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TITLE: Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans

AUTHOR: ['Felipe H. Coutinho', 'Cynthia B. Silveira', 'Gustavo Bueno Gregoracci', 'Cristiane C. Thompson', 'Robert A. Edwards', 'Corina P. D. Brussaard', 'Bas E. Dutilh', 'Fabiano L. Thompson']

ABSTRACT:

Marine viruses are key drivers of host diversity, population dynamics and biogeochemical cycling and contribute to the daily flux of billions of tons of organic matter. Despite recent advancements in metagenomics, much of their biodiversity remains uncharacterized. Here we report a data set of 27,346 marine virome contigs that includes 44 complete genomes. These outnumber all currently known phage genomes in marine habitats and include members of previously uncharacterized lineages. We designed a new method for host prediction based on co-occurrence associations that reveals these viruses infect dominant members of the marine microbiome such as *Prochlorococcus* and *Pelagibacter*. A negative association between host abundance and the virus-to-host ratio supports the recently proposed Piggyback-the-Winner model of reduced phage lysis at higher host densities. An analysis of the abundance patterns of viruses throughout the oceans revealed how marine viral communities adapt to various seasonal, temperature and photic regimes according to targeted hosts and the diversity of auxiliary metabolic genes.

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