Viral ecology

Lecture 23
Biology 4310
Virology
Spring 2020

All have their worth and each contributes to the worth of the others
J.R.R. Tolkien
November 17-20, 2019

4th Ringberg Symposium on Giant Virus Biology
Ringberg Castle, Tegernsee, Germany

- Scientific Program -

Sunday, November 17
15:00 Arrival, Coffee & Cake
16:00 Welcoming Remarks
16:15 - 17:15: Alexandra Warden
GEOBARR, Kiel, Germany
A Sea of Giant Viruses
17:30 - 20:00 Poster Session
with Sandwiches & Beverages

Monday, November 18
08:00 - 09:00 Breakfast

Diversity of Giant Viruses
Chair: TBA
09:00 - 09:30: Ruth-Anne Sandaa
University of Bergen, Norway
Diversity of Giant Viruses Infection
Haptoptyles
09:30 - 10:00: Grgur Steward & Chris Schwarz
University of Hawaii Manoa, USA
Comparative Genomics of Floroviricella viruses
10:00 - 10:15: Keiko Nagasaki
Kochi University, Japan
NCLDVs of Deinogemadites and Raphidophytes
10:15 - 10:30 Coffee Break

Structure of Giant Virus Particles
Chair: Dennis Banfield with short intro
10:45 - 11:10: Choon Kao
University of Texas at El Paso, USA
In Memoriam Michael Hossmann
11:00 - 11:30: Thomas Klose
Purdue University, USA
High-resolution Structures of Large dsDNA Viruses and What We Can Learn From Them
11:30-12:00: Steven Wilhelm
University of Tennessee, USA
The Proteome and Structure of the Adder Particle: a Virus With a Sweet Tooth

Monday, November 18 - continued
12:00 - 12:30: Jim Van Etten
University of Nebraska, USA
Chloroviruses Encode Many Glycogen Transferases
12:30 Lunch

Genetics and Cell Biology
Chair: TBA
14:30 - 15:00: Jean-Michel Cazier
IGS Aix-Marseille University, France
A Spectacular Anomaly in the Known Composition of the Giant Pandoravirinae Genomes
14:30 - 14:45: Matthieu Legrand
IGS Aix-Marseille University, France
The Metaphylogeny Landscape of the Pandoravirinae
14:45 - 15:00: Motohiro Akashi
Tokyo University of Science, Japan
DNA Replication, Repair, and Evolution of a Giant Virus
15:00 - 15:15: Rodrigo Rodrigues
Federal University of Ouro Preto, Brazil
Stages suggest a complex evolutionary history of ephemeral mammana
Vertebrates Circumventing Faustovirus Transmission Dissemination by Enclosing Viral Progeny Inside Cysts
15:15 - 15:45 Coffee Break

Host-Virus (Virophage) Interactions
Chair: TBA
15:45 - 16:00: Steven Short
University of Toronto Mississauga, Canada
Distributions of Giant Viruses and Their Stooges Suggest a Complex Ecology
16:00 - 16:30: Chantal Abergel
IGS Aix-Marseille University, France
Propulsion of the Progeny of Transvirus Within Mimivirus Reveals a Unique Example of Commensalism in the Viral World

Monday, November 18 - continued
16:30 - 17:00: Matthias Fischer
Max Planck Institute for Medical Research, Germany
Endogenous Virophages Populate the Genomes of Caulobacteriobacteria
17:00 - 17:30: Assaf Vardi
Weizmann Institute of Science, Israel
Inducibility in Host-Virus Interactions in the Ocean
17:30 Guided Tour of Ringberg Castle
18:30 Dinner

20:00 Podcast Recording
"This Week in Virology"
With Vincent Racaniello, Rich Condit, Nils Elie & Guests

Tuesday, November 19
08:00 - 09:00 Breakfast

Evolution of Nucleocytoplasmic Large DNA Viruses
Chair: Curtis Stuttle
09:00 - 09:30: Rich Condit
University of Florida, USA
Poxviruses: A Window on the World of NCLDVs
09:30 - 10:00: Nils Elie
University of Utah, USA
Post Evolution: A Big Virus Among Giants
10:00 - 10:15: Natacha Yulin
National Institutes of Health, USA
Comparative genomics of fish mimiviruses provides insights into animal host adaptation
10:15 - 10:45 Coffee Break
10:45 - 11:00 Morgan Gaia
Institut Pasteur, France
The Co-evolution of NCLDV Core Genes
11:00 - 11:30 Eugene Koszin
National Institutes of Health, USA
Does Every Family of NCLD Include Both Giant and Dwarf Viruses?
11:30 - 12:00: Mart Krupovic
Institut Pasteur, France
Chimeric Scenario for the Origin of Viruses

