



Dear SEA-PHAGES Community,

The 2018 Annual Symposium is a red-letter event, reflecting ten very exciting productive years of phage discovery and genomics, and engagement of over 20,000 undergraduate students in authentic research experiences. This is a good moment to write our first [Annual Letter](#) to celebrate some of the accomplishments of the past year, and provide some thoughts on the year to come.

### 2017-18 Program Highlights and Accomplishments

- **Program growth.** This year marks the first time we've had **more than 100 schools concurrently active** in the SEA-PHAGES program. During the fall, 113 schools delivered SEA-PHAGES courses to **more than 4,500 undergraduates**. These students isolated more than 2,500 new bacteriophages, including almost 1,200 on hosts other than *Mycobacterium smegmatis* mc<sup>2</sup>155. (By contrast, in the first year of SEA-PHAGES, twelve schools were active, 201 phages were discovered, and 13 were sequenced that academic year.)
- **Global reach.** This year two more international schools joined the program (in [Mexico](#) and [Nigeria](#)), and next year we will add two more, bringing the total number of international partner schools to five.
- **It works!** A major goal of the SEA-PHAGES program is to provide research experiences to early-career undergraduates that will engage and excite them, and enhance their continuation in STEM disciplines. The outcomes of a major assessment study led by David Hanauer clearly demonstrate enhanced persistence by SEA-PHAGES students. A huge thank you goes to all the faculty and students that participated and helped to make this happen. The data were published in [a paper in the Proceedings of the National Academy of the Sciences](#) (PNAS), and framed the SEA-PHAGES program as a model for an inclusive Research Education Community (iREC).
- **Advancing phage biology.** SEA-PHAGES discoveries continued to be a major impetus for new biological insights and were published in several notable papers this past year. These include the discovery of [prophage-mediated defense systems](#), [phage evolutionary modes](#), and the genomics of [Arthrobacter](#) and [Gordonia](#) phages. A special thanks to everyone that contributed to these publications.
- **Genome Announcement Workshop.** Forty-three SEA-PHAGES faculty attended a [Genome Announcement Workshop](#) aimed at the publication of phage genome sequences in the journal *Genome Announcements*. The workshop resulted in the publication of 14 *Genome Announcement* papers. Spoiler alert: *Genome Announcements* is about to be incorporated into the journal [Microbiology Resource Announcements](#), with a mission beyond genomics.

- **New bioinformatics tools.** The fantastic web version of [Phamerator](#) has made requiring the Virtual Machine obsolete, and new functionalities are regularly being added to it. [PECAAN](#) collects evidence relevant to annotation in a single place, facilitates calling functions, and outputs DNA Master files with proper notes.
- **Online guides for phage discovery and bioinformatics.** The bioinformatics guide underwent a major revision and is now available [online](#). This will allow access from a variety of devices and let us update the guide regularly as new tools and practices are developed. The phage discovery guide is just going online now and will be available to use this fall.
- **New Archive-Tracking System (and Hidden Freezer Gems).** The astonishing collection of over 13,000 individual phages isolated are in theory archived at the University of Pittsburgh, in duplicate collections stored at -80°C. To convert the theory into a reality, SEA-PHAGES faculty can help by determining the archiving status of their phages at their [institutional home page](#). As a prompt, the panel is colored **Raging Red** when there are unarchived phages, but **Pleasing Purple** if everything is up to date. The archive is used actively, and the [DOGEMS](#) strategy is being applied to find the hidden gems amongst the unsequenced phages. For example, [a new Singleton, Kumao](#), from Lehigh University is a terrific find.
- **Roto Rooter of the annotation pipeline.** Currently, the genome annotation pipeline spanning from gene sequence to GenBank submission is badly clogged, with many hundreds of genomes currently stagnant. The new Annotation Tracking System – available at your institution home page at <http://seaphages.org> – enables you to see where your genomes are in the pipeline, due dates for completion, and an expanded [Genome Exchange](#). The goal is to facilitate high quality annotation submissions for all genomes sequenced in that academic year, and to clear the backlog. Updated [guidelines](#) and the [online bioinformatics guide](#) should be helpful too. We are also hoping to increase the number of SEA-PHAGES faculty with **Expedited Submitter** status that recognizes excellence in genome annotation and facilitates direct submission to GenBank.

### The Coming Year

The 2018-2019 academic year promises even more successes and excitement:

- **Program growth.** An additional 18 institutions were accepted into the SEA-PHAGES program this year, and Cohort 11 will soon start their training at the UMBC facility. Please join us in extending a warm welcome to our new faculty colleagues.
- **New bacterial hosts.** More and more schools are using the newer hosts for phage isolation, and Cohort 11 will be using *Microbacterium* for their phage isolation.
- **Hitting 5,000.** Not wanting to count the chickens yet, but it is likely that we will approach a total of almost 5,000 SEA-PHAGES students this current year.

Wishing all of you a successful and fun year, and we look forward to seeing you at the Symposium.

Sincerely,  
David Asai and Graham Hatfull