**An exploration of the molecular evolution of *Cressdnaviricota*, a phylum of highly diverse and ubiquitous ssDNA viruses**

Alvin’s research focuses broadly on understanding the evolutionary dynamics of circular, rep-encoding single stranded (CRESS) DNA viruses. His research is mainly focused on understanding the evolution of cassava mosaic begomoviruses (CMBs), a group of CRESS DNA viruses that cause cassava mosaic disease (CMD). Cassava is a staple food crop throughout Africa and an important industrial crop in Asia, two continents where production is severely constrained by CMD, which accounts for billions of dollars in annual crop losses. The CMD disease complex is comprised of 11 viral species exhibiting accelerated rates of evolution, driven by high mutation rates and genetic recombination. These two processes generate vast amounts of genetic diversity that constrain disease management. Recombination is especially implicated in the emergence of new CMD viral strains; most notably in the emergence of a highly virulent recombinant in the late 1990s that caused severe epidemics in sub-Saharan Africa. While there has been an increase in scientific efforts surveying CMB evolution (including their own NSF-funded international collaboration), a systematic examination of CMB recombination was lacking. Through bioinformatics approaches, he and his lab assessed the role of recombination on the molecular evolution of all field-surveyed, publicly-available CMB isolates. Their results support that recombination has significantly impacted the CMB phylogeny and has driven speciation in the CMD species complex.

Alvin also works on identifying genomic signatures in the genomes of CRESS DNA viruses that can shed light on how their genomes evolve and possibly aid in taxonomical efforts. High-throughput sequencing methods have led to the discovery of many novel groups of uncultivated viruses during the past decade, causing a paradigm-shift from traditional virus taxonomy involving biological features like host range and serology to sequence-guided classification. Consequently, scientists have focused on finding intrinsic genomic patterns that can help define taxonomic ranks for unclassified viruses. Among viral phyla, perhaps none has had a more drastic increase in discovery rate than *Cressdnaviricota*. Some CRESS-DNA viruses are classified, in part, by which genes are found in sense and which in antisense in the virus’ ambisense genomic DNA. Previous studies suggest that there is an unequal usage of synonymous codons, or codon usage bias, in favor of T-ending codons among CRESS-DNA viruses, which is consistent with the observation that single-stranded DNA is highly vulnerable to C->T transitions. Their current goal is to determine if codon usage bias patterns driven by the C->T substitution bias could help identify sequence orientation in ambisense CRESS-DNA viral genomes.

Alvin’s research is funded by a Howard Hughes Medical Institute Gilliam fellowship for Advanced study. He is also involved with DEI efforts as the co-chair of the Ecology and Evolution Graduate Student Association Diversity Committee and functions as a member of both the Ecology and Evolution Graduate Program DEI Committee and the SEBS-wide DEI Committee.