Tuesday, November 19 - continued
12:00 - 12:15: Curtis Stuttle
University of British Columbia, Vancouver, Canada
Viruses - Unlocking Secrets of the Most Abundant "Life" on Earth
12:30 Lunch
Free Afternoon (Hiking, Discussions, Sports, etc.)
16:00 - 16:30: Coffee Break

Metagenomics, Isolation & Ecology
Chair: TBA
16:30 - 17:00 Frederik Schulz
Joint Genome Institute, USA
Global Diversity of the Megaviruses as Determined by Metagenomic Analysis
17:00 - 17:15: Bernard La Scala
IMU Aix-Marseille University, France
Running After Metagenomics: New Strategies and New Tools to Discover and Study New Giant Viruses
17:15 - 17:30: Hiro Ogata
Kyo University, Japan
Global Genetic Data Reveal Lineages of Giant Viruses and Other Eukaryotic Viruses Associated With Carbon Export Efficiency
17:30 - 18:00: Philippe Colson
IMU Aix-Marseille University, France
The Significance of Giant Viruses in Humans
18:00 - 18:30: Lutz Becker
University of California, Germany
The Molecular Evolution of Eco-Evolutionary Dynamics in a Coevolving Host-Virus System
18:30 Conference Dinner

20:00 Open Mic (Music Room)

Wednesday, November 20
08:00-09:00 Breakfast

Biochemistry
Chair: TBA
09:00 - 09:30: Gerhard Thiel
Technical University Darmstadt, Germany
Viral Membrane Transport Proteins: They are Everywhere

Virology Lectures 2020 • Prof. Vincent Racaniello • Columbia University
THIS WEEK IN VIROLOGY

#575 ENDLESS GIANT VIRUS FORMS MOST BEAUTIFUL
Ecology

- A study of the relationships of organisms to each other and to their environment
- Microecology - the interaction of viruses within their hosts
- Macroecology
  - Ecological disruptions that lead to zoonotic spillover
  - Global effects of viruses
Ecology and emerging viruses

- Disruption or invasion of ecological niches can lead to cross-species transmission
- Origins of every human virus, and zoonotic viruses, can be traced to such invasions and disruptions
- Measles virus, Ebolavirus, Nipah virus, SARS-CoV
The Phytobiome

Not only plant viruses, but the viruses of everything that interacts with plants, including other microbes, insects and other invertebrates, other plants and herbivorous animals
Virus-host symbioses

- **Antagonistic:** Tomato bushy stunt virus infection of eggplants
- **Commensal:** Viruses with no apparent impact
- **Conditionally mutualistic:** Virus induces formation of winged morph of rosy apple aphid, smaller and less fecund but able to move to a new plant when crowding occurs
- **Mutualistic:** Phage infection of Vibrio cholera causes toxin production and invasion of host gut
- **Symbiogenic:** Exaption of retroviral gene to form placenta
Beneficial viruses

Many viruses confer drought tolerance to plants.
Factors leading to Nipah virus emergence

• First outbreak Malaysia 1998
• Reservoir: Fruit bats (*Pteropus vampyrus*)
• 1970s-1990s Deforestation for pulpwood and industrial plantations reduced fruit bat habitat
• Haze from slash-and-burn blanketed much of Southeast Asia in months before outbreak
• Exacerbated by drought driven bit severe 1997-98 El Niño Southern Oscillation
• Acute reduction in availability of flowering and fruiting forest trees for foraging flying foxes
• Encroachment of flying foxes into cultivated fruit orchards
• Location of open piggeries in fruit orchards
Web of Nipah virus emergence

Natural Reservoir Hosts of Nipah Virus

- *P. vampyrus*
- Deforestation
- Wildlife Habitat
- Food Supply
- Migration
- Pattern of pig and orchard farming
- Pigs
- Humans
- Anthropogenic forest fires
- Haze
- Drought
- El Niño
Ecology of Nipah virus spillovers
Argentine hemorrhagic fever, Junin virus

- Use of herbicides to convert the Argentine pampa to land for growth of maize
- Weeds controlled with herbicides to allow growth of maize
- A new shade-tolerant grass grew in shadow of maize
- This grass led to emergence of new dominant mouse, *Calomys musculinus*, reservoir of Junin virus
- Argentine hemorrhagic fever first described in 1953, virus isolated 1958
The number of viruses on Earth is staggering.

