The Connecticut Agricultural Experiment Station

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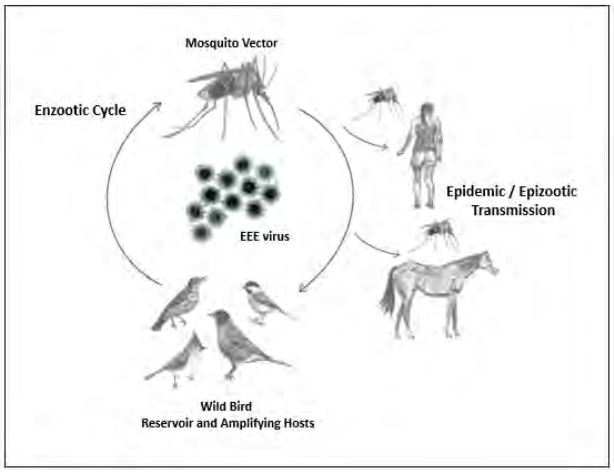
Wood Thrushes Identified as Superspreaders of Eastern Equine Encephalitis, a Highly Pathogenic Mosquito-borne Virus in the Northeastern U.S.

Scientists with the Center for Vector Biology & Zoonotic Diseases, at the Connecticut Agricultural Experiment Station have discovered that the common wood thrush, *Hylocichla mustelina* plays a leading role in introduction and seasonal amplification of eastern equine encephalitis (EEE) virus, a deadly virus transmitted by mosquitoes. The findings published in *PLoS Neglected Tropical Diseases* further identified the blood feeding behavior of the primary mosquito vector, *Culiseta melanura* as the single most important factor affecting local maintenance and build-up of the virus in freshwater woodland swamp habitats in Connecticut.

“EEE virus is a highly pathogenic mosquito-borne zoonosis that is responsible for outbreaks of severe disease in humans and equines, resulting in high mortality and neurological impairment in most survivors,” said Dr. Theodore Andreadis, Center Director and one of the co-authors of the study. "In the past, human disease outbreaks in the northeastern U.S. have occurred intermittently with no apparent pattern. However, during the last decade the region has witnessed recurring annual emergence and expansion into northern New England and southern Canada where the virus had been previously unknown”. According to the CDC, 55 human cases have been documented in the northeast resulting in 23 fatalities since 2003. The underlying factors responsible for this sustained resurgence have eluded scientists and public health officials.

According to Dr. Goudarz Molaei, lead author of the study, “in the northeastern U.S., EEE virus is maintained in an enzootic cycle involving a bird-biting mosquito, *Cs. melanura*, and wild perching birds in freshwater hardwood swamps. However, the identity of key bird species that may serve as superspreaders of the virus in these swamps leading to spill over into humans and equines, has not been established.”



The team tackled this issue by analyzing the blood meal contents of more than 1,100 *Cs. melanura* mosquitoes collected from four EEE virus swamp foci in Connecticut using PCR-based molecular methods and direct sequencing of the mitochondrial cytochrome b gene. Bird abundance in the swamps was also estimated through the use of avian point count surveys that were conducted from April through October for two years. In cooperation with scientists at Oregon State University, they developed an empirically informed mathematical model for EEE virus transmission, the first of its kind, based on the proportion of mosquito blood meals identified from individual bird species in relation to their observed frequency in the swamp.

The authors found that in these swamps, mosquitoes were exposed to a diverse community of birds, feeding on no fewer than 65 different species throughout the course of the season. However, mosquitoes exhibited larger feeding indices on Wood Thrush and a few other virus competent species including: American Robin, Tufted Titmouse, Common Grackle, Chipping Sparrow, Black-capped Chickadee, Northern Cardinal, and Warbling Vireo, thus demonstrating that these birds play prominent roles in supporting EEE virus amplification.

Noted Molaei, “this research provides a basis to better understand the involvement of *Cs. melanura* and key avian hosts in the transmission and ecology of EEE virus and the risk of human infection.”

Journal Reference:

Molaei, G, Thomas MC, Muller T, Medlock J, Shepard J, Armstrong PM, and Andreadis TG. 2016. Dynamics of vector-host interaction and the role of avian species as superspreaders of eastern equine encephalitis virus in the northeastern U.S. *PLoS Neglected Tropical Diseases* 10(1):e0004347. doi:10.1371/journal.pntd.0004347

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