

Chasing Viruses: An 'omics dive into viral diversity of the North Sea

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While being the most abundant biological entities in the world's oceans, marine viruses play a pivotal role in the biogeochemical cycling of our planet. Viruses are obligate parasites that require their host for metabolism and reproduction. In the process, they lyse their host and thereby shunt the flow of energy away from higher trophic levels. Although in recent years marine viruses have been a topic of intensive research, their diversity is yet to be unraveled completely. With the help of VLIZ BMRI grant 2022, we have dived into dissecting the composition of planktonic viral communities in the North Sea and their life-history strategies using metagenomic approaches.

We collected water samples from 21 stations and filtered the host cells out using 0.22 µm membrane filters. The filtrate containing viruses (< 0.22 µm) was subjected to iron chloride flocculation and viruses were collected on 1 µm membrane filters. Flocculated viruses were resuspended, and nucleic acids were extracted. After clean-up, extracted viral DNA was used to prepare genomic libraries using xGen ssDNA & Low-Input DNA Library Preparation Kit, which is meant to have lower bias towards ssDNA fragments. The libraries were sequenced using Illumina NextSeq500 PE75 chemistry.

Preliminary analyses of the sequenced data revealed a total of over 32000 viral contigs. Double-stranded DNA (dsDNA) viruses comprised of about 88% of these sequences. Around 40% of these dsDNA viruses belonged to the family Kyanoviridae and are predicted to infect cyanobacteria (photosynthetic bacteria). We also identified potential viruses (subfamily Arquatrovirinae and family Rudiviridae) that infect archaea. Single-stranded DNA (ssDNA) viruses comprise 4% of total sequences and are predicted to infect invertebrates, and the gut bacteria of marine vertebrates. Around 25% of the identified phage contigs displayed traits for temperate lifestyle, where they can switch between lytic and lysogenic life-history strategies. When in lysogeny, viruses incorporate themselves within the host genome as proviruses. Around 1% of the total contigs were predicted to be proviruses.

Giant viruses, also known as Nucleocytoplasmic Large DNA Viruses (NCLDV), were found to be abundant in our samples (around 7%). These viruses are known for their large genomes containing genes for DNA replication, repair, transcription, and translation, which are absent in other viruses. We also identified around 8% of the contigs as Lavidaviridae, also known as virophages. As the name suggests, virophages are viruses of viruses. These are relatively small viruses, with small genome size, that are known to co-infect a host cell along with giant viruses.

Some of the contigs were predicted to be (-)ssRNA (5%), (+)ssRNA (2%), and dsRNA (0.5%) viruses. We also identified 0.3% of the contigs as ssRNA-RT viruses that use RNA-dependent DNA polymerase to construct a DNA intermediate that incorporates itself within the host genome as a provirus.

We are in the process of identifying auxiliary metabolic genes in viral genomes that could play a role in evolution of planktonic communities through horizontal gene transfer.

With this project, we have identified and classified viruses in the North Sea, commented on potential life-history strategies, and have plans to examine auxiliary metabolic gene content of these viruses.

Keywords

Marine Viruses; North Sea; Metagenomics; Phages; Virus-Host Interactions