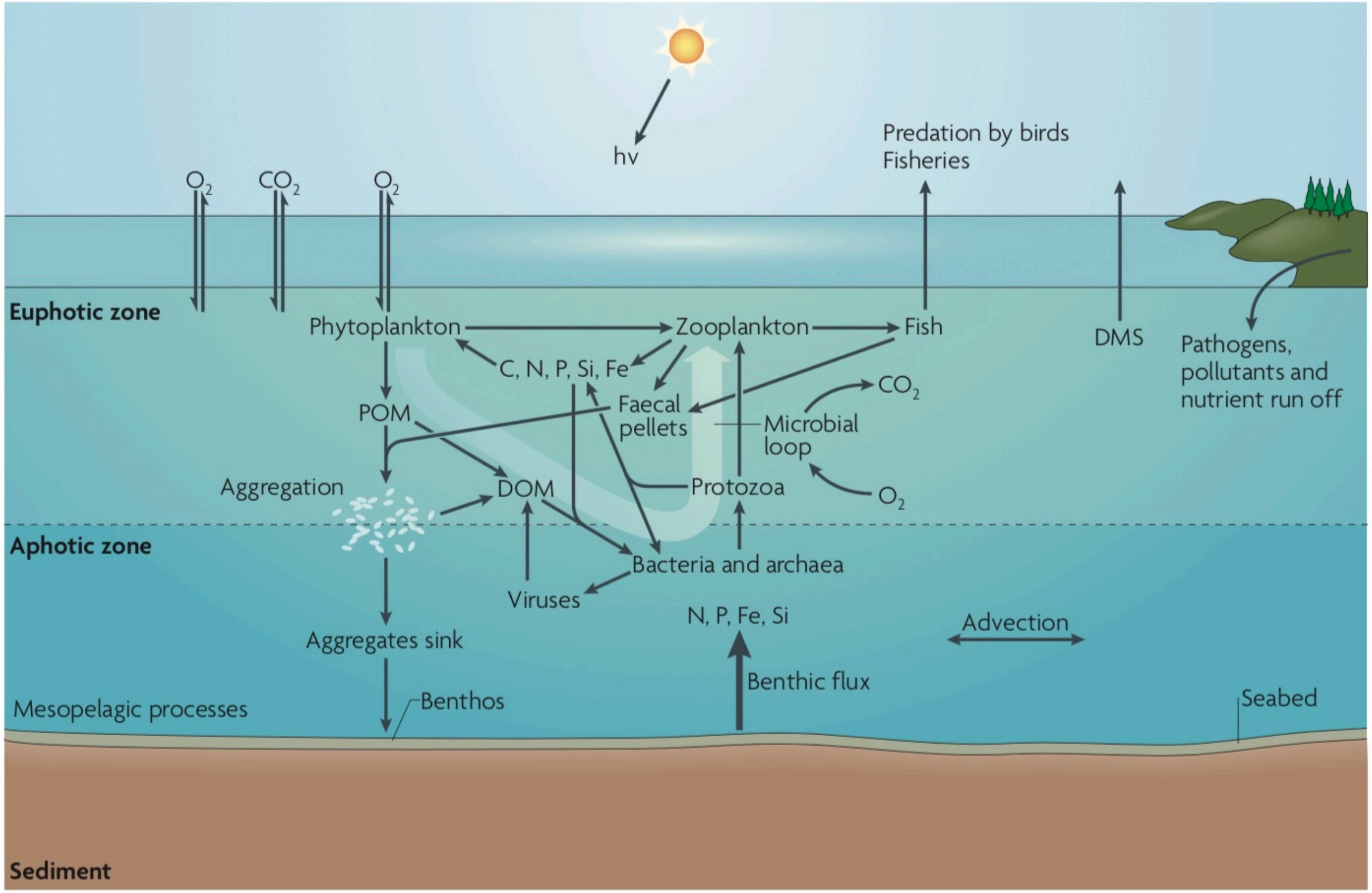
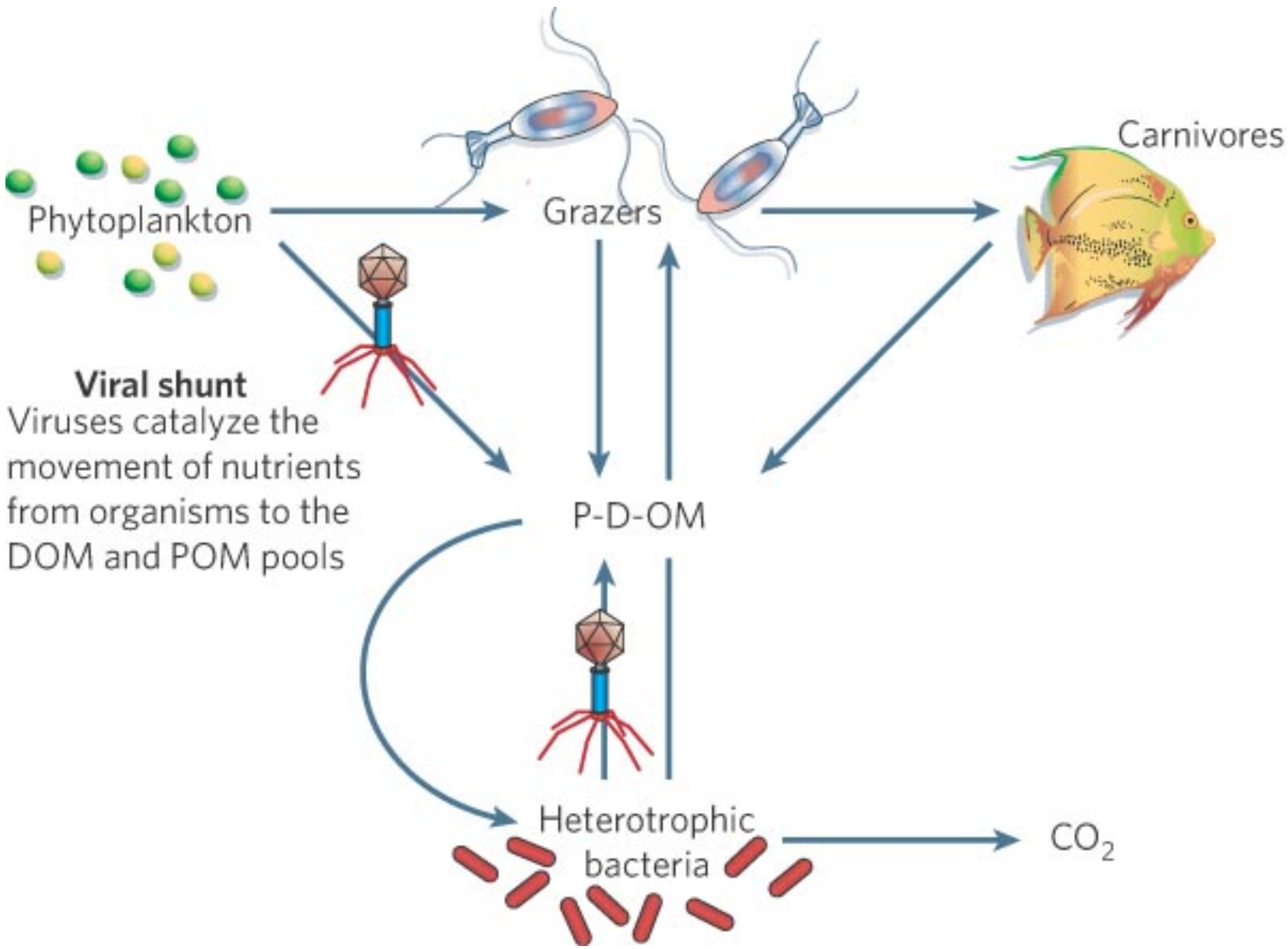


