METAGENOMICS

A global marine viral metagenome

The first global survey of marine viral genomes has shown that the oceans are awash with viruses. Calculations of viral diversity indicate there might be as many as a few hundred thousand distinct marine viral species. The majority of viral species are widely dispersed, but local environmental conditions dictate which are most common in a particular oceanic region.

The group of Forest Rohwer and their collaborators collected 184 samples from 68 different marine sites located in four main regions: the Sargasso Sea, the Arctic Ocean, the Gulf of Mexico and the coastal waters of British Columbia. They extracted and amplified DNA from uncultured viral particles and used pyrophosphate sequencing to determine the DNA sequences that were present. Fewer than 10% of the sequences in this viral assemblage were significantly related to sequences in current genomic and metagenomic databanks. The sequences were also phylogenetically distinct from those of known phage genomes, and indicated that marine phages share distinctive characteristics.

The richness of viral species varied along a latitudinal gradient. Diversity was highest in regions nearest the equator and lower towards the poles, in common with other marine biota. The marine virome from British Columbia, a region that is affected by seasonal upwelling and the outflows of many rivers, was exceptionally genotype-rich. The authors speculate that the richness of such regions could be boosted to levels approaching global diversity by the inward migration of viral species from other regions.

The prevalence of viruses differed among the four oceanic regions. The Arctic metagenome had the most prophage-like sequences. Cyanophages and a novel ssDNA microphage dominated the Sargasso sample. As the majority of viral species are widespread and shared between oceanic regions, the observed geographical distribution is largely the result of differences in the abundance of viral species rather than the exclusion of particular species.

Metagenomic analysis has provided important information on the abundance, distribution and dynamics of marine viruses. A more comprehensive characterization of marine viral diversity and, as a result, a better understanding of marine microbial ecosystems, can be anticipated with further improvements in the power of DNA sequencing technology.

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ORIGINAL RESEARCH PAPER Angly, F. E. *et al.* The marine viromes of four oceanic regions. *PLoS Biol.* **4**, e368 (2006)
FURTHER READING Edwards, R. A. & Rohwer, F. Viral metagenomics. *Nature Rev. Microbiol.* **3**, 504–510 (2005) | Tringe, S. G. & Rubin, E. M. Metagenomics: DNA sequencing of environmental samples. *Nature Rev. Genet.* **6**, 805–814 (2005)
WEB SITE
SDSU Center for Universal Microbial Sequencing: http://scums.sdsu.edu/phage/Oceans

DEVELOPMENT

It takes a lot to make the segmentation clock tick

The segments that give rise to the vertebrate spine and muscles of the trunk — the somites — are produced sequentially with each oscillation of the segmentation clock. A new microarray study shows that the molecular mechanism that underlies the clock is a large network of genes, transcribed in two groups that are exactly out of phase with each other.

The mRNA levels of a few genes are known to oscillate with the segmentation clock. Most of these are members of the Notch signalling pathway, although a component of the Wnt pathway, *Axin2*, is known to oscillate out of phase with them. Olivier Pourquié and colleagues used microarrays to obtain a more comprehensive list of the molecular components of the clock. They used the expression pattern of one known oscillator, *Lfng* (lunatic fringe), to select a series of 17 mouse embryos that covered an entire oscillation cycle. Microarray data from these samples confirmed the oscillations of known clock genes, and a statistical algorithm was applied to detect other oscillating transcripts.

The transcripts clustered into two groups that were directly out of phase. The known Notch-pathway components clustered with further Notch components, including the Wnt inhibitor *Nkd1* (naked cuticle 1 homologue), and also with fibroblast growth factor (FGF)-pathway components. Analysis of a mutant that is defective in Notch signalling revealed that FGF components oscillate in parallel with Notch rather than being dependent on it. The other cluster consisted mainly of Wnt components and their downstream targets, although only a subset of Wnt targets was involved.

The authors anticipate that technical improvements — in microarray coverage and transcript amplification — will increase the number of identified oscillating targets from their 29 to between 50 and 100. Nevertheless, these results are a significant advance on models that involved only a few genes, and they suggest a model in which Notch/FGF and Wnt components mutually inhibit each other. It will be interesting to see whether the half-lives of the proteins are as short as those of the transcripts, or whether mutual inhibition is required to maintain the oscillations at the protein level.

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ORIGINAL RESEARCH PAPER Dequéant, M.-L. *et al.* A complex oscillating network of signaling genes underlies the mouse segmentation clock. *Science* 9 November 2006 (doi:10.1126/science.1133141)