# MESSAGE IN A BOTTLE

SEA PHAGES

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Welcome to the first edition of ***Message in a Bottle***, a periodic newsletter about the SEA-PHAGES program. This fall we begin year seven of the program and welcome eight new schools. With 80 participating institutions and more than 2,000 students digging for new phages, these are exciting times. We look forward to keeping you abreast of SEA-PHAGES news and insights in Message in a Bottle.

The SEA-PHAGES program is at an interesting juncture, having completed six successful years since the first cohort of 12 schools joined in 2008. We look forward to further programmatic developments and extending its impact over the next five years. There will be many interesting challenges ahead, but we are excited at the prospects for defining viral diversity and identifying mechanisms of viral evolution. The thrill of discovery is unabated!

We hope that you will contribute to future issues of Message in a Bottle and invite you to email us your suggestions. We are keen to hear from you, whether it is a paper accepted for publication, student or faculty awards, or fascinating plaque or viral morphologies. Email your suggestions to **info@seaphages.org**.

## IMPORTANT DATES

- **October 31, 2014**
  Application deadline for new schools
- **November 21, 2014**
  DNA submission deadline: schools on semeseter calendar
- **December 8-12, 2014**
  In Silico Workshop for new institutions at HHMI HQ
- **December 19, 2014**
  DNA submission deadline: schools on quarter calendar
- **June 12-14, 2015**
  Annual Symposium at JFRC

## EIGHT NEW SCHOOLS JOINING SEA-PHAGES IN 2014

We are delighted to welcome the students and faculty at eight institutions starting their first experiences in phage discovery and genomics. The new schools are: Old Dominion University, University of Kansas, Florida International University, Indian River State College, St. Edwards University, North Carolina Agricultural & Technical State University, Truckee Meadows Community College, and Lincoln University. We wish you the best of luck in your endeavors. Please don't hesitate to call upon the folks at Pitt, Steve at JMU, Lu, Kevin and Darisa at HHMI, your buddy school partners, and your colleagues in the SEA-PHAGES community for questions or assistance. We look forward to hearing how the year goes at the symposium.

## DON'T MISS SOUNDS OF THE SEA


Had a chance to listen to any episodes of the ***Sounds of the SEA*** podcast yet? You can access them via PhagesDB or directly from iTunes. There are now a total of five episodes and we hope to add to the collection on a regular basis.

In the current episodes you can hear about events from the 2014 SEA-PHAGES Symposium, phage hunting in Durban as it pertains to the state of tuberculosis in South Africa, as well as discussions of several recent papers with useful insights into phage biology. We plan to discuss a variety of topics about phage hunting and genomics in the coming episodes.

## Did you know?

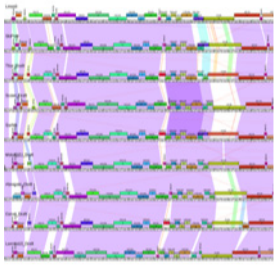
**"I found two phage", or "I found two phages"?**

In their Microbial Genetics textbook, Maloy, Cronan and Freifelder state: "The word 'phages' refers to different types of phage, whereas in common usage the word 'phage' can be both singular and plural, referring in the plural sense to particles of the same phage. Thus P1 and P22 are both phages, but a test tube might contain either 1 P22 phage or 100 P22 phage."

So if you really have two distinct entities, you did, in fact, find two phages!

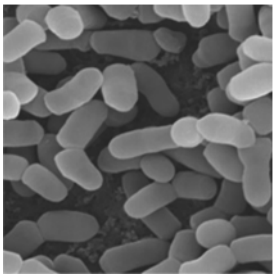
**See this (PubMed PMC3109450) for more info.**

## SOFTWARE UPGRADES



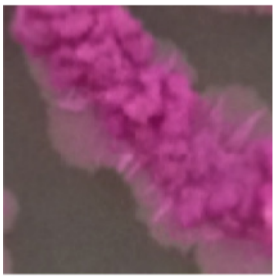
Even though virtual machine distribution is unchanged this year, we are working to improve the software. Improvements to Phamerator database building using kClust for phamily construction has sped up the process by a couple of orders of magnitude, and reduced overall database size – which means faster updates and downloads. You may notice some changes in phamily composition, as kClust uses different metrics to group the proteins, although the relationships are not substantially different. These updates will be pushed automatically to your virtual machine when you launch Phamerator (provided you have an internet connection). Watch out for more software developments in the coming year, including a new mobile App!

## NEW HOSTS



As we continue to explore bacteriophage diversity, the use of different bacterial hosts provides an opportunity to broaden the findings. *Mycobacterium smegmatis* mc2155 remains a sturdy workhorse and is the host for the largest collection of sequenced phage genomes for any single bacterium – thanks to the efforts of SEA-PHAGES students and faculty. Meanwhile, in 2013 twelve schools began to work with Arthrobacter as an alternative host, and we are excited that several schools are starting to work with *Rhodococcus globerulus* (ATCC 15903) this year as we venture out across the Actinomycetales landscape. Together with the ongoing efforts at SEA-PHAGES schools to use *Streptomyces spp.*, several *Bacillus* species, and *Paenibacillus larvae* among others, we look forward to the isolation and characterization of many novel phages and genes.

## NEW PAPER ON MYCOBACTERIOPHAGE PROMOTER ANALYSIS



Mycobacteriophage transcriptional promoters remain rather poorly characterized. All phages must have them and they are typically among the most active types of promoters so as to optimize phage gene expression and phage growth. However, predicting their locations and strengths using bioinformatic approaches is tricky. Some mycobacteriophage promoters can be identified using the same consensus as for *E. coli* sigma-70 promoters, whereas others cannot. A new paper by Oldfield and Hatfull (2014) uses mutagenesis to dissect the PR promoter of phage BPs (Cluster G) and to determine the critical bases for promoter strength. Mutations are then combined to generate a calibrated series of promoter variants that are active in both *M. smegmatis* and *M. tuberculosis* and can be used for foreign gene expression in these strains.

## WHAT'S GOING ON AT YOUR PLACE?

We are always delighted to hear of news and events going on in the SEA-PHAGES community and would be delighted to share them via the Message in a Bottle newsletter. Please send them to info@seaphages.org.

## PUBLICATIONS OF INTEREST


- **Breakwell et al. (2014)**
  Genome sequences of five B1 subcluster mycobacteriophages. *GenomeA* 1 pii: e00968-13.
- **Pope et al. (2014)**
  Cluster M mycobacteriophages Bongo, PegLeg, and Rey with unusually large repertoires of tRNA isotypes. *J.Virol*. **88**, 2461-2480.
- **Gissendanner et al. (2014)**
  A web-based restriction endonuclease tool for mycobacteriophage cluster prediction. *J. Basic Micro*. Epub ahead of print.
- **Franceschelli et al. (2014)**
  Complete genome sequences of nine mycobacteriophages. *GenomeA* 2 pii: e00181-14.
- **Oldfield, L. A. and Hatfull, G. F. (2014)**
  Mutational analysis of the mycobacteriophage BPs promoter $P_R$ reveals context-dependent sequences for mycobacterial gene expression. *J. Bacteriol*. Epub ahead of print.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