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Abstract

Unveiling Infection Strategies across Diverse Marine Phage–Host Systems †

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Abstract: Bacterial viruses (phages) are amongst the smallest, most powerful biological entities on Earth. Through infection, phages impact host metabolism, bacterial mortality, and evolution. In the oceans, 20–40% of surface microbes are infected, with 10^{23} new infections each second. Yet, infections remain virtually uncharacterized, as the available phage isolates underrepresent the diversity of marine phage–host interactions. Additionally, while sequencing efforts reveal "who is there?", a gap between sequence and function prevents answering "what are they doing?" and "how?". We have developed new Bacteroidetes and Proteobacteria marine phage–host model systems with which to connect genomes, infection strategies, and functions using both traditional and genome-wide "-omics" experiments. We ask: How do infections by genomically divergent phages compare? Are there links between phage–host genomes and infection strategies? Our findings are as follows. In *Bacteroidetes*, a phage infecting two nearly identical strains (host38 and host18) under identical conditions is more fit and efficient on host38. By contrast, on host18, it is less fit and, except for phage transcription, it fails at efficiently mastering all stages of the infection: from adsorption through to cell lysis. In *Proteobacteria*, genomically unrelated podovirus and siphovirus phages infecting the same strain reprogram host metabolisms very differently. Namely, siphovirus-infected cells hardly differ from uninfected and mainly repress energy-consuming processes such as motility and translation. By contrast, podovirus-infected cells greatly differ from uninfected cells in transcription and in uniquely shifting central carbon and energy metabolism. Additionally, the siphovirus is more complementary to the host than the podovirus in %GC, amino acids, and codon usage. We found that phage–host genome complementarity may drive the resource demand and fitness of a phage: the phage most complementary to its host easily accesses intracellular resources, infects with little reprogramming, and accomplishes the largest fitness, which has not previously been shown. Together, this work helps to uncover infection efficiency strategies, and connect genomes with metabolisms in marine phage–host systems.

Keywords: bacteriophages; bacteria; omics; phage-host interactions