Figure 1 | **Microbial structuring of a marine ecosystem.** A large fraction of the organic matter that is synthesized by primary producers becomes dissolved organic matter (DOM) and is taken up almost exclusively by bacteria. Most of the DOM is respired to carbon dioxide and a fraction is assimilated and re-introduced into the classical food chain (phytoplankton to zooplankton to fish). The action of bacteria on organic matter plays a major part in carbon cycling through DOM. It therefore influences the air–sea exchange of carbon dioxide, carbon storage through sinking and carbon flux to fisheries. DMS, dimethylsulphide; hv, light; POM, particulate organic matter.

Azam and Malfatti 2007

Viruses in the Marine Environment

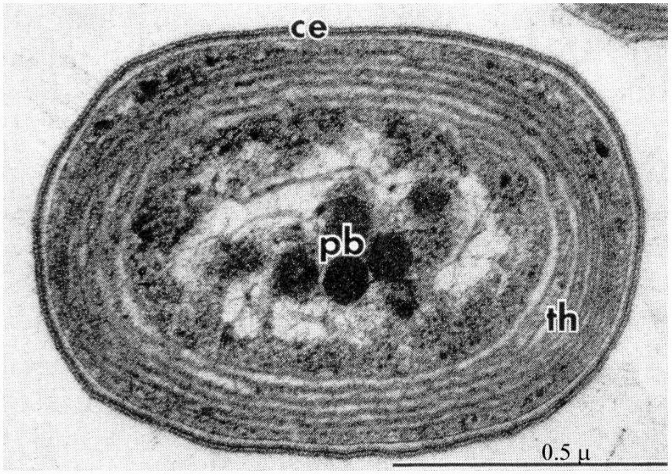


Suttle 2005 (Nature)

