

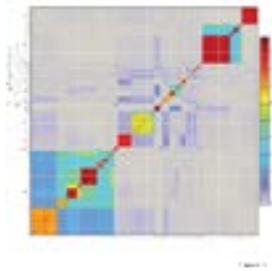


Graham F. Hatfull  
Lead Scientist

Welcome to Message in a Bottle! Although the spring semester may be winding down for many, we can see from the symposium abstracts that this has been a very busy and productive year. We are excited to hear all about it at the symposium, and to share our plans and aspirations for the coming SEA-PHAGES year. It is an especial delight to see the *eLife* paper emerge from a somewhat complex manuscript preparation, submission, review, and production process. But it is a real landmark publication and we extend a big thank you to everyone for helpful input at every step of the process. The broad genomic analyses described in the paper have also facilitated constructive consideration of how the sci-

ence should progress in the next few years. I think it is evident that as exciting as the analysis is, that claiming even a slight scratch on the surface of viral diversity would be an optimistic description. So what's next? Clearly, we need to keep clawing away at phage genomics, and continue the process that we've already started to discover and characterize phages of additional – but phylogenetically-proximal – hosts. We've not met a phage that we didn't like, but we look forward to the exploration and genomics of Actinomycetales phages as being the primary scientific focus of the SEA-PHAGES community over the next few years. We predict it will be an especially rich seam of viral diversity in which to explore.

### A CONTINUUM OF DIVERSITY



We are excited at the publication of the paper “Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity” in the open access online journal *eLife*. The 627 phages analyzed in this collection were isolated and annotated by 2644 students at 81 institutions, and in addition to the scientific insights, supports the effectiveness of the SEA-PHAGES program as an authentic research experience for early-career undergraduate students. With a grand total of 2,863 authors, it is one of the most highly-authored

papers ever, and it must be a record for the number of undergraduate authors on a single paper! We've not yet caught up with the current division leader (the Higgs-Boson report has about 6,000 authors) but it's nice to be in such distinguished company. Congratulations to everyone.

### NEW ACTINOMYCETES HOSTS FOR FALL 2015



Now that we've examined the whole genome sequences of 627 mycobacteriophages, what next? We will continue to isolate and sequence *Mycobacterium smegmatis* phages, but will also move towards the use of other hosts within the phylum Actinobacteria for phage isolation. In addition to the *Arthrobacter* and *Rhodococcus* strains already in use by some schools, we are looking forward to distributing new strains of *Dietzia*, *Gordonia*, *Rhodococcus*, *Mycobacterium*, *Nocardia*, *Tsukamurella*, *Corynebacterium* and others. Exploring this segment of viral diversity-space will

be the signature focus of SEA-PHAGES in the next few years, and evaluating these strains will require a community effort. We look forward to further discussions at the symposium.

### IMPORTANT DATES

- **May 15, 2015**  
Final genome annotations due. See [phagesdb.org](http://phagesdb.org) for protocols
- **June 12-14, 2015**  
Annual Symposium at JRC
- **June 15-17, 2015**  
Advanced In Silico Workshop at HHMI HQ
- **June 21-27, 2015**  
In situ workshop A at UMBC
- **July 12-18, 2015**  
In situ workshop B at UMBC
- More at [seaphages.org](http://seaphages.org)

### Did you know?

#### Temperate vs. lysogenic

A common error in phage-related vocabulary is to use the phrase “lysogenic” to indicate that a phage is capable of establishing itself harmlessly in the cell as well as undergoing lytic growth. Such cells are “lysogens” and the dormant phage genome is a “prophage”. However, phages with this ability are called “temperate” phages, not “lysogenic” phages.

Lysogeny is maintained by a repressor, but the prophage may be either integrated site-specifically into the host chromosome, or can replicate autonomously extrachromosomally --similar to a large plasmid --and use a plasmid partitioning system to prevent prophage loss during cell division.

## 2015 SEA-PHAGES SYMPOSIUM



We are looking forward to the 2015 Annual SEA-PHAGES Symposium at the Janelia Research Campus (June 12-14th), and are delighted that **Eric Betzig** will be our keynote speaker on Friday evening. Eric shared the Nobel prize for **Chemistry** in 2014 for the development of super-resolved fluorescence microscopy and is a Group Leader at the Janelia Research Campus. This year will also feature student moderators for the scientific sessions, and student introducers for Drs. Betzig and Hatfull. Thanks to all the faculty members who submitted nominations for these positions. We will also hear from some of our SEA-PHAGES faculty members in a session highlighting their research. Photo: <http://janelia.org/people/scientist/eric-betzig>

## 2015 SEA-PHAGES ASSESSMENT WORKSHOP



The first SEA-PHAGES assessment workshop was held at HHMI HQ in March 2015. Led by Dr. David Hanauer, 15 SEA-PHAGES faculty members met to review and improve assessment tools they developed and implemented at their institutions. Faculty members learned how to validate their assessment instruments, how to measure student socio-emotional variables accurately, and discussed methods for student tracking. We look forward to future workshops and assessment reports.

## TRANSITIONS



We are busily adding functionality to the new <http://seaphages.org> website, which is now the go-to place for SEA-PHAGES programmatic information. You've probably already visited the site to submit course data, update faculty contact information, see the calendar of upcoming events, and read the blog; and there's much more to come in the next

couple of months. Please note that primary program information will be disseminated through [info@seaphages.org](mailto:info@seaphages.org), so please add the email to your address book! The list of SEA-PHAGES membership benefits and responsibilities is also posted there, which we hope will provide useful and practical guidelines as you plan for your upcoming year of phage discovery and genomics. As the SEA-PHAGES community grows, being mindful of these will be increasingly important.

## SEA HIGHLIGHTS

We are delighted to welcome Viknesh Sivanathan as the newest addition to the SEA-PHAGES leadership team. Vic comes to us from Ann Hochschild's lab at Harvard Medical School, and has much experience working in bacterial and bacteriophage biology. Welcome aboard, Vic!

We also welcome Gonzaga faculty member Marianne Poxleitner, who will be spending her sabbatical working on SEA-PHAGES projects in the coming year, as well as Sharon Isern and Scott Michael from Florida Gulf Coast University who are working with Kevin to teach the In Situ workshops for Cohort 8 this summer.

Want to contribute to Message in a Bottle? Send your information to us at [info@seaphages.org](mailto:info@seaphages.org)!

## PUBLICATIONS OF INTEREST

- **Cresawn et al. (2015)**  
Comparative genomics of Cluster O Mycobacteriophages. *PLoS ONE*. **10**:e0118725.
- **Hoskisson et al. (2015)**  
The phage growth limitation system in *Streptomyces coelicolor* A(3)2 is a toxin/antitoxin system, comprising enzymes with DNA methyltransferase, protein kinase and ATPase activity. *Virology* **477**, 100-109.
- **Liu et al. (2015)**  
The diversity and host interactions of *Propionibacterium acnes* bacteriophages on human skin. *ISME J*. doi: 10.1038/ismej.2015.47.
- **Pope et al (2015)**  
Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity" *eLife* **4**:e06416.

### THE SEA-PHAGES TEAM:

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David Asai (HHMI)  
Billy Biederman (HHMI)  
Charlie Bowman (Pitt)  
Kevin Bradley (HHMI)  
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hhmi



SEA-PHAGES: A community of researchers  
exploring phage diversity

Message in a Bottle  
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