

MESSAGE IN A BOTTLE



Welcome to Message in a Bottle. We hope you are off to a wonderful start with your new school year. SEA-PHAGES students isolated an amazing 1942 phages in 2016, over a third of which infect bacteria other than *M. smegmatis mc²155*, expanding our scope to explore phage genomic diversity across the broad spectrum of Actinobacterial hosts. We are looking forward to another spectacular year of phage discovery, and further expansion of the varieties of actinobacteria for phage isolation. Don't hesitate to contact the SEA-PHAGES team if you need assistance with a new host.

Welcome Cohort 10! We are delighted at the overall variety of the 17 new participating institutions, especially schools from Mexico and Nigeria, expanding the international reach of the SEA-PHAGES program. The growth of the program facilitates broader and greater scientific findings, and expansion of the amazing resource of sequenced and annotated phage genomes. We are also excited about our DOGEMS strategy to identify interesting phages in the unsequenced archives. The biggest prize thus far: a new singleton, Kumao, isolated at Lehigh University in 2015. Make sure you send us all your lysates for archiving; you could be the next big winner!

Graham F. Hatfull
SEA-PHAGES Lead Scientist



17 NEW SCHOOLS IN 2017

We are delighted to welcome 17 new schools (in blue and listed right) to the program and our community in 2017. In 2016 - 2017, 100 institutions (in purple) participated in SEA-PHAGES, with 4,146 students, primarily freshmen, enlisted last fall.



Aaniiih Nakoda College
Bowling Green State University
Coastal Carolina University
Indiana University of Pennsylvania
Iowa State University
Northwest Indian College
Salish Kootenai College
St. Louis Community College
SUNY Old Westbury
Tarleton State University
United Tribes Technical College
Universidad Autónoma de Nuevo León
University of Central Oklahoma
University of Lagos
University of Nevada Las Vegas
University of South Florida
Virginia Western Community College

Did you know?

Size matters!

Sometimes we see electron micrographs of phages and think "wow, that picture cannot possibly go with that genome sequence." How do we know?

Two ways:

The first is the length of the phage tail and the length of the tape measure protein-- so named because the length of the protein is directly proportional to the length of a flexible tailed phage's tail at a ratio of $1aa \sim 0.15nm$, with few exceptions. (Katsura and Hendrix, 1984).

The second is that phages tend to pack DNA at similar densities into their capsids, resulting in a direct correlation between the length of the phage genome and the diameter of the phage capsid. A phage with a 50kb genome is likely to have a capsid diameter of $\sim 55nm$, while a phage with a 150kb genome is likely to run closer to a $\sim 80nm$ diameter.

REGIONAL SYMPOSIA

More and more SEA institutions are hosting regional SEA symposia. In 2016-2017, 17 institutions (stars) participated in 5 regional symposia. These meetings offer many benefits to SEA students and faculty, and HHMI is pleased to offer a moderate contribution to help offset the associated costs.

To learn more about regional SEA symposia and how to request HHMI support, visit seaphages.org/blog/



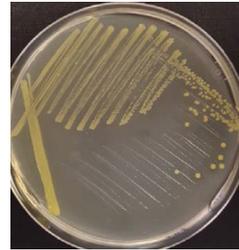
Singletons

- A1 Over the past few years, Steve Cresawn and his team of students from James Madison University have made tremendous progress in moving the integral SEA-PHAGES program, Phamerator, online. The ongoing work is available at Phamerator.org, and is freely available for students and faculty in the program to use.
- A2 The majority of the functionality of Phamerator has been incorporated into the online version, which only displays phages from the latest version of the Actino-Draft database. For 2017-2018, schools may choose to use either Phamerator online or Phamerator on the SEA Virtual Machine for their bioinformatics semesters.
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- A4
- A5
- A6
- A7 Steve and his team will be continuing to add functions to Phamerator.org throughout next year, and plans to retire the Ubuntu version within the next few years.
- A8

A NEW HOST: MICROBACTERIUM FOLIORUM

In line with our program-wide scientific goal, the isolation of ever more diverse Actinobacteriophages, we are pleased to announce the availability of a new Actinobacteria host: *Microbacterium foliorum*. Phage hunting with *M. foliorum* at the University of Pittsburgh was so successful (68 phages!) that we introduced it at the Cohort 10 Phage Discovery Workshops, making Cohort 10 the first cohort to be trained with a non-smegmatis host.

M. foliorum is a lovely lemon yellow color and grows under similar conditions as *Gordonia terrae*. A version of the Phage Discovery Guide for Microbacterium is now available on seaphages.org, along with guides for Streptomyces, Gordonia, Arthrobacter, and of course, Mycobacterium.



M. foliorum forms bright yellow colonies

WELCOME



SEA-PHAGES welcomes a new member to the team, Dr. Joslynn Lee. Joslynn comes to HHMI from Cold Spring Harbor Laboratory's DNA Learning Center, where she was a Data Science Educator. She will work closely with the SEA Team at HHMI to support the SEA-PHAGES program, and to develop genomics-based research programs for undergraduates.

A SPEEDY RECOVERY

As our thoughts go out to all those affected by hurricane Harvey, we are thankful that our SEA colleagues, Rachna Sadana and Sanghamitra Saha from the University of Houston-Downtown, and Rob Hatherill and Daisy Zhang from Del Mar College, are safe. We hope that their colleagues, students, friends, and family managed through the storm, and wish their schools and towns a speedy recovery.

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

- **Pope et al (2017)**
Bacteriophages of *Gordonia* spp. Display a Spectrum of Diversity and Genetic Relationships. *MBio*, Aug 15;8(4). pii: e01069-17
- **Klyczek et al (2017)**
Tales of diversity: Genomic and morphological characteristics of forty-six *Arthrobacter* phages. *PLoS One*. Jul 17;12(7):e0180517
- **Mavrich and Hatfull (2017)**
Bacteriophage evolution differs by host, lifestyle and genome. *Nat Microbiol*. Jul 10;2:17112
- **Russell and Hatfull (2017)**
PhagesDB: the actinobacteriophage database. *Bioinformatics*. Mar 1;33(5):784-786
- **Dedrick et al (2017)**
Prophage-mediated defence against viral attack and viral counter-defence. *Nat Microbiol*. Jan 9;2:16251
- **Tzipilevich et al (2017)**
Acquisition of Phage Sensitivity by Bacteria through Exchange of Phage Receptors. *Cell*, Vol. 168, Issues 1-2, p186-199.e12
- **Erez et al (2017)**
Communication between viruses guides lysis-lysogeny decisions. *Nature*. 2017 Jan 26; 541(7638): 488-493

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