More than $10^{30}$ bacteriophage particles in the world’s waters!

- A bacteriophage particle weighs about a femtogram ($10^{-15}$ grams)

\[ 10^{30} \times 10^{-15} = \text{the biomass on the planet of BACTERIAL VIRUSES ALONE exceeds the biomass of elephants by more than 1000-fold!} \]

- The length of a head to tail line of $10^{30}$ phages is 100 million light years!
Viruses are not just purveyors of bad news

More viruses in a liter of coastal seawater than people on Earth

Biomass

Abundance

94%

Prokaryotes
Protists
Viruses

doi:10.1038/nrmicro1750
Viruses in seawater - $10^7$ viruses per ml

Seawater: 0.2 micron filtered, stained with SYBR Green

Bacteriophage T7
Table 1 Sample estimates for virus-like particles (VLP) and bacterial abundances in selected freshwater systems

<table>
<thead>
<tr>
<th>Lake</th>
<th>Environment</th>
<th>VLP ($\times 10^{10}$ L$^{-1}$)</th>
<th>Bacteria ($\times 10^9$ L$^{-1}$)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lake Pfaffsee, Germany</td>
<td>Epilimnion</td>
<td>1.37</td>
<td>4.6</td>
<td>Weinbauer &amp; Hofle (1998b)</td>
</tr>
<tr>
<td></td>
<td>Metalimnion</td>
<td>4.3</td>
<td>7.7</td>
<td></td>
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<tr>
<td></td>
<td>Hypolimnion</td>
<td>2.8</td>
<td>5.8</td>
<td></td>
</tr>
<tr>
<td>Lake Constance, Germany</td>
<td>1–4</td>
<td>0.5–4.0</td>
<td></td>
<td>Hennes &amp; Simon (1995)</td>
</tr>
<tr>
<td>Sproat Lake, BC, Canada</td>
<td>Epilimnion (summer)</td>
<td>c. 0.15–0.2</td>
<td>1–1.5</td>
<td>Klut &amp; Stockner (1990)</td>
</tr>
<tr>
<td></td>
<td>Epilimnion (winter)</td>
<td>0.06</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lake Superior</td>
<td>Surface microlayer</td>
<td>0.07–0.92</td>
<td>1.7–18.3</td>
<td>Tapper &amp; Hicks (1998)</td>
</tr>
<tr>
<td></td>
<td>Subsurface, 20m</td>
<td>0.02–0.09</td>
<td>1.2–4.6</td>
<td></td>
</tr>
<tr>
<td>Lake Ontario</td>
<td>Eastern basin</td>
<td>17.7</td>
<td>13.8</td>
<td>Gouvêa et al. (2006)</td>
</tr>
<tr>
<td></td>
<td>Central basin</td>
<td>10.0</td>
<td>6.5</td>
<td>DeBruyn et al. (2004)</td>
</tr>
<tr>
<td></td>
<td>Western basin</td>
<td>11.6</td>
<td>3.7</td>
<td></td>
</tr>
<tr>
<td>Lake Erie, 2002</td>
<td>Western basin</td>
<td>0.1–3.4</td>
<td>1.4–5.1</td>
<td>Leff et al. (1999)</td>
</tr>
<tr>
<td>Lake Erie, 1997</td>
<td>Western basin</td>
<td>14–190</td>
<td>1–12</td>
<td>Brum et al. (2005)</td>
</tr>
<tr>
<td>Mono Lake, CA</td>
<td></td>
<td>14–190</td>
<td>1–12</td>
<td></td>
</tr>
<tr>
<td>Several Antarctic lakes</td>
<td></td>
<td>0.4–3.4</td>
<td>NA</td>
<td>Kerper et al. (1998)</td>
</tr>
<tr>
<td>Lake Bourget, France</td>
<td></td>
<td>5.8–26</td>
<td>0.03–0.28</td>
<td>Dorigo et al. (2004)</td>
</tr>
<tr>
<td>Lake Erken, Sweden</td>
<td>Epilimnion</td>
<td>12–37</td>
<td>1.6–8.5</td>
<td>Lymer et al. (2008)</td>
</tr>
<tr>
<td>Lake Fyrsjön, Sweden</td>
<td>Epilimnion</td>
<td>18–29</td>
<td>3.5–6.9</td>
<td></td>
</tr>
<tr>
<td>Lake Klocktjön, Sweden</td>
<td>Epilimnion</td>
<td>5–6</td>
<td>0.5–2.0</td>
<td></td>
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<tr>
<td></td>
<td>Pelagic zone</td>
<td>7.2 / 32</td>
<td>134</td>
<td>Bettarel et al. (2006)</td>
</tr>
<tr>
<td></td>
<td>Benthic zone</td>
<td>56.2 / 15.3</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>Djoudj Pond, Senegal*</td>
<td>Pelagic zone</td>
<td>3.9 / 2.5</td>
<td>5.3</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Benthic zone</td>
<td>55.9 / ND</td>
<td>219.3</td>
<td></td>
</tr>
<tr>
<td>Lake Guiers, Senegal*</td>
<td>Pelagic zone</td>
<td>0.89–12.0</td>
<td>7.7–8.5</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Benthic zone</td>
<td>0.02–0.16</td>
<td>0.1–0.2</td>
<td></td>
</tr>
<tr>
<td>Lake Ganzirri, Italy*</td>
<td>Whole water column†</td>
<td>0.005–0.754</td>
<td>0.06–30.9</td>
<td>Vanucci et al. (2005)</td>
</tr>
<tr>
<td>Antarctic lakes</td>
<td>Ultra-oligotrophic lakes</td>
<td>0.89–12.0</td>
<td>c. 0.5–2.0</td>
<td>Madan et al. (2005)</td>
</tr>
</tbody>
</table>