Host: *Synechococcus*

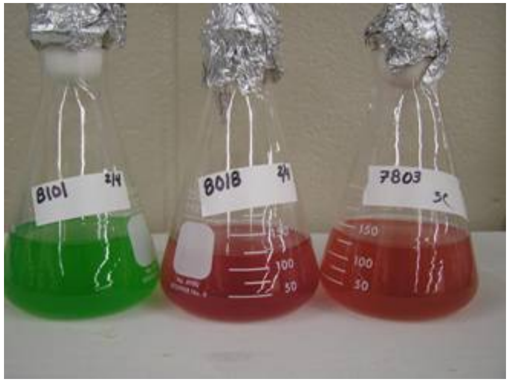
Small unicellular cyanobacteria

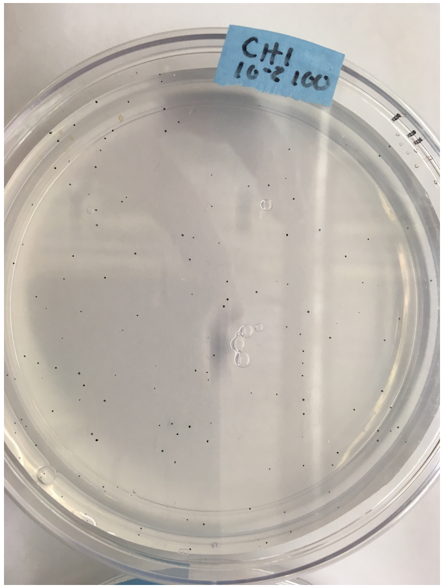
Photosynthetic primary producers



ce: Cell Envelope
pb: Polyhedral Bodies
th: Thylakoids

http://www.bio.ic.ac.uk/research/barber/psIIimages/PSII.jpg





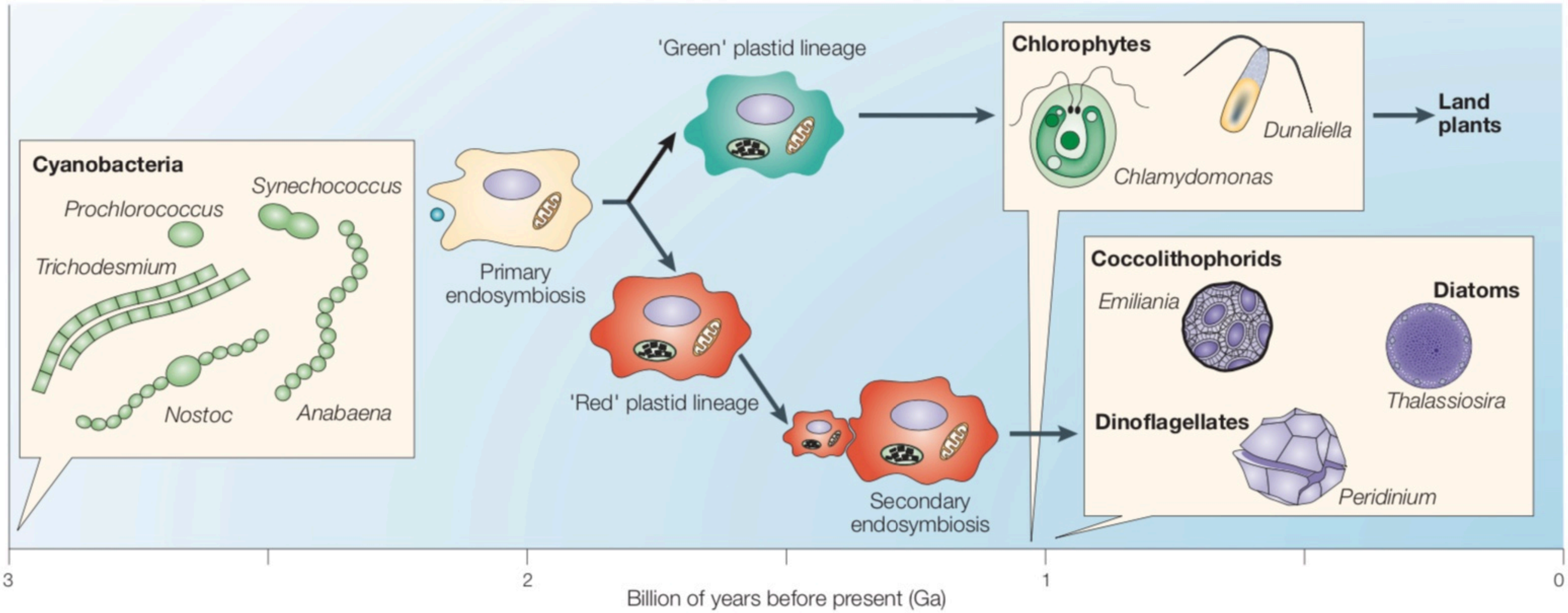


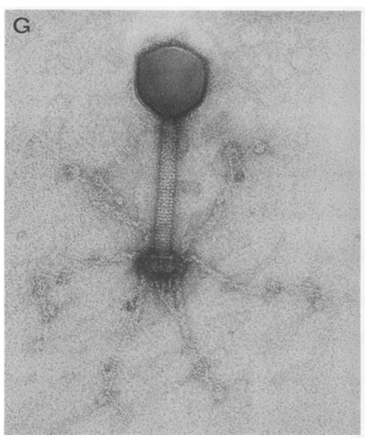
Figure 4 | **Placement of phytoplankton PCD into an evolutionary context.** Phytoplankton evolution spans both bacterial and eukaryotic domains of life and at least eight major eukaryotic divisions or phyla[141], some of which are shown here. Most phytoplankton in the contemporary ocean are cyanobacteria, which, based on the presence of molecular markers, were present in marine ecosystems at least 2.8 billion years ago (Ga)[69] and probably evolved much earlier[70]. The photosynthetic origins of eukaryotic phytoplankton can be traced to an endosymbiotic event between an ancestral, mitochondrion-containing eukaryotic cell and a coccid cyanobacterium[72]. Photosynthetic eukaryotes inhabited coastal waters by 1.4–1.9 Ga[73–75], with a schism early in the evolution of eukaryotic phytoplankton giving rise to two major plastid types and, consequently, two ancient superfamilies — the 'green' and 'red' lineages[76]. Each lineage evolved independently after the primary endosymbiotic event. The Chlorophytes (for example, *Dunaliella* and *Chlamydomonas*) are members of the green lineage which gave rise to land plants ~0.45 Ga. The green lineage is thought to have dominated eukaryotic marine phytoplankton communities in the Mesoproterozoic (900–1,600 million years ago (Mya)) and Paleozoic (251–544 Mya) oceans but have become much less abundant since the end-Permian extinction (251 Mya)[142]. The red lineage includes diatoms (for example, *Thalassiosira*), coccolithophorids (for example, *Emiliania*) and dinoflagellates (for example, *Peridinium*), and has come to dominate the modern ocean[142].

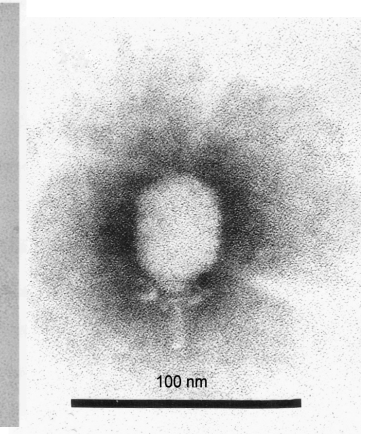
Bidle and Falkowski, 2004

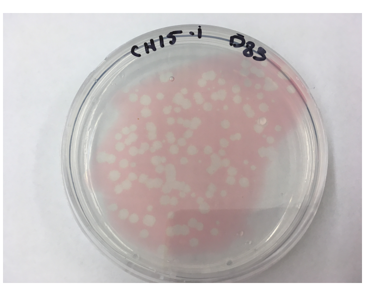
Virus: Cyanophages

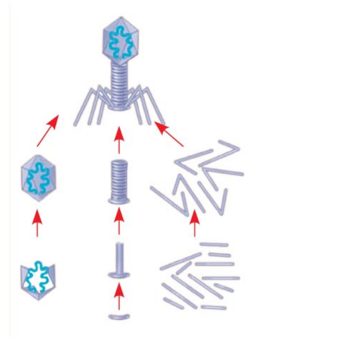
dsDNA bacteriophages

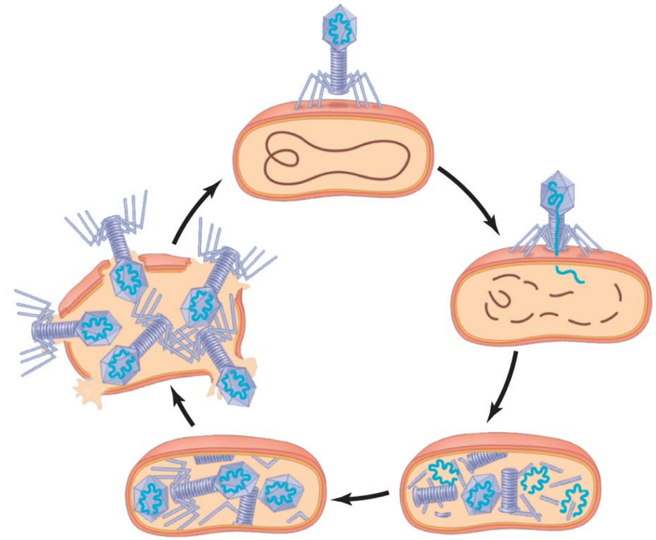
Myoviruses and Podoviruses
180,000 bp 48,0000 bp





