Errantiviruses are insect analogues of vertebrate retroviruses. Because retroviruses have high utility for genetic transformation, we wish to investigate whether errantiviruses have a similar potential for genetic modification of pest insects such as mosquitoes. To choose suitable viruses for investigation, we have made a catalog of intact errantiviral sequences in dipteran genomes (those of mosquitoes and flies) and determined the phylogenetic relationship among these viruses. These intact proviral sequences represent "fossil relics" of recent infections that have not experienced inactivating mutational drift and, in many cases, might be used to re-express the virus.

Our search of dipteran genomic sequences has identified 61 distinct errantiviral proviruses in addition to 17, mostly from *Drosophila melanogaster*, that had been previously characterized. Half of these newly identified errantivirus sequences come from the *Aedes aegypti* genome. These 78 errantiviruses divide phylogenetically into 8 major classes, five of which are restricted to mosquitoes, two restricted to flies and one with sublineages in both flies and mosquitoes.

To further characterize these candidate mosquito viruses, we intend to identify those that are transcriptionally active by using RT-PCR of RNA isolated from adult and larval mosquitoes. The tissue-specific expression of the transcriptionally active viruses will then be assayed by *in situ* hybridization. Because of the importance of the gut and salivary gland in the transmission of mosquito-borne pathogens, errantiviruses active in these tissues would be the most suitable to develop as vectors for introducing genetic modifications modulating the transmission of those pathogens.