# A novel finding in how chikungunya virus has spread to new vectors and locations

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Researchers at the University of Texas Medical Branch have discovered how a key protein switch allows Chikungunya Virus (CHIKV) to spread to new vectors. The study, published December 7 in PLoS Pathogens, explains how the virus has increased its ability to infect and be transmitted by the Asian tiger mosquito, Aedes albopictus.

CHIKV is an emerging arbovirus associated with several recent large-scale epidemics of arthritic disease. The virus has formerly been known to be carried primarily by the mosquito Aedes aegypti. However, a recent epidemic in the Indian Ocean islands suggested that something else was carrying the virus, as Ae. aegypti are not found there. In fact the relative Asian tiger mosquito, Ae. albopictus, was present. This prompted the team, led by Dr. Stephen Higgs, to look further into the virus.

In an earlier study it had been found that the epidemics on islands in the Indian Ocean were associated with a strain of CHIKV with a mutation in the envelope protein gene (E1-A226V). Therefore, the researchers investigated the role of the E1-A226V mutation on the fitness of CHIKV in both types of mosquitoes. The team infected mosquitoes with two genetically-engineered clones of the virus, one with the mutation and the other without.

The team found the mutant virus out-competed the other virus with respect to transmission by the tiger mosquito. This proved that EI-A226V is directly responsible for CHIKV adaptation to the Asian tiger

mosquito, explaining why the virus was found in an area which lacks the typical vector mosquito.

The Asian tiger mosquito is present in many countries. Both mosquito species are currently present in the U.S. and the Asian tiger mosquito is spreading in Europe. The findings suggest that, especially with the global climate warming, CHIKV could expand to new geographic locations.

Citation: Tsetsarkin KA, Vanlandingham DL, McGee CE, Higgs S (2007) A single mutation in Chikungunya virus affects vector specificity and epidemic potential. PLoS