Tracing Evolutionary Patterns in West Africa: A Phylogenetic Analysis of the HIV-1 and HIV-2 Strains

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The human immunodeficiency virus, or HIV, is responsible for causing the AIDS pandemic and killing millions of people around the world. This project seeks to shed light on the evolutionary relationships between West African subtypes of HIV, including HIV-1 and HIV-2, as well as simian immunodeficiency virus, or SIV, a related virus found in non-human primates. Past studies have not documented the same region and subtypes in detail, and the few trees that have been published lack strong bootstrap or posterior probability support. HIV and SIV sequences from infected humans and primates in West Africa were taken from the National Center for Biotechnology Information and Los Alamos HIV databases. Alignment of the sequences was completed with MAFFT, after which two trees were created. The first was a parsimony-constraint tree produced by PAUP*, while the second was a phylogram produced with a strict molecular clock using BEAST, where the Markov Chain Monte Carlo method of Metropolis-Hastings was run for 120,000,000 iterations. The two trees have much stronger bootstrap values and posterior probabilities on each branch than in previous work, providing a strong foundation for any future research in this area. In addition, they provide powerful evidence for the theory that HIV-1 Subtype O originated from gorilla SIV, strongly suggest that HIV-2 Subtypes A and B came from a single transmission, support multiple new theories for the movement of HIV across West Africa, and propose earlier dates of divergence than the current models predict. These results can be used to better understand the origin of the virus as well as design new treatments targeting specific continuities between strains and subtypes.

Awards Won:
Third Award of $1,000