SEA PHAGES

Dear SEA-PHAGES Community,

The 2019 SEA-PHAGES Annual Symposium marks yet another highly successful year with a plethora of exciting events. The program continues to expand with inclusion of a new cohort of schools and we are especially pleased to welcome the Cohort 12 faculty to the Symposium. We are delighted to share with you a few of the highlights from the past year.

2018-19 Program Highlights and Accomplishments

• Program Growth and Milestones

This fall, we will welcome 18 new institutions into the SEA-PHAGES program as Cohort 12. Included among these are our first schools from Arizona, New Hampshire, and Canada, as well as a second institution in Puerto Rico. Geographical diversity is great, but phage diversity is even better, so Cohort 12 will be trained using *Arthrobacter globiformis* and *Gordonia rubripertincta* as hosts. And SEA-PHAGES schools now represent 43 different US states, as well as the District of Columbia and Puerto Rico.

Because of our collective efforts, we will soon pass 3,000 sequenced Actinobacteriophage genomes, and nearly 2,500 of those genomes are published in GenBank. We reached 2,000 sequenced genomes in May 2017, so we are now finding and sequencing the genomes of nearly 500 novel phages per year, which is a tremendous accomplishment and rich collection and data set. And there are now five genera on which we've isolated and sequenced at least 200 genomes: *Mycobacterium, Arthrobacter, Gordonia, Microbacterium*, and *Streptomyces*. Thank you for all your work in making this happen!

• Mycobacteriophage therapy

One of the most exciting scientific developments over the past year culminated in the <u>publication of</u> a paper in *Nature Medicine* this May describing the use of a phage cocktail to treat a disseminated drug-resistant Mycobacterial infection in Isabelle Holdaway, a British 15-year-old with cystic fibrosis who had received a lung transplant. After receiving the three-phage cocktail—which contained two BRED-engineered phages—Isabelle showed substantial health improvement, and the story received <u>international media attention</u>. One of the three phages used, ZoeJ, was found by a SEA-PHAGES student at Providence College, but many of your SEA-PHAGES phages were screened to find the few that were useful.

The primary scientific goals of SEA-PHAGES are to understand the basic principles of phage diversity, but this development illustrates a key point: that translational applications depend on and emerge from basic scientific exploration. It is hard to imagine how this life-saving intervention could have occurred without the SEA-PHAGES program.

Microbiology Resource Announcements

In June 2017, we held a Genome Announcement Workshop where we encouraged SEA-PHAGES faculty members to learn to write and submit papers describing the phage genomes they'd found. The seed planted at that workshop has begun to bloom, as the past year has seen at least 12 Microbiology Resource Announcements on which (non-Pitt) SEA-PHAGES faculty members are the corresponding authors. Congratulations!

• Future Symposia, Faculty Meetings, and Workshops

If you're from one of the earlier SEA-PHAGES cohorts, you probably remember when you could bring a faculty member and two students to the Symposium each year. But the growth of the program has bumped up against the capacity of Janelia Research Campus, and we've had to moderate the number of attendees per institution to fit everyone. In the interests of long-term sustainability, therefore, the 2020 Symposium will be held at a new location, the <u>National</u> <u>Conference Center</u> in nearby Leesburg, VA. This facility has been carefully vetted and should provide an excellent location and atmosphere to accommodate our ever-growing group of student researchers and faculty members.

Each year, immediately following the Symposium, we hold another meeting for faculty only. In even-numbered years, this is a full faculty meeting where one representative from each institution is invited, and in odd-numbered years it is a specialized workshop of some sort, where invitations are based on the topic covered in the workshop. This year we are hosting a *Microbacterium* Phage Genomics workshop, whereas next year will be a full faculty meeting.

Removing Annotation Bottlenecks

With nearly 500 genomes being sequenced each year, the task of getting high-quality annotations into GenBank in a timely fashion has grown. This past year saw a number of developments that aimed to remove some of the bottlenecks in the annotation pipeline.

First, the June 2018 full SEA-PHAGES faculty meeting focused on improving the quality of phage genome annotations and bringing everyone up to speed with the current best practices. There were lots of "aha" moments and many genomes were submitted directly to GenBank as a result of the meeting.

Second, the number of expedited submitters has grown to include 50 SEA-PHAGES faculty members representing 39 institutions. Expedited submitters use a streamlined submission form and their genomes go quickly into GenBank, easing the QC burden. We thank those of you who have worked to achieve this status and hope to add many more this coming year.

Third, a sustained effort from a dedicated team at Pitt allowed us to completely clear out the pile of genomes awaiting QC in early 2019. We have new plans in place to make sure your genomes are processed as expeditiously as possible in the future, and your adherence with the annotation deadlines will help to make this a reality!

We will continue to improve this pipeline in ways that it is helpful to you. This will include an online file-checker that will allow you to identify and fix any issue with your submission files before entering them in PhagesDB, and will avoid them being returned to you for common errors. Watch out for announcements soon!

• Feedback

We are always interested in hearing your feedback, suggestions, concerns, and questions about the larger aspects of the SEA-PHAGES program's direction. We've created a new forum called "Larger Program Questions" and encourage you to share items there.

Thanks for being part of this vibrant and productive community. 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