

CULTIVATION AND CHARACTERIZATION OF VIRUSES INFECTING
EUKARYOTIC PHYTOPLANKTON FROM THE TROPICAL NORTH
PACIFIC OCEAN

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Abstract

Death by viral infection rivals predation as a source of mortality for all types of microscopic plankton in the ocean, including phytoplankton that are the foundation of the marine food web. This has profound consequences for plankton ecology and nutrient cycling in the sea. Viruses tend to be quite specific in the cells they infect, so the known extraordinary diversity among the marine phytoplankton implies that there is a similar high diversity of viruses in the sea. Our knowledge of viral diversity in the ocean has dramatically improved in recent years using metagenomic techniques (random sequencing of genome fragments from mixed communities). However, basic information about the viruses being detected, such as which organisms they infect and the details of their infection cycle cannot be reliably determined from sequence data alone. Having more model virus-host systems in culture that can be experimentally manipulated and studied in the lab would provide valuable new insights into the functional roles of the viruses in the marine food web.

In this dissertation, cultivation-based techniques were used to characterize novel virus-host systems for eukaryotic phytoplankton from the tropical North Pacific Ocean, thereby identifying new virus-host linkages and establishing model systems for further study. Over 300 phytoplankton strains were cultivated and used in the isolation of over 60 virus strains. Described herein is a summary of these isolation efforts, including preliminary characterizations for 19 virus isolates using electron microscopy and genome sequencing. This is followed by more in-depth analyses of the genome and virion proteome of the giant virus *Tetraselmis virus 1* (TetV-1), which infects the cosmopolitan green alga *Tetraselmis*. This work establishes new virus-host linkages and highlights previously uncharac-

terized viral diversity, including the first protist-infecting isolates from viral families previously only known to infect plants or animals. Furthermore, the genomic analyses have revealed a high number of viral encoded metabolic genes not previously seen in viruses, and the proteomic analyses have identified novel virion-associated enzymes. Marine viruses continue to represent an enormous amount of unknown or uncharacterized taxonomic and metabolic diversity, and this work demonstrates the utility of cultivation-based approaches in illuminating some of these mysteries.