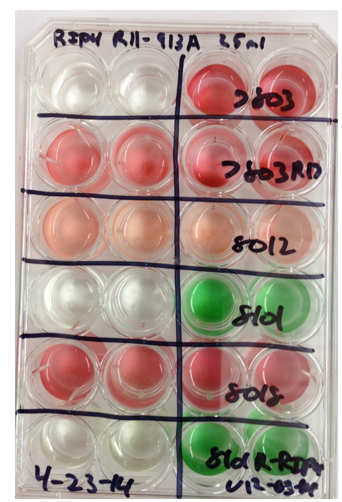




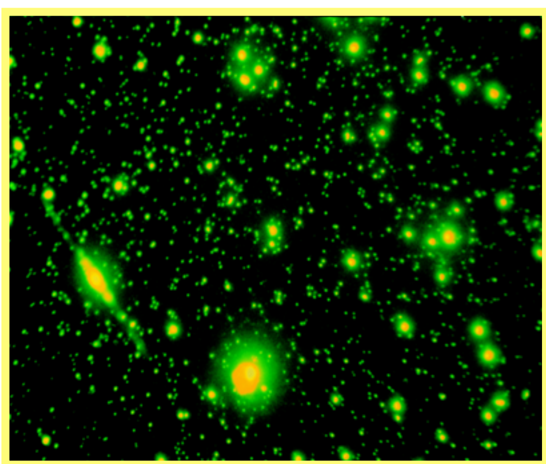


Virus 1 control cells

Virus 2 control cells

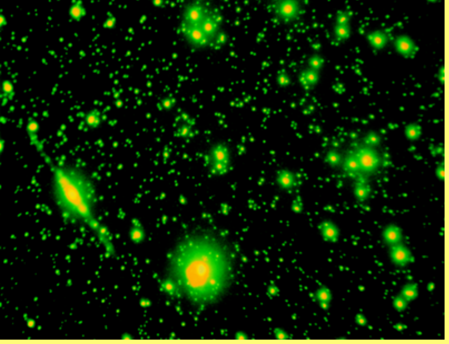


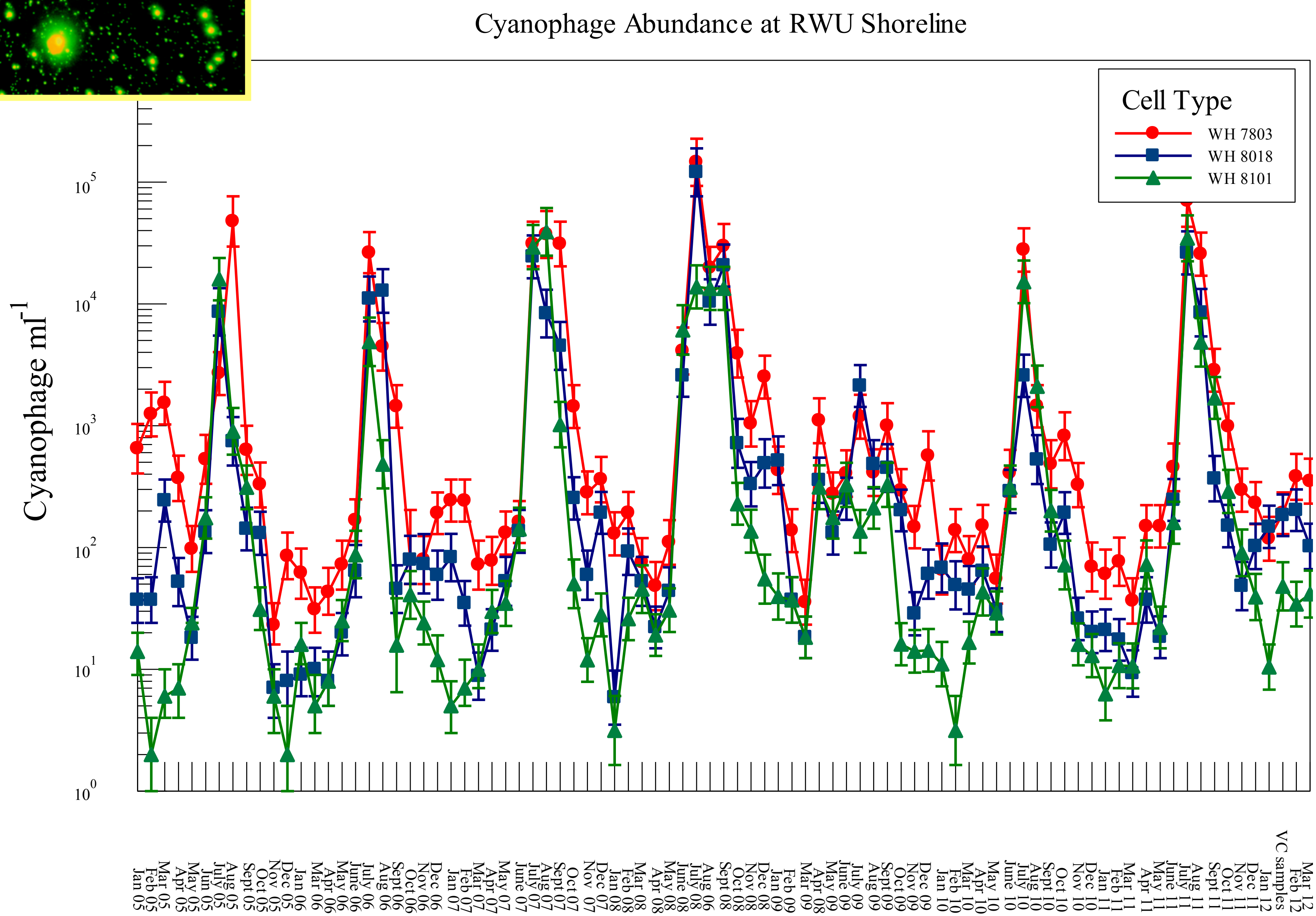
The Secret Lives of Marine Viruses



Furhman 1999 Nature

1. How many different types of marine cyanophages are there?
2. What is the biogeography of marine cyanophages?
3. How much genomic diversity is present in natural populations of cyanophages?
4. How do cyanophages evolve and coexist with their hosts?





Cyanophage Abundance at RWU Shoreline
Cyanophage ml^{-1}
10^0
10^1
10^2
10^3
10^4
10^5
Cell Type
WH 7803
WH 8018
WH 8101
Jan 05
Feb 05
Mar 05
Apr 05
May 05
Jun 05
July 05
Aug 05
Sept 05
Oct 05
Nov 05
Dec 05
Jan 06
Mar 06
Apr 06
May 06
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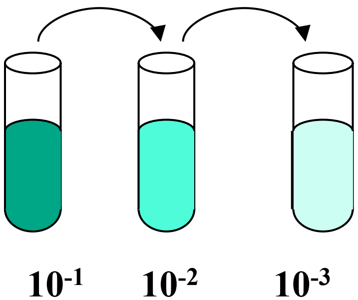
Dec 10
Jan 11
Feb 11
Mar 11
Apr 11
May 11
June 11
July 11
Aug 11
Sept 11
Oct 11
Nov 11
Dec 11
Jan 12
VC samples
Feb 12
Mar 12

