



BIOINFORMATICS 2016 SPRING SEMINAR SERIES

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<http://bioinformatics.udel.edu/Seminars/Current>

MONDAY, April 25, 2016
3:30pm
DBI Room 102

Tapping the Marine RNA Genome Pool

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ABSTRACT: Hallmarks of RNA viruses include their high rates of mutation and rapid replication times, which lead to inherently vast genetic diversity. Marine RNA viruses are known to infect hosts from many cellular lineages across trophic levels. However, much of the research and data to date on RNA virus diversity and phylogeny arises from human, plant and animal RNA viruses; leaving the marine RNA viral pool, which encompasses major components of total RNA viral diversity, largely unknown and woefully under-sampled. Our research seeks to characterize RNA viral populations using a combination of size-fractionated community transcriptomes targeting eukaryotic phytoplankton, RNA from viral particles and infection studies. To date, our global study includes samples that traverse salinity, temperature and depth gradients as well as ocean basins. These data are providing insight into the taxonomic diversity and distribution of RNA viral populations. Using high-throughput sequencing ample coverage of complete RNA viral genomes was achieved further revealing abundant and diverse communities of RNA viruses, some of which exhibit sequence homology pervasive between marine provinces, and others display population level micro-diversity. From our environmental transcriptomes (n=287) targeting marine eukaryotic algae communities, and the Moore Marine Eukaryotic Transcriptome Sequencing Project (MMETSP) we have recovered >100 new RNA virus genomes, thereby building the available marine RNA virus database and furthering our knowledge of presence and genetic diversity.