

Evolution of a deadly virus

May 24 2018, by Leigh Macmillan

Infections caused by the mosquito-borne eastern equine encephalitis virus (EEEV) are severe and have high mortality rates for horses—90 percent—and humans—33 percent, with significant brain damage in most human survivors.

Florida has been hypothesized to be the source of EEEV epidemics, but little is known about the evolutionary characteristics of the [virus](#).

Suman Das, Ph.D., and colleagues have now sequenced and analyzed complete genomes of 433 EEEV strains collected within the United States from 1934 to 2014.

They report in the *Journal of Virology* that EEEV appears to evolve relatively slowly and that strains have long-term persistence and higher genetic diversity in Florida, compared to strains from northeastern [states](#) such as New York and Massachusetts.

The findings support a model in which Florida is a major source of EEEV, with viruses that are endemic in Florida migrating and seeding outbreaks in northern states. The results may have important implications for the control and prevention of other mosquito-borne viruses in the Americas.

More information: Yi Tan et al. Large scale complete genome sequencing and phylodynamic analysis of eastern equine encephalitis virus reveal source-sink transmission dynamics in the United States, *Journal of Virology* (2018). [DOI: 10.1128/JVI.00074-18](https://doi.org/10.1128/JVI.00074-18)

Provided by Vanderbilt University

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