VIROMICS

What is it?

Viromics is essentially "meta-omics" of viruses. While viruses are extremely important to natural ecology, viromics can be considered the most elusive of the "-omics" fields because it is difficult to collect samples, even though there are an estimated 10^{10} viruses per liter of seawater. Viruses play an important role in infection and mortality of all branches of life, but have also recently been shown to be beneficial to their hosts in some cases. The first virome was sequenced in 2002.[1] This was a huge advancement because unlike for prokaryotes and eukaryotes, there is no universal genetic marker that is common for all viruses.[4] Before viromics, the study of viruses was biased by PCR and the need to use degenerate primers.[5]

Types of Viruses:

Nucleic Acids → DNA → double-stranded / single-stranded

RNA → double-stranded / single-stranded

Lab Groups to Watch

Matt Sullivan, Ohio State University- This group is responsible for the development of bioinformatics interfaces that are freely available, such as iVirus.

Mya Brietbart, University of South Florida- This lab continues to push forward the field of Viromics in a variety of natural environments, including plants, insects, and the ocean. They are responsible for the technique of "vector-enabled metagenomics," in which the vector of disease is used as the sample, rather than the host, in order to integrate the genomes of various viruses of the hosts.

Joaquin Martinez, Bigelow Lab - Look out for this lab to lead the way in "single virus" genomics, a parallel technique to single cell genomics.

Penny Chisholm, Massachusetts Institute of Technology- This lab has been using the Prochloorococcus/ cyanophage system as a model system to study host- virus interactions in the ocean and develop hypotheses based around beneficial relationships between viruses and their hosts.

Challenges

Viromics has been challenging because typical filtration methods often yield very little material for standard sequencing libraries even when large volumes are filtered. However, new techniques have allowed the development of libraries from <1ng of DNA.[5] Furthermore, most studies can only focus on one type of virus (see figure).[4] There is also the problem of the lack of viral annotations. Typically, 60-99% of viral reads have not been previously annotated.[4] This has improved somewhat with the increased coverage of viral genomes from culture studies, single-cell genomics project, and even the assembly of viral genomes from environmental metagenomes.[5] Virome databases are still underdeveloped relative to their microbial and eukaryotic counterparts. But new interfaces have been developed, such as MetaVir, VIROME, and iVirus.[5]

Recent Major Findings

Viral genomes have been found to have genes that are necessary to their hosts, and likely play a role in horizontal gene transfer. In this way, viruses are thought to "reprogram" their hosts by manipulating the distribution of particular metabolic genes.
→Viruses of the common ocean microbe, SUP05, suggested that these viruses manipulate growth of their hosts by sharing sulfur-cycling genes among the hosts.[5]

→Viruses of *Prochlorococcus* contain full-length genes for photosynthesis and phosphorus uptake, that are necessary for growth of and are phylogenetically identical to those from *Prochlorococcus*.[3]
→ Aphotic carbon metabolism genes, like those for chemoautotrophy, were found widespread among aphotic viruses, suggesting they share those genes among their aphotic hosts, similar to those in photic habitats.[2]

Martinez et al.[4] developed a method to target single viruses using fluorescent tagging and cell sorting without the need for culturing. Using this method, this group can capture and sequence the fraction of viruses that are typically missed by normal filtration.

References: 1. Breitbart, M., P. Salamon, B. Andresen, J.M. Mahaffy, A.M. Segall, D. Mead, F. Azam, and F. Rohwer. (2002) Genomic analysis of uncultured marine viral communities. *PNAS* 99(2): 14250-14255. 2. Hurwitz, B.L., S.J. Hallam, M.B. Sullivan (2013) Metabolic reprogramming by viruses in the sunlit and dark ocean. *Genome Biol.* 14:R123 3. Lindell, D., M.B. Sullivan, Z.I. Johnson, A.C. Tolonen, F. Rohwer, and S.W. Chisholm (2005) Transfer of photosynthesis genes to and from Prochlorococcus viruses. *PNAS* 101(30: 11013-11018. 4. Martinez, J.M., B.K. Swan, and W.H. Wilson (2014) Marine viruses, a genetic reservoir revealed by targeted viromics. *The ISME Journal* 8(5): 1079-1088. 5. Sullivan, M.B. (2015) Viromes, Not Gene Markers, for Studying Double-Stranded DNA Virus Communities. *J. Virol.* 89:2459-2461.