

MESSAGE IN A BOTTLE

Welcome to message in a bottle and to the 10th Annual SEA-PHAGES Symposium!

It is hard to believe that it has been ten years since the beginning of the SEA-PHAGES program. We've come a long way from the early days of twelve schools, Mycobacterium phage genome sequences arriving after the final exam, and annotations in GBrowse and Apollo, to more than 130 member institutions, hundreds of genomes sequenced in a few short weeks annually, thousands of student alumni, and the rise and fall of the SEA Ubuntu Virtual Machine.

The scientific and educational accomplishments of the program speak for themselves, with more 2500 genomes sequenced, 1500 annotations in GenBank, and more than 20 peer-reviewed papers in the literature with undergraduate authors.

Where will the next ten years take us?

Graham F. Hatfull
SEA-PHAGES Lead Scientist



18 NEW SCHOOLS IN 2018

In 2017 - 2018, 117 institutions participated in SEA-PHAGES, with 4,605 students, primarily freshmen, enlisted last fall. We are now delighted to welcome 18 new schools to the program and our community in 2018. Welcome to

College of Southern Nevada
Columbia State Community College
Ekiti State University
Hillsborough Community College
Minnesota State University Moorhead
Mitchell Community College
Monmouth College
Neumann University
Northern State University

Radford College
Saint Leo University
Salem State University
Thiel College
University of Connecticut
University of Hawaii at Manoa
University of Ibadan
University of the Ozarks
Virginia State University

REGIONAL SYMPOSIA

More and more SEA institutions are hosting regional SEA symposia. In 2017-2018, 17 institutions participated in 7 regional symposia, which included

Florida Symposium
Western Pennsylvania Symposium
NYC Symposium
South Central Symposium

Phage Phest
Phall Phage Fair
Philly Phage Phestival

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, email info@seaphages.org

Did you know?

What is the phage portal?

"The portal is a dodecameric ring made of 12 copies of the portal protein that sits at one vertex of the capsid, replacing one of the capsid pentamers. During assembly, the terminase binds to the portal and pumps the phage's genomic material into the capsid. The terminase then dissociates and the tail binds to the portal vertex to form an intact virion."

- phagesdb.org glossary

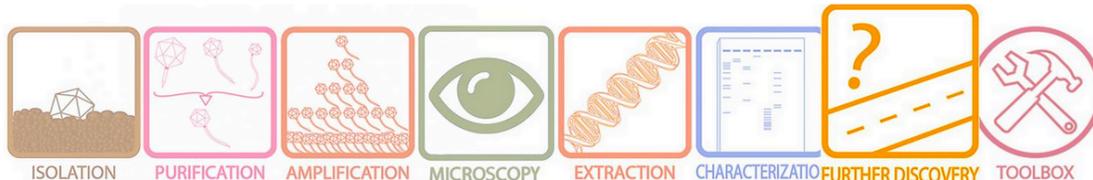
The portal protein has one of the most highly conserved protein sequences found in tailed phages and thus is also one of the most easily identifiable functions in a genome. Phage genomes have one and only one portal gene. Some phage biologists call the portal protein the "head-to-tail connector" protein. This leads to all kinds of confusion, as portal genes can be mislabeled in global databases. Phages also have "neck" proteins that make a complex with the portal that the tail joins to after DNA packaging. These smaller proteins are called "head-to-tail connector complex proteins" and have been co-crystallized with true portal proteins, resulting in a protein data bank entry that contains both types of proteins. How do you tell the difference? Synteny! The true portal gene is likely to be found adjacent to the terminase and upstream of the major capsid protein.

SEA-PHAGES COURSE GUIDES ARE NOW ONLINE!

We are delighted to announce that the SEA-PHAGES Course Guides are now online.

After its test run in December at the Cohort 9 Bioinformatics Workshop, the new Bioinformatics Guide went live in December for use across the SEA. Compared to the retired DNA Master Annotation Guide, the Bioinformatics Guide is expanded in content, including sections on common tools and the field of Bioinformatics, as well as descriptions of the underlying algorithms and statistics behind our annotation programs. The online platform is easy to update, allowing us to respond quickly to user comments or changes in the third party websites we use, thus getting the latest information out to faculty and students immediately –even during the semester.

The Phage Discovery Guides are now also available online, with few changes content-wise. Moving these guides online streamlines the annual update process and supports the development and dissemination of new material, like host-specific guides and new bioinformatic tools.



NEW BACTERIAL HOSTS FOR PHAGE-HUNTING

In line with our program-wide scientific goal, the isolation of ever more diverse Actinobacteriophages, we are pleased to announce the availability of new Actinobacteria host: *Gordonia rubripertincta* and *Microbacterium testaceum*. Protocols for isolating phages with these bacterial hosts are now available as part of the new online Phage Discovery Guides.

If you are working with an Actinobacterial hosts that is not included in the Phage Discovery Guide, we would like to work with you to validate these hosts and generate protocols that can be shared across the SEA. Let us know by emailing us at info@seaphages.org

WELCOME



HHMI welcomes a new member to the SEA team, Dr. Danielle Heller. Danielle comes to HHMI from Harvard Medical school, where she was a post-doctoral fellow studying the mechanism of toxicity of a family of prophage-encoded toxins.

As a Science Education fellow at HHMI, Danielle works with the SEA to develop a new Course-based Research Experience for undergraduates.

A SPEEDY RECOVERY

As our thoughts go out to all those affected by hurricane Harvey and Maria last year, we are thankful that our SEA colleagues were safe. We hope that their colleagues, students, friends, and family managed through the storm, and wish their schools and towns a speedy recovery.

STAYING INFORMED

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.

Please add info@seaphages.org and no-reply@phagesdb to your email address book to that you do not miss program communications.

PUBLICATIONS OF INTEREST

- **Ko and Hatfull (2018)**
Mycobacteriophage Fruitloop gp52 inactivates Wag31 (DivIVA) to prevent heterotypic superinfection. *Mol Microbiol.* 2018 May;108(4):443-460
- **Hanauer et al (2017)**
An inclusive Research Education Community (iREC): Impact of the SEA-PHAGES program on research outcomes and student learning. *Proc Natl Acad Sci U S A.* 19;114(51):13531-13536
- **Dedrick et al (2017)**
Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. *BMC Microbiol.* 2;17(1):225
- **Mehla et al (2017)**
Virus-host protein-protein interactions of mycobacteriophage Giles. *Sci Rep.* 28;7(1):16514
- **Doron et al (2018)**
Systematic discovery of anti-phage defense systems in the microbial pangenome. *Science.* 2;359(6379)viruses guides lysis-lysogeny decisions. *Nature.* 2017 Jan 26; 541(7638): 488–493

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