Cyanophage Isolation

1. Collect surface seawater

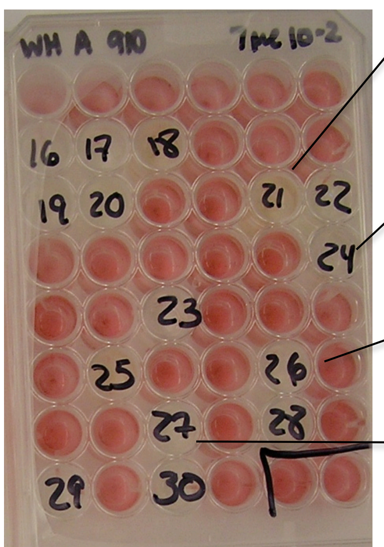
2. Seawater dilutions

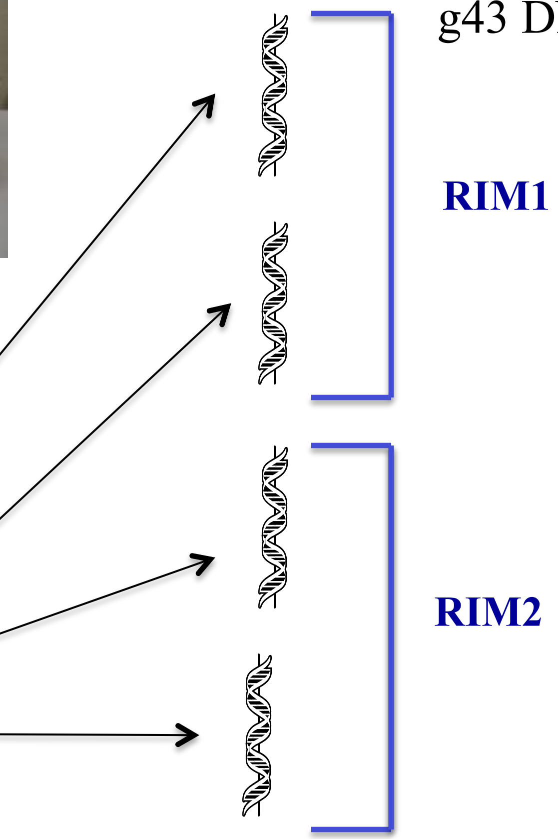


+

3. Extinction dilution plates

Clear wells indicate viral lysis

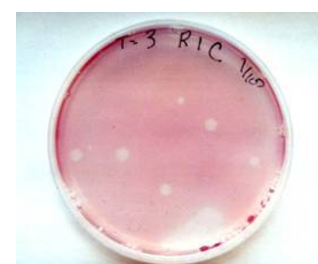




4. Polymerase Chain Reaction & DNA Sequencing

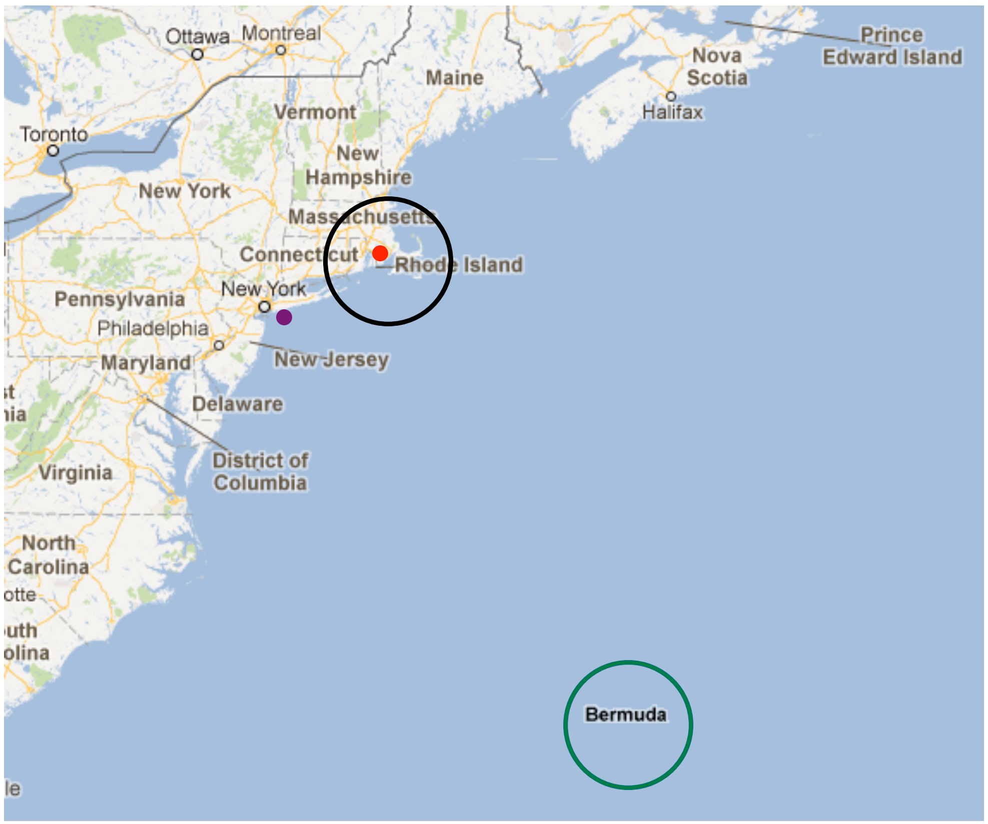
g43 DNA polymerase gene

5. Plaque-purify for host range tests, experimental evolution and genome sequencing



Biogeography

What are the local and regional spatial and temporal patterns of cyanophage community composition?



Marston *et al* 2013

Cyanophage communities analyzed over different temporal and spatial scales.

~3,000 viral isolates genotyped

● **1 site RW: 800 isolates**
41 samples over 6 years

○ **9 sites SNE: 1726 isolates**
7 samples over 15 months

● **1 site Long Island: 102 isolates**
7 samples over 13 months

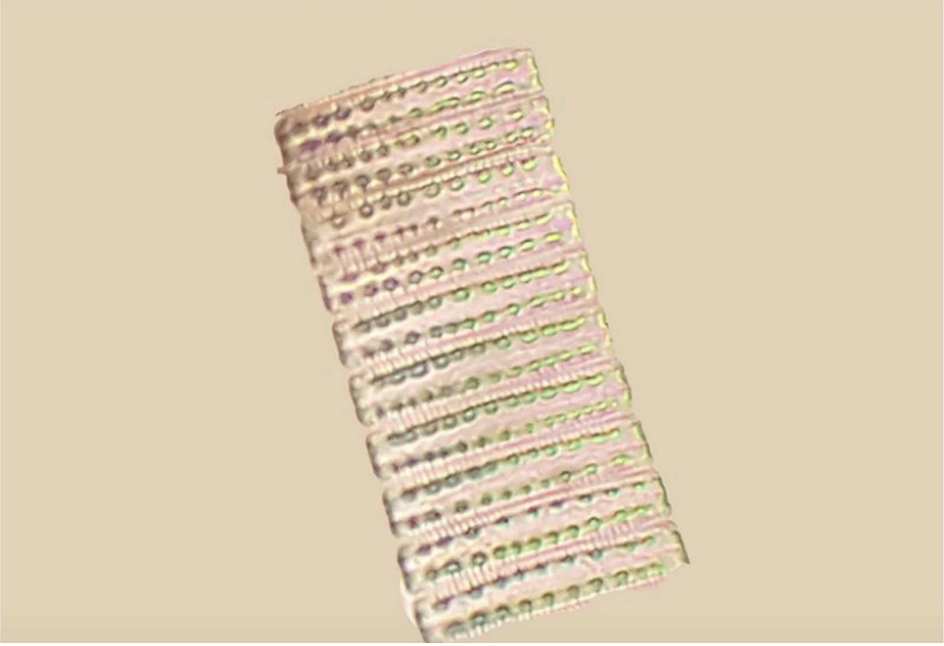
○ **12 sites Bermuda: 488 isolates**
6 samples over 22 months

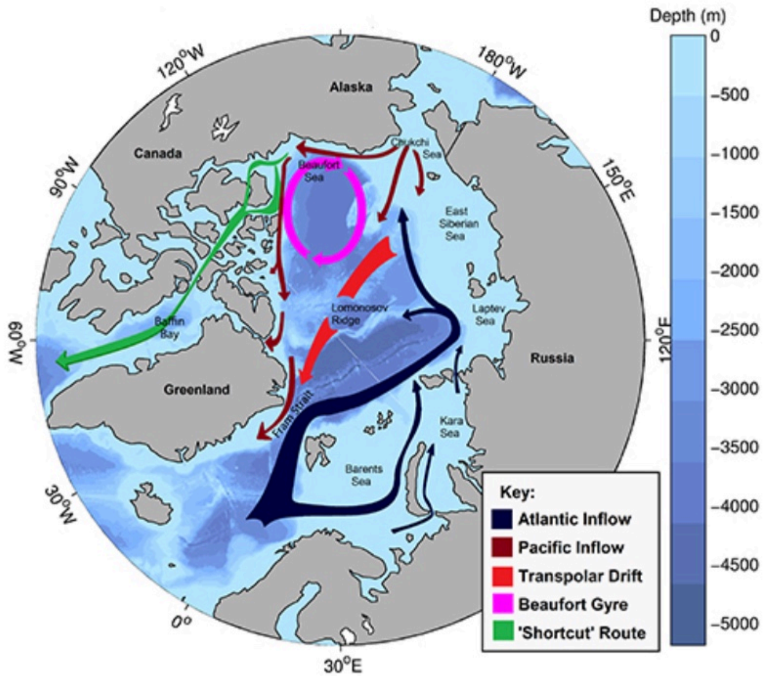
OCEAN SCIENCES

News

New Paths for Plankton in Warming Arctic?

