Siobain Duffy

Siobain Duffy is a born and raised New Jerseyan interested in the molecular evolution of emergent viruses. She graduated from Rutgers with a degree in Molecular Biology and Biochemistry while working as an undergraduate researcher in food microbiology. After a Fulbright fellowship, she studied viral experimental evolution as an HHMI predoctoral fellow at Yale University. She was an NSF postdoctoral fellow at the Center for Infectious Disease Dynamics at Penn State University before returning to Rutgers to join the Department of Ecology, Evolution and Natural Resources in the School of Environmental and Biological Sciences. Over the past twelve years the NSF, NIH, DoE and BMGF have supported her lab's computational research on emergent plant and animal viruses and experimental work with bacteriophages. She is an active member of the Council on Microbial Sciences of the American Society for Microbiology, is part of the International Committee on the Taxonomy of Viruses (bacterial viruses subcommittee) and won the American Society for Virology's Ann Palmenberg Junior Investigator Award in 2017. She has twice won university-wide awards for her teaching which focuses on microbial evolution, evolutionary medicine and science communication.

Abstract:

As everyone in the world has been reminded of this year, we frequently see RNA viruses jump into new hosts. Typically a host shift requires a mutation that expands a virus' host range to include one or more novel hosts, making host range mutations the first step in emergence. Little research has been done on how different host range mutations affect the subsequent steps of emergence of an RNA virus in a novel host. Using a safe bacteriophage model system (the RNA phage phi6, which infects *Pseudomonas* bacteria), we investigate how host range mutations influence the future evolution of viruses forced to emerge on novel hosts. First, we assessed how much having one host range mutation affects a virus' ability to serially host shift into a second novel host. A comparison of wildtype phi6 and two isogenic host range mutants (E8G, G515S — different expanded host range mutations in the host attachment protein P3) showed that there were at least 9 point mutations in P3 protein that could confer entry into a novel host, *Pseudomonas syringae* pv *atrofaciens*. The host range mutants were restricted to a subset of these mutations: only two, or only one, of the nine available to wildtype phi6. Sequencing revealed that wildtype phi6 had additional ways to infect the novel host involving genes other than the host attachment protein P3 that were also unavailable to the E8G and G515S host range mutants. This extreme constraint on serially host shifting was not seen in longer-term studies on the effects of phi6 host range mutations on future evolution. A comparison of the wildtype phi6 and the E8G mutant grown on one of their only common

hosts, the typical lab host *P. syringae* pv *phaseolicola*, showed that there was no difference in the total genetic variation accumulated over 30 days' passaging (ANOVA, $p > 0.05$). There was a single shared high frequency single nucleotide polymorphism (SNP) between one wildtype and one E8G lineage (non-coding a830g on the M segment), but there was no parallel mutation of high frequency SNPs within lineages descended from the same ancestral phi6 strain. Carrying a host range mutation does not appear to affect the evolution of phi6 on the typical lab host. Finally, we compared the evolution of three expanded host range mutants on novel hosts: E8G, E8A and E8K grown on novel hosts *P. syringae* pv *tomato* (tomato) and *P. pseudoalcaligenes* ERA (ERA) for 30 passages. All lineages evolved on tomato performed similarly well on tomato, but there was some effect of the different initial mutations when lineages were grown on ERA. Lineages started with E8A were poorer at growing on ERA than those lineages founded by E8G and E8K. The lineages evolved on tomato showed high levels of parallel mutation compared to those evolved on ERA. Overall, our work shows that initial host range mutations impose both immediate and long-term constraints on evolution on novel hosts.