Characterization of Viral-Host Interactions Following Antagonistic Co-Evolution

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Cyanobacteria and the viruses that infect them are abundant in coastal marine environments. When cyanobacteria and viruses interact, co-evolution occurs in which the cyanobacteria evolve resistance to the viruses, and viruses then evolve to overcome that resistance. As the viruses evolve, their host range increases with the virus infecting both ancestral and co-evolved bacteria. However, few studies have explored the infection kinetics of pairwise interactions among co-evolved cyanobacterium and virus. In this project, we examined the level of viral resistance in four co-evolved hosts and the degree of infectivity of four co-evolved viral isolates. To examine the genetic mutations that are responsible for host resistance and virus host range expansion, we sequenced the whole genomes of all ancestral and co-evolved cyanobacterial hosts and viral isolates. In cyanobacterial isolates, viral resistance typically resulted from only a few single point mutations, and different combinations of mutations could lead to resistance to the ancestral virus. Likewise, in the co-evolved viral isolates, different sets of mutations enable the virus to overcome host resistance. One noted difference in the virus, however, was that multiple mutations were often observed in the same gene. Pairwise cross-infectivity assays among all viral isolates and cyanobacterial host isolates revealed that levels of resistance vary among the cyanobacterial isolates and similarly, the degree of infectivity differs among the viral isolates. For example, the co-evolved viral isolate RIM8 G-167-3 did not infect cyanobacterial isolate WH7803 G-84-sc3, however it evolved to overcome resistance and infect cyanobacterial isolates WH7803 G-112-sc3 and WH7803 G-167-sc2, but with varying degrees of infectivity. Even when co-evolved viral strains can infect bacterial host isolates, cross-infectivity assays suggest that the rate of replication may differ between cell types. The next step of this study is to analyze how well co-evolved viral isolates replicate on the ancestral and co-evolved cyanobacterial isolates. Understanding how co-evolution influences viral-host interactions will elucidate the effects viruses have on overall host mortality in natural environments.

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