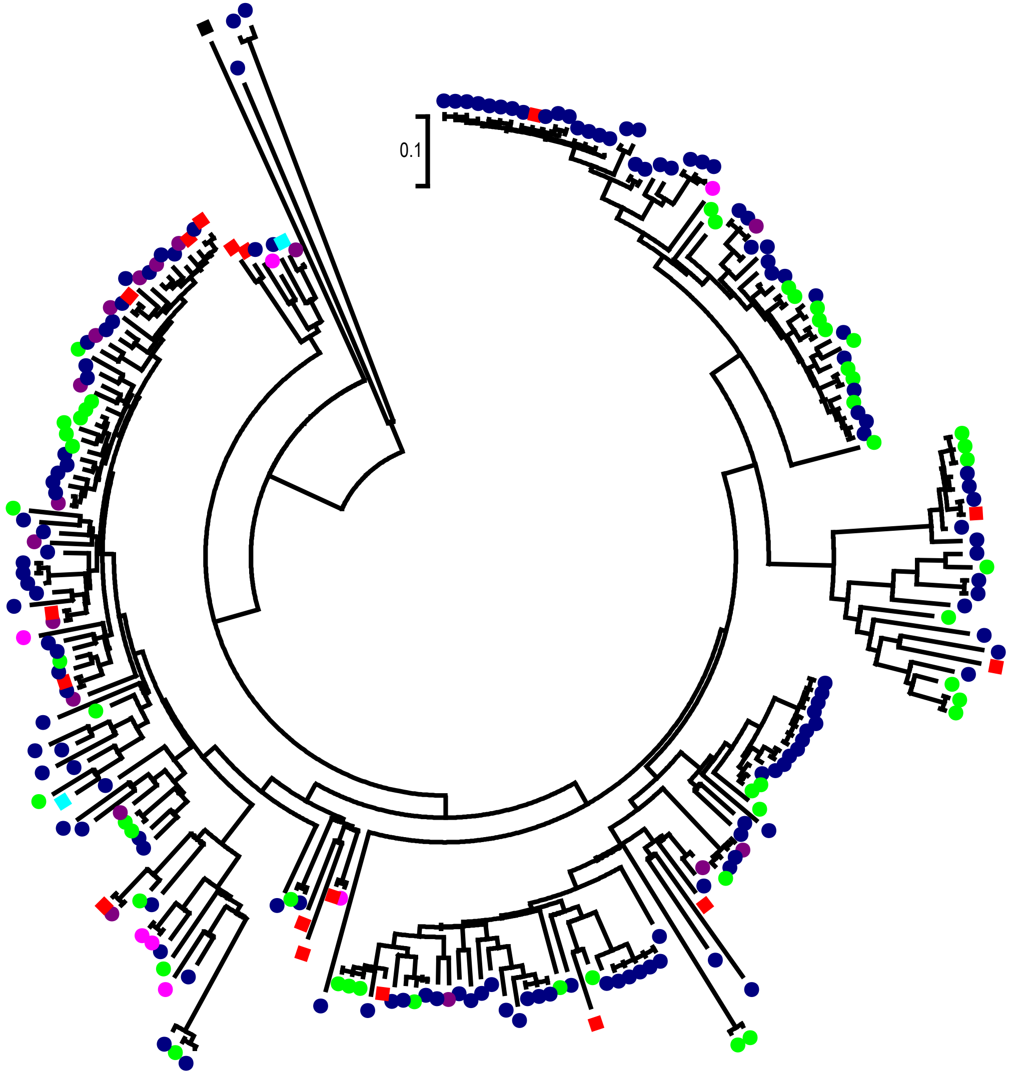
Water flowing from the Pacific to the Atlantic could find new shortcuts, enabling plankton to survive the trip through the cold polar region.





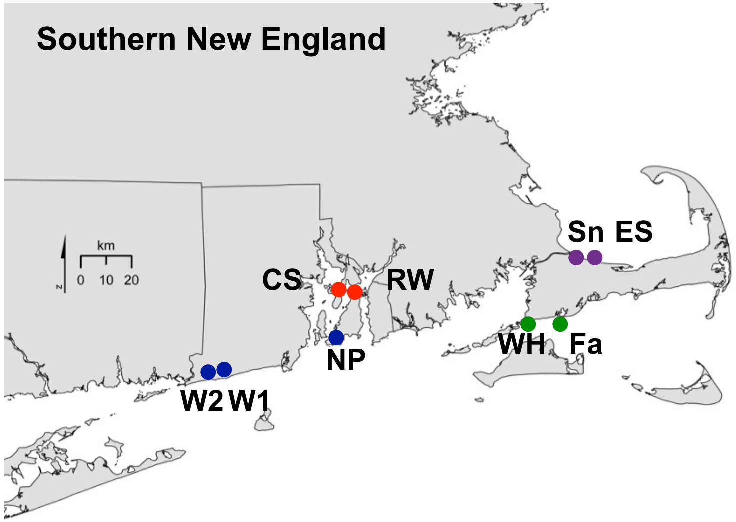
Currents in the Arctic Ocean provide net transport from the Pacific into the Atlantic. Pacific water (red brown) usually follows three pathways but sometimes, according to model calculations, takes a shortcut through the Canadian Arctic Archipelago (green). Shown also are the Beaufort Gyre (magenta) and the Atlantic inflow (dark blue). The Transpolar Drift Stream (orange) exits, together with some water from the Pacific, through the Fram Strait off northeastern Greenland. A portion of the Atlantic inflow enters the Arctic Ocean through the same passageway but farther to the east. Credit: Stephen Kelly, University of Southampton