NA, not available.

*Viruses were enumerated by both epifluorescence microscopy and TEM.

†Brackish system, 21–37 practical saline units.

‡Three lakes ranging from brackish to saline.

§Density is given for picocyanobacteria only.
What do aquatic viruses do?

• Most viruses thought to infect heterotrophic bacteria

• Also abundant viruses infecting cyanobacteria

• Some viruses infect eukaryotic phytoplankton and can collapse large blooms
Emiliania huxleyi

- Single-cell coccolithophore (photosynthetic plankton) found in all oceans
- One of many parts of marine food web
- Forms extensive blooms in nutrient-depleted waters after reformation of summer thermocline
- Covered with calcite disks
- Important source of calcium carbonate and dimethyl sulfide (cloud formation)
Emiliania huxleyi virus 86, a coccolithovirus

Linear, dsDNA genome of 410-415 kb encoding ~472 proteins
Nucleo-cytoplasmic replication (NCLDV)
Viruses are catalysts for biogeochemical cycling

Viral shunt
Viruses catalyze the movement of nutrients from organisms to the DOM and POM pools
Viruses can affect the efficiency of the biological pump

*In oceans: ~10^{29} virus infections d^{-1}, destroying 20-40% of marine bacteria and releasing 10^8-10^9 tonnes of Carbon*
Metagenomics to study ocean viruses

The TARA Oceans Expedition 2009–2013
Rethinking the tradition of the great expeditions of the 18th Century, Tara sailed the world oceans for three and a half years. For the first time, seawater plankton in its entirety was collected and studied - from viruses and bacteria to the large and majestic.

Why this expedition?

TARA explored the climate and atmosphere of our planet. Phytoplankton produce half of the oxygen generated globally each year by photosynthesis, and absorb atmospheric CO₂. Affected by pollution, overfishing, and climate change, phytoplankton are increasingly under threat. Metagenomics helps us understand these threats and develop solutions.

New techniques allow us to collect DNA directly from seawater and analyze it.

