concentrations. In addition, the bleached, unhealthy samples resulted in higher DNA concentrations, whilst the healthy samples yielded higher RNA concentrations. Unhealthy samples possibly contain a higher amount of DNA viruses. All samples have been send for sequencing twice, but due to the COVID-pandemic (restricted access to the laboratory, a shortage of lab-supplies related to the extraction of viruses, and a big sequencing pressure on sequencing companies) we still await these results.