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Editorial: The 3Ds of marine viruses: discovery, diversity, and dynamics

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Editorial on the Research Topic

The 3Ds of marine viruses: discovery, diversity, and dynamics

Viruses are the most abundant ‘biological entities’ in the oceans, can infect any life form, from microbes to whales, and could deeply influence marine trophic webs. Accordingly, marine viruses contribute to the evolution of life on our planet since are key drivers of host diversity, mediate the transfer of genetic material between organisms, affect population dynamics and can drive biogeochemical cycling, contributing to the daily flux of billions of tons of organic matter. Additionally, viral diseases prevalent in economic-relevant marine species could cause mass mortalities associated with high economic losses. Therefore, a comprehensive understanding of marine viruses is urgent and significant, which should be prioritized in future research directions.

The abundance of marine viruses mirrors the diversity of viral genomes and morphotypes. Since the first phage was isolated from the marine environment more than 60 years ago, the number of newly found viruses had increased sharply due to the advent of genomic and metagenomic techniques. Indeed, the emergence of new technologies has drastically contributed to our knowledge on viral communities as well as of single viruses. The application of multi-omics approaches to marine viruses, which is currently challenging, will contribute to a comprehensive understanding of viral biodiversity and virus-host interaction. In this context, the advent of innovative sequencing technologies has opened an avenue for viral research, highlighting the “dark matter” of virus and *virus-like* particles from almost all environmental niches. This enormous bubble of data challenged the research community in order to identify connections between viruses and hosts, consequently disclosing the “*functional biology*” of these viruses. Since this data production trend will likely grow in the next years and decade, paired high-throughput methods to complement the discovery of novel viruses with functional data are needed.

The main goal of this Research Topic was to bring together research papers focusing on innovate virus identification methods and on the exploration of novel marine viruses and of their specialized hosts. The published contributions revealed relevant heterogeneity, both in the investigated viruses and in the applied methods.

The infection dynamic of a RNA virus was studied by [Walde et al.](#), using an advanced quantitative image analysis based on 3D confocal microscopy, showing evidence of a possible host defense reaction. Notably, this approach that was applied to the marine diatom, *Guinardia delicatula*, revealed a great potential for future applications in the field of marine virology.

[Qiu et al.](#) focused their contribution to an emerging virus causing relevant mortalities in shrimps and crabs, the Decapod iridescent virus 1 (DIV1). Their study demonstrated that the virus can effectively infect the kuruma shrimp *Penaeus japonicus*. The significant abundances of DIV1 found in farmed *P. japonicus* samples from five coastal provinces in China was 5.3%, supporting the multi-host behavior of this virus and giving support for developing DIV1 preventive and control strategies.

Similarly, another viral family, the *Malacoherpesviridae*, causing relevant mortalities in economic relevant shellfish species was considered by the paper of [Rosani et al.](#) The authors reported four novel malacoherpes-like viruses retrieved from global metagenomic datasets, highlighting the need to update detection protocols and preventive measures to possible future viral outbreaks impacting aquaculture.

Two novel phages, putatively representing a novel family and a novel genus were described in the research papers of [Ren et al.](#) and [Jing et al.](#), respectively. The novel viral family, named *Psaeviridae*, included the vB_PsaP_M1 phage that can infect *Pseudomonas* and can represent a novel tool to investigate host-virus interactions. Likewise, the phage genus *Qingschitovirus* described in [Jing et al.](#) can infect *Vibrio hangzhouensis* and will likely contribute to a better understanding of interactions between *Vibrio* phages and their hosts, for example providing novel reference genomes to determine the taxonomic status of unknown phages in the metagenome and meta-transcriptome datasets.

[Segura-Göthlin et al.](#) monitored the infection by poxvirus in the skin of dolphins under human care, posing relevant questions about the currently unknown viral etiology, which is possibly influenced by environmental stimuli, viral load, or the health/immunological status of the animals.

Altogether, the articles published within this Research Topic contributed to further state the importance of viruses at all the trophic levels. The understanding of the fascinating “viral world” holds great potential for answering fundamental questions in biology, like the evolution of viruses and of antiviral defense systems.

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