Temporal dynamics of microbe-virus interactions in the Baltic Sea

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Abstract

Bacteria and archaea are key drivers of all major element cycles. Viruses that infect bacteria and archaea also play a fundamental role by altering the metabolic state of their host during infection and causing cell death. The CRISPR-Cas system is one of many strategies employed by bacteria and archaea to defend against viral infection. Invading viral DNA is incorporated into a CRISPR array as a short sequence (spacer) that is then recognised during the next viral encounter providing an adaptive immunity. The temporal dynamics of this system in the environment, however, is not well constrained. Using a meta-omic dataset spanning several years of sampling, we leveraged the CRISPR-Cas system to explore microbe-virus interactions in the Baltic Sea. Our goal was to understand how quickly microbes in the environment adapt to virus predation, and conversely how quickly viruses adapt to the microbial defence mechanism by developing mutations in the spacer-targeted region. To explore these interactions, we first generated a database consisting of thousands of complete and high-quality viral genomes recovered from viromes collected from the Baltic Sea. CRISPR arrays were then identified in microbial metagenome assembled genomes (MAGs), metagenomic contigs, and unassembled metagenomic reads from corresponding sampling time points. Virus-host dynamics were uncovered by matching quality-filtered spacers from CRISPR arrays to the viral database. The results show that spacer turnover over time can be captured in temporal meta-omic datasets. In the Baltic Sea, this has implications for the termination of microbial blooms, biogeochemical cycling, and resource turnover.

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Conflicts of interest

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