Cyanophages are genetically diverse

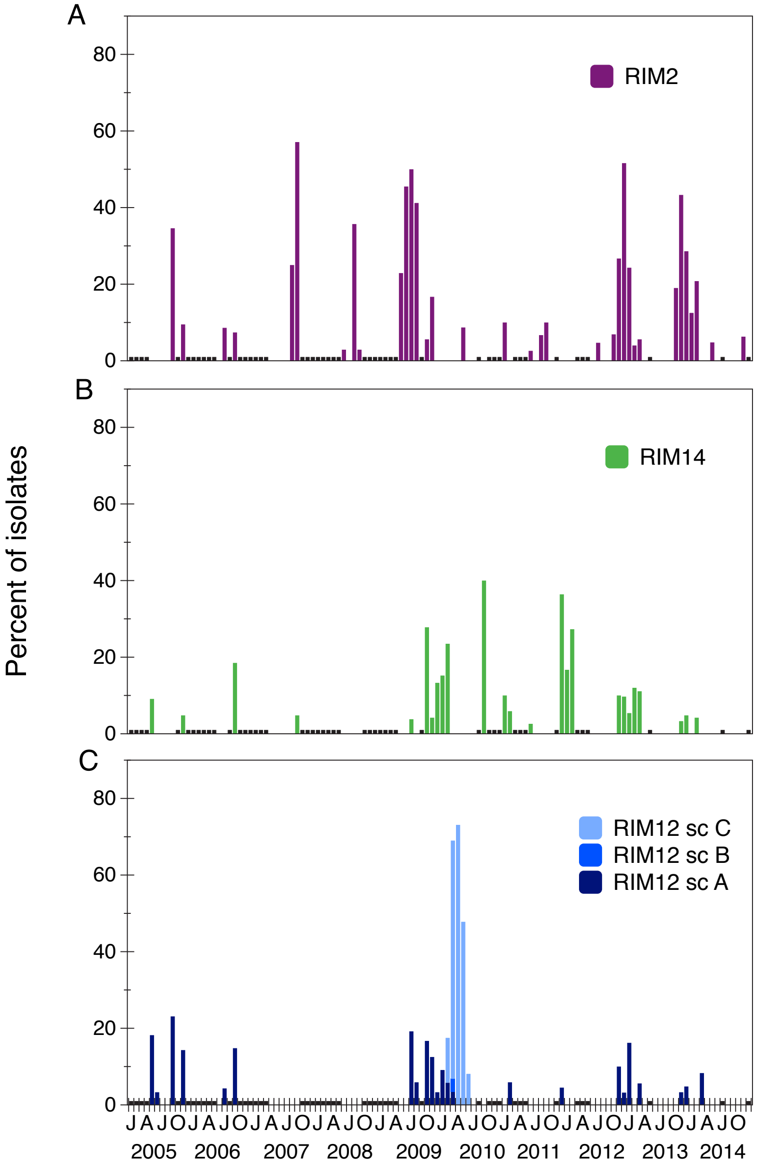


218 different g43 genotypes were identified.

Amino acid neighbor-joining tree of 218 genotypes and 18 sequenced cyanophages based on g43 DNA polymerase gene



Longer Temporal Patterns of Abundance

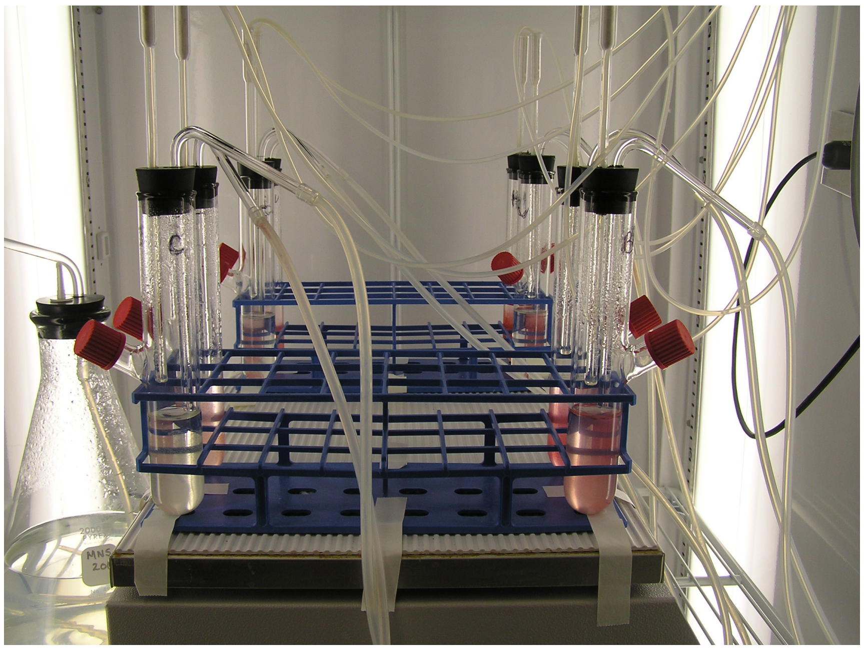


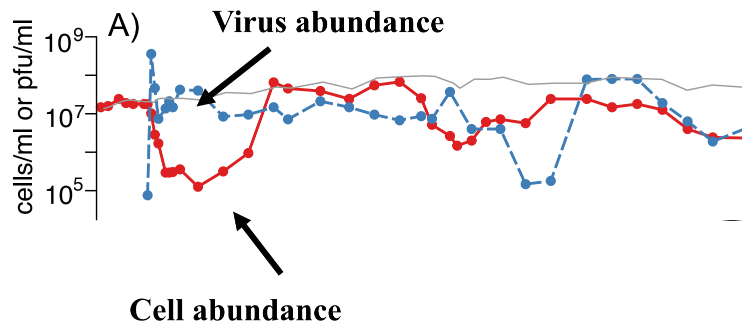
Individual virus types can be isolated year after year and exhibit seasonal patterns of abundance

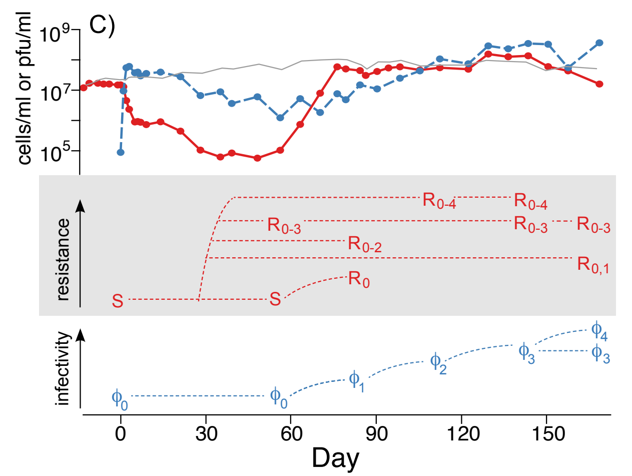
Marston *et al* 2013

Evolution of Viral – Host Interactions: An experimental approach

What are the genes involved in viral-host interactions?



