Geneticists trace the evolution of St. Louis encephalitis

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Before West Nile virus arrived in this country, we had (and still have) a home-grown relative of this pathogen. An epidemic of unknown origin exploded around St. Louis, Missouri in the autumn of 1933, a disease that is now known to be transmitted by mosquitoes from birds to people. Now, a new analysis of the genome of St. Louis encephalitis completed at the Sackler Institute for Comparative Genomics at the American Museum of Natural History (AMNH) is shedding light on the evolution of this virus.

Under the direction of Susan Perkins, Assistant Curator of Microbial Genomics, postdoctoral fellows Gregory Baillie, Sergios-Orestis Kolokotronis, and Eric Waltari sequenced the entire genetic code of 23 strains of the virus that cause St. Louis encephalitis, all from the genus Flavivirus.

Previous research had found that recombination (the cutting and pasting of strands of genetic material, in this case RNA) explained the evolution of this virus, but these studies sequenced just a single gene of the virus. Because the whole-genome approach turned a microscope on the entire set of instructions for St. Louis encephalitis, the AMNH researchers were able to determine that a single mutation in the coding for an envelope protein rather than recombination most likely caused changes that made the virus pathogenic to humans.

“Recombination is important for disease; it makes novel proteins or genes that the immune system has never seen before,” explains Perkins.

“But in this case, it was population dynamics combined with slight changes in the form of point mutations that have been important in the evolution of this virus.”

Genetic analysis also allowed Perkins and colleagues to trace the evolutionary path of the Flavivirus virus. They determined that the older, less derived strains, or more ancestral strains, are from South America.

The North American and Haitian strains were passed from common bird hosts such as finches, robins, blue jays, and doves into humans by the Culex mosquito after the virus exploded into a new continent. To time this event, researchers again turned to the genomic code: by determining the rate of mutation in the virus, Perkins found that the division between the South and North American strains happened about 116 years ago. “St. Louis encephalitis is a perfect storm between infected bird hosts coming into a new area and the mosquito vectors transferring the virus to humans,” says Perkins. “It is the North American version of West Nile.”

St. Louis encephalitis is currently found throughout the United States, and, according to the Centers for Disease Control, there were 4,651 cases between 1964 and 2005. Symptoms range from a mild headache to high fever and tremors. Mortality is between 5 and 30% and is higher among the elderly.

Source: American Museum of Natural History

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