Three methods of collection and observation:

- Nets
  Tara deployed 7 types of nets (mesh sizes range from 10 to 400 microns). The nets are hoisted from the surfaced to 1000 metres depth. The sampled DNA is extracted and re-sequenced on the mothership.
- Phytoplankton pump
  This pump is inserted at a depth of 10 to 120 metres, then powered through a series of strainers and filters to collect phytoplankton. An important change in seawater pH is monitored.
- Core Russian
  These are privileged places for specific phytoplankton, but they are suffering from climate change. Tara searched for the ideal platform for studying phytoplankton and its role in global equilibria.

Three concentrations of high tech:

- A unique array for microscopic imaging
  Set up aboard Tara - the dry lab - where researchers characterize the organisms collected, their functional diversity, and their complexity.
- Niskin bottle
  Some of the largest ecosystems on Earth are deep and difficult to access. Tara used Niskin bottles to collect samples from different depths.
- The FlowCam
  The FlowCam is a filter-free, high speed, 4K camera that allows to sample and identify marine organisms as they pass through the filter.

Overview of the samples

- In open ocean
  To study viruses,
  - Tara used several methods to collect samples from the open ocean.
  - Viruses are collected and sequenced directly from seawater.
  - Viral communities are studied from different depths using the FlowCam.

Scientific results

Based on the data from Tara Oceans, many scientific articles describing the phytoplankton communities of the open ocean have been published, or are on the way to being published.

Enjoy a snapshot of this data thanks to the Oceanscope project* which has established a database of ocean communities and set up a platform for publishing and following the evolution of these communities in relation to climate change.

*Oceanscope is a long-term effort to develop a public database of ocean diversity. It is a collaborative effort among the Tara Oceans partners to make the Tara Oceans data available to the scientific community.
Ruler of the seas - Where is the Carbon?

Total Carbon - $10^6$ tonnes

Whales
4.1 - 12

Bacteria
2740 - 27400

Viruses
27 - 270
This heat map displays the relative abundance of each virus population (y axis) in each sample (x axis). Relative abundance of one population in a sample is based on recruitment of reads to the population reference contig and is only considered if more than 75% of the reference contig is covered.

Longhurst provinces are indicated below samples and are outlined in black on the heat map.
Viruses not only shape activity, they shape potential

Horizontal gene transfer: although the true ecological extent remains unknown, it is thought that viruses move genes between related (and unrelated) hosts.

- Are these movements important?
- Can we observe one in progress?
- Can viruses utilize these other genes?
A giant virus infecting green algae encodes key fermentation genes

Christopher R. Schvarcz, Grieg F. Steward*

Department of Oceanography, Daniel K. Inouye Center for Microbial Oceanography: Research and Education, University of Hawai’i at Mānoa, 1950 East-West Road, Honolulu, HI 96822, United States

Giant ChoanoVirus encodes rhodopsin photosystem
ChoanoVirus
ViR in the oceans

TARA Oceans Data

VirR or Mimiviridae PolB per predicted assembled protein (x 10^5)

Depth (m)

Photosynthetically active radiation (μMol^1m^2s^1)

VirR read recruitment (normalized and divided by 10^2)

Deep Chlorophyll Maximum (DCM)
Aureococcus anophagefferens

- Alga responsible for NY/NJ brown tides
- In mid-Atlantic US estuaries since 1985
- Detrimental to bivalve populations
- Detrimental to beds of Zostera marina (eelgrass)
- $50 million losses annually
Of course there is an *Aureococcus* virus
Aureococcus anophagefferens virus

- Giant virus, isolated during a brown tide bloom
- Likely regulates blooms
- Has acquired genes from a variety of cellular sources
Paramecium bursaria chlorella virus

- Large icosahedral dsDNA viruses (331 kb)
- Worldwide in fresh waters
- Chlorella hosts is a symbiont of protozoan Paramecium bursaria
How does chlorella virus infect its host?

*Virus particles are excluded from Paramecium*
Virus Ecology - we have barely scratched the surface

• Just a sampling of interactions among viruses, hosts, and their environments

• A growing field with the addition of metagenomics, needs a transition to experimental science

• Plants and their viruses

• Unicellular inhabitants of oceans, fresh water, land environments

• How mutualism function
Next time: HIV and AIDS