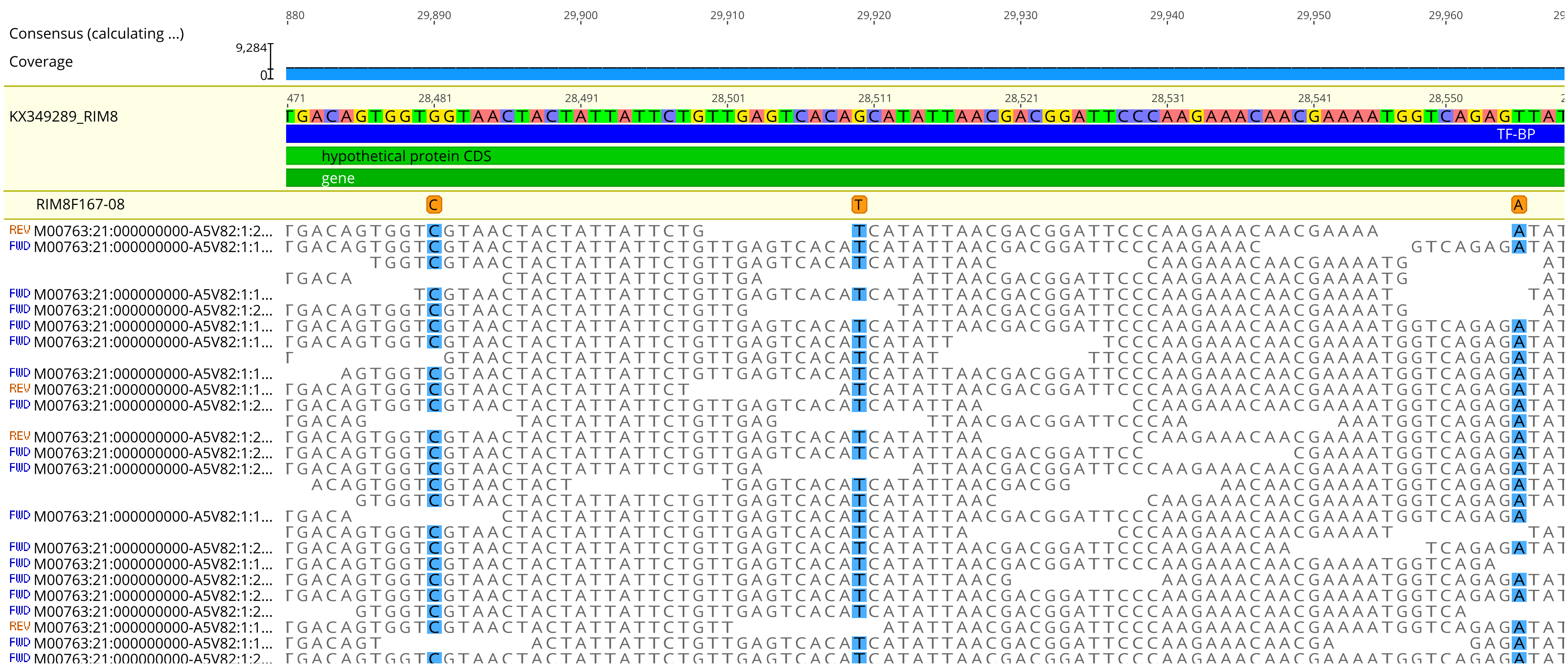




RIM8 and Synechococcus WH7803

Marston et al 2012 PNAS

Next-Gen Sequencing of evolved genomes and then map the reads back to the ancestral genomes to look for SNPs or Indels.



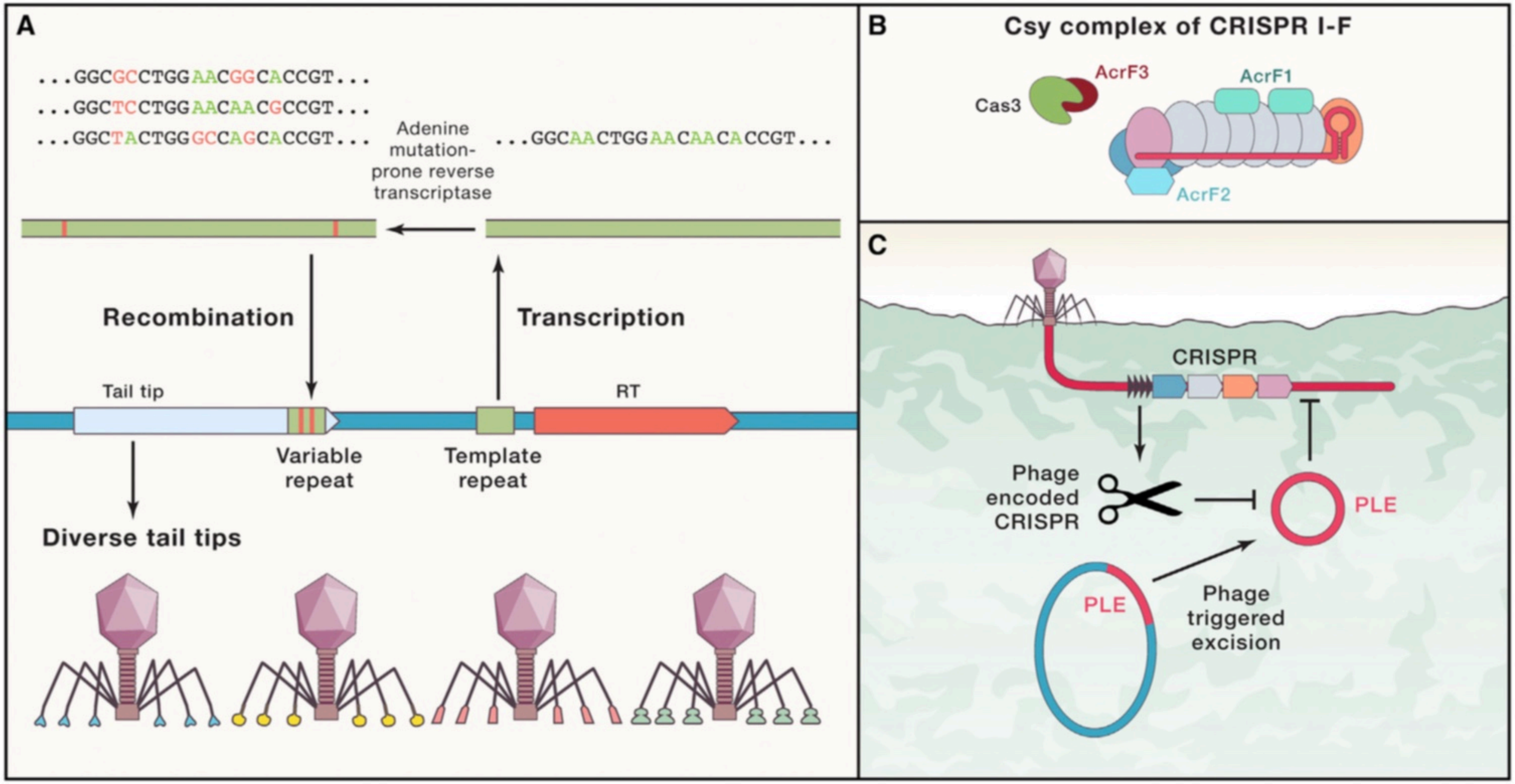


Figure 3. Mechanisms of Phage Escape from Bacterial Defenses

(A) Diversity-generating retroelements (DGRs) diversify phage tail tips. The template repeat is transcribed and then reverse-transcribed by a phage-encoded error-prone reverse transcriptase (RT) that converts adenines into random nucleotides. The cDNA is then recombined with the C terminus of the gene encoding the tail-tip, generating a population of phages that can encode an extremely diverse repertoire of tail tips.

(B) Anti-CRISPR proteins can target various components of the CRISPR machinery.

(C) Phage-encoded CRISPR targets a chromosomal island in *Vibrio cholerae* that excises upon phage infection and interferes with the phage-replication process.

Ofir and Sorek, 2018 Cell