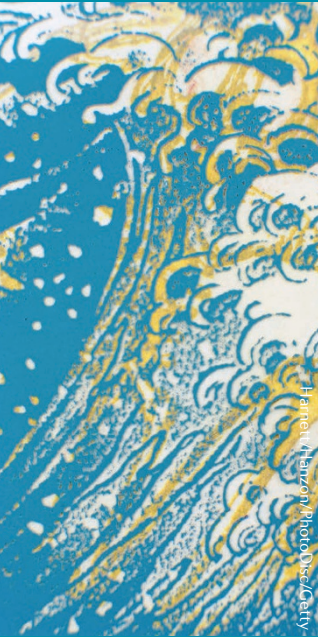


 METAGENOMICS

Marine genomics goes viral



The systematic collection and processing of the global ocean virome (GOV) data set, now reported in *Nature*, reveals the underlying structure of marine viral communities worldwide, providing an unprecedented view into the genetic diversity of double-stranded DNA (dsDNA) viruses.

Viruses are thought to play a major part in marine ecosystems, but their identification and quantification has been challenging owing to the lack of conserved genomic signatures and technical limitations. Roux *et al.* assembled complete genomes and large contigs from environmental samples obtained during two previous research expeditions from several oceans and seas, at varying depths to sample surface as well as deep-ocean viruses on a community-wide scale. The resulting marine viral metagenomes (also known as viromes) comprised a total of 15,222

epipelagic and mesopelagic viral populations, thus tripling the number of known marine viral populations.

Viruses could be categorized into 867 viral ‘clusters’ (groups of approximately similar genus) on the basis of gene-content information and network analytics. Characterization of the oceanic viral clusters revealed 38 dominant clusters, which constituted almost half of the viral populations present in any sample. Of these clusters, 4 were globally abundant, as they could be determined in samples obtained from more than 25 different sampling stations.

To predict virus–host pairings for the dominant dsDNA virus clusters, the authors used three different sequence-based approaches that examined similarities between viral genome sequences and host CRISPR spacers, between viral and microbial

genomes due to integrated prophages or gene transfers, or between viral and host genome nucleotide signatures. These analyses indicated that the four ubiquitous and abundant viral clusters target seven of the eight globally most abundant microbial groups.

The authors also identified 243 virus-encoded auxiliary metabolic genes (AMGs), of which 148 were unknown. Characterization of several viral AMGs involved in sulfur and nitrogen cycles revealed new biological insights into how these viruses directly manipulate microbial metabolism.

In the future, this fundamental ecogenomic resource will support marine microbiology studies and the interpretation of new genomic and metagenomic data sets to hopefully yield a holistic and predictive understanding of the many roles of viruses in diverse ecosystems.

Linda Koch

ORIGINAL ARTICLE Roux, S. *et al.* Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. *Nature* <http://dx.doi.org/10.1038/nature19366> (2016)