Implementation of the 2008-2009 NGRI Bacteriophage Genomics Laboratory Course at Carnegie Mellon University

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Selection of Students

In the summer of 2008, all incoming freshman in the Mellon College of Science (~200 individuals) were informed about the course via a brochure that was sent to them by land mail and email.

To apply, a student was required to write an essay about why the course appealed to him or her. Approximately 30 students applied.

Based on the essay, we admitted 10 female and 11 male students to the course. We did not use the students' academic records or intended majors as criteria. Most of the 21 students were intended biology majors; a few were intended chemistry majors.

The students represented a broad range of backgrounds, interests and personalities. All developed high levels of engagement and proficiency.

Fall Semester

The primary instructor in the Fall semester was Jon Jarvik.

Students were assigned to bench locations in the laboratory through a blind lottery. Each student belonged to a pair (side-by-side students), to a group of four (side of a bench), and to an island (8 students). These sets of widening allegiances worked very well socially and scientifically.

Each student isolated and purified at least one mycobacteriophage and characterized its morphology and restriction pattern. Each island nominated one phage for sequencing, and the entire class voted to choose the winner. "Island3" was chosen for genome sequencing due to its distinctive prolate ellipsoidal head morphology, and due to the fact that it yielded large quantities of DNA using the standard SEA protocol.

All of the above activities were completed before Thanksgiving. To fill the few remaining weeks of the semester, we did some brainstorming to identify projects that might be finished quickly, and the students worked in self-selected groups on several of these. Projects included:

1. Examination of Ca^{++} and Mg^{++} sensitivity/dependence for phage infection and growth.

2. Generation of lysogens and analysis of patterns of cross-immunity among individual phages.

3. Scanning and transmission electron microscopy of individual phage plaques.

These efforts were successful and kept the students fully engaged until the last day.

Spring Semester

The primary instructor in the Spring semester was Javier Lopez.

The Spring, which was to be devoted to genome annotation, presented challenges due to delays in receiving the completed sequence and the fact that Island-3 was nearly identical to a known phage.

We maintained student engagement in two ways.

First, students carried out their own finishing experiments to fill large gaps and resolve poor quality regions in the preliminary sequence.

Second, we compared the genomes of Island-3 and its two relatives to generate and test hypotheses about their life cycles and regulation, including ability to lysogenize, integration into the bacterial genome, and patterns of immunity.

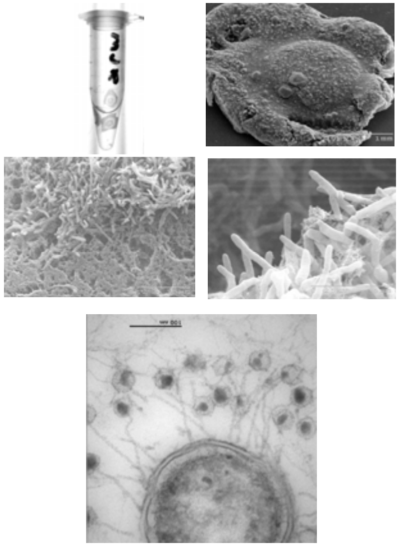
This approach was successful and had multiple benefits:

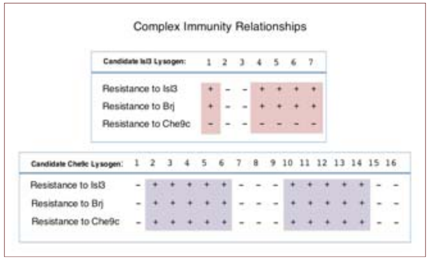
1. The value of the bioinformatic analysis became much more obvious.

2. Students experienced the entire research cycle, including initial observations, generation of hypotheses, design of tests and experimental validation.

3. The value of combining computational and experimental approaches was highlighted by experiments that revealed novel and unexpected behavior.

4. Students made novel discoveries about the biology of their phage and its relatives, which rescued the course from an initial disappointment at having isolated a seemingly already-known phage.





Complex Immunity Relationships

Candidate Isl3 Lysogen:	1	2	3	4	5	6	7
Resistance to Isl3	+	–	–	+	+	+	+
Resistance to Brj	+	–	–	+	+	+	+
Resistance to Che9c	–	–	–	–	–	–	–

Candidate Che9c Lysogen:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Resistance to Isl3	–	+	+	+	+	+	–	–	–	+	+	+	+	+	–	–
Resistance to Brj	–	+	+	+	+	+	–	–	–	+	+	+	+	+	–	–
Resistance to Che9c	–	+	+	+	+	+	–	–	–	+	+	+	+	+	–	–