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Title: Recurrent evolution of a virulent viral haplotype in a *Drosophila*/DNA virus system

Abstract: Viruses are a significant burden on animal populations and, as a consequence, host genes involved in antiviral immunity are often rapidly evolving. However, viruses also rapidly adapt to evade host immune defense. Thus, we expect a coevolutionary arms race between hosts and viruses. We study coevolution between *Drosophila innubila* and the *Drosophila innubila* Nudivirus. *D. innubila* lives in the wooded regions of the Sky Islands in southwestern North America. The Sky Islands are mountain ranges surrounded by vast swaths of desert likely limiting migration of flies between populations. Nudiviruses have large circular DNA genomes that experience considerable recombination. In principal the system allows us to study host/virus coevolution in replicate Sky Island populations. To do so, we performed whole genome resequencing of about 100 individuals each from four different populations. To our surprise, we found evidence for significant movement of hosts between populations but almost no movement of the virus. We then performed a genomewide association study to ascertain genetic variants in both the host and virus that are associated with increased viral titer in individuals. We find several tightly linked viral polymorphisms upstream of known virulence factors to be strongly associated with viral titer. These polymorphisms form two 'types' of virus which seem to be maintained under balancing selection. Furthermore, reconstruction of the evolutionary history of the viruses suggests that the polymorphisms re-evolved independently in each population. These results suggest an impressive evolutionary potential in nudiviruses to quickly and repeatedly adapt to their hosts.