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Because most ecosystems depend on microbes for their success, the field of environmental microbiology has become the focus of many researchers who seek to understand the complex inner workings of those ecosystems. Only in the last 25 years has the importance of bacteria in marine ecosystems started to become clear. As part of this discovery process, marine viruses were found to be 10-fold more numerous than the co-occurring bacteria in a number of natural environments. These viruses most commonly infect members of the bacterial communities rather than larger, multi-cellular organisms. As a result of this series of relatively recent discoveries, it seems clear that viral infection plays a role in shaping bacterial communities, and thereby can impact entire ecosystems from the bottom up. This is true for terrestrial as well as marine ecosystems, and is why I am studying viral communities in types of environments.

There are a few methods that can be used to study environmental viruses. The most straightforward method is to use a very high power microscope (usually a Transmission Electron Microscope or TEM) to look at the different shapes of viruses. However, there are only about five or six different shape categories that have been observed in viruses, and it is difficult to draw meaningful conclusions about the viral community with so few morphologies. Therefore, I have focused on the use of molecular methods based on studying the DNA found within the viruses to study these simple organisms. The first method is called Pulsed Field Gel Electrophoresis (PFGE), and is based on separating viral DNA simply by the size of the genome. After the viruses are separated from all other organisms, a single viral community is run in a lane on the gel, resulting in a distinct banding pattern that represents the genomes of the viruses found in that community. The banding pattern can be considered the “fingerprint” of that viral community at that point in time.

By applying PFGE to the viral community in the Chesapeake Bay, I have found that there are distinct changes that occur in the viral community over an annual cycle. It is not surprising that there are seasonal patterns emerging, since it has been well established that the microbial community (the hosts for the viruses) in the Chesapeake undergoes seasonal changes as well. And while it seems intuitive that the co-occurring viruses would also show temporal variations, we are the first multi-year study of the viruses themselves. Thereby, we are providing the first empirical evidence for this phenomenon. In contrast, there do not seem to be large differences in the viruses found at different locations through out the Bay. This finding is quite surprising because of the drastic variation in the marine environment from near fresh water at the top of the Bay, to full sea-water salinity at the mouth of the Bay. Intuition would suggest that organisms would be adapted to a much more narrow set of biochemical parameters, but our results are not showing this to be the case. These PFGE results are good examples of how much we have to learn about natural viral and microbial communities.

In addition to looking at the community fingerprints of environmental viruses, we are also looking directly at the DNA sequences of these viruses. Through the use of metagenomics (i.e., genomics of a group of organisms, rather than a single organism), I have been able to examine these viruses in a way that was previously impossible. In the past, researchers were required to isolate a culture of a microbe to gain biochemical information about that microbe, or to have enough DNA for sequencing. Unfortunately, researchers have not been able to isolate cultures of the vast majority (>99.9%) of microbes found in nature, even with very advanced culturing

techniques. This large hurdle has been overcome through advances in molecular biological methods. We can now generate DNA sequences from tiny amounts of starting DNA. This has been critical in the study of viruses which have the smallest genomes of any known organisms. I am currently in the process of analyzing two sets of viral DNA sequences, or metagenomes. One of these is from the Chesapeake Bay, and will provide additional detail for the fingerprint studies mentioned above. The second is from Delaware agricultural soil, and will provide the first glimpse into the viruses found in this environment.

In my preliminary analysis of these metagenomes, it is becoming clear that viruses have different life strategies based on their environment. Perhaps the most striking observation has been that over two thirds of these DNA sequences are unique, and are not similar to anything in the entire database of known DNA sequences. Again, this illustrates how much we have to learn about the microbes which are critical for all ecosystems on our fragile planet.