virus

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Bacteria impact human health and disease, industrial processes and natural ecosystems, but do so under the influence of viruses. Problematically, knowledge of viral infection efficiencies and outcomes (*e.g.* lysis, lysogeny) derives from few model systems that over-represent efficient, lytic infections and under-represent virus-host natural diversity. Here we sought to understand how infection efficiency is regulated in an environmental *Bacteroidetes* virus that has drastically different infection efficiencies when infecting two genetically and physiologically nearly identical bacterial host strains. To this end, we quantified bacterial virus (phage) and host DNA, transcripts and phage particles throughout both infections. While phage transcription was similar in both hosts, transcriptional differences between hosts suggested host-derived regulation of infection efficiency. Specifically, host transcriptomes suggested that the phage failed to repress early host expression in the inefficient infection, thereby allowing the host to respond against infection by delaying phage DNA replication and protein translation. Experimental measurements then revealed that these transcriptional responses targeted phage DNA and particle production, as they were both significantly delayed (by >30 minutes) and reduced (by >50%) in the inefficient versus efficient infection. This suggests that the phage failing to repress early host expression in the inefficient infection allowed the host to respond against infection by delaying phage DNA replication and protein translation. Given that this phage type is ubiquitous and abundant in the global oceans and that variable viral infection efficiencies are central to dynamic ecosystems, these data provide a critically needed foundation for understanding and modeling viral infection efficiencies in nature.

Morphological characteristics and complete sequences of two cold-active *Pseudoalteromonas* phages

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Cold-active bacteriophages are generally defined as bacterial viruses that are capable of infection and production at low temperature (≤ 4°C). Several studies of cold-active bacteriophages isolated from aquatic environments have been reported. However, characteristics of cold-active bacteriophage-host systems in deep-sea sediments are still poorly understood, despite high viral abundance maintain in persistently low temperature. Two bacteriophages, ϕCA1 and ϕCA2, were isolated from a deep-sea sediment core taken from the Mendeleev Ridge in the western Arctic Ocean. Host bacteria of ϕCA1 and ϕCA2 were affiliated with the genus *Pseudoalteromonas* based on 16S rRNA gene sequences. The *Pseudoalteromonas* bacteriophages of ϕCA1 and ϕCA2 turned out to exhibit successive propagations at low temperature of 1°C,

indicating that they are cold-active ones. Each phage has a contractile tail, which is a morphological feature of the family *Myoviridae*. To find genomic characteristics of the cold-active phages, a complete genome sequence of each phage was obtained by Illumina MiSeq sequencing technology. The genome sizes of ϕCA1 and ϕCA2 were 36,825 bp and 36,989 bp, respectively, with an identical G+C content of 43.1 mol%. Details of genomic content of the cold-active phages and their relatedness with other phages will be provided.

Battle of two molecular parasites in *Salmonella*

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Phages and plasmids are both molecular parasites, which infect, compete for and interact in the same host cells. For *Salmonella* sp. it has been recurrently reported that acquisition of certain plasmids might lead to a phage type conversion e.g. lost of sensitivity to one or more phages during phage typing. Some of these plasmids belong to incompatibility group X1 (IncX1), such as the well studied and fully sequenced plasmid pOLA52. Phage typing has confirmed that also pOLA52 is able to increase resistance against phages in *Salmonella*. Interestingly, although some type of incompatibility exists between the two, the pOLA52 plasmid does not code for any identified phage resistance mechanism making the resistance mechanism unknown. In order to elucidate the possible mechanism of this phage-plasmid interaction we have fully genome sequenced 17 phages used for typing of *Salmonella* in Denmark. We analyzed and grouped the phages and compered their sequence to available IncX1 plasmid sequences and phages of *Salmonella* followed by transcriptome analysis of the infected cells. Additionally, we generated pOLA52 knockout mutants to reveal a possible mechanism of this interaction. Both phages and plasmids are shaping bacterial communities and there is a need for better understanding of their relations using modern molecular methods.

Distinct communities of phytoplankton viruses in the St. Lawrence estuary transition zone

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The St. Lawrence hydrographic system is composed of a diversity of freshwater, brackish and marine habitats and is one of the largest and most important waterways in North America. This region is a crucial breeding ground for invertebrates, fish and marine birds and mammals. Ultimately, the health of these groups is dependent on phytoplankton, therefore understanding the forces that determine the productivity and composition of this keystone group of protists is critical to understanding the overall