Viral ecogenomics across the Porifera

Cecília Pascelli
Patrick W. Laffy
Emmanuelle Botté
Marija Kupresanin
Thomas Rattei
Miguel Lurgi
Timothy Ravasi
Nicole S. Webster

Video Byte

Keywords: Viromics, viral ecology, functional diversity, AMGs, coral reef sponges, coral, reef, virus, Porifera, sea sponge, ecology, Microbiome

Posted Date: November 12th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-107384/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Abstract

Marine sponges are an ecologically important component of the sea floor. In addition to providing a habitat for a diverse array of marine species, they also mediate biogeochemical fluxes by filtering organic matter, facilitating nutrient consumption and release. But while their interaction with picoplankton, bacteria, and archaea has been extensively studied, the interaction of sponges with viral-like particles is poorly understood. A recent study examined this 'dark matter' in this ecologically important symbiosis. Researchers assessed nine sponge species from the Great Barrier Reef and seven species from the Red Sea. Viomic sequencing revealed host-specific and site-specific patterns in viral communities. All sponge species were dominated by the bacteriophage order Caudovirales, but large DNA virus families were also represented. While core viral functions were consistent across viromes, putative auxiliary metabolic genes (AMGs) were differentially represented. These AMGs, derived from viral hosts, were associated with herbicide resistance, heavy metal resistance, and nylon degradation. AMGs also varied with the composition and abundance of the sponge-associated microbiome. These results highlight the diverse functional roles that viruses can play in marine sponges and demonstrate the important role of viral AMGs in helping sponges thrive in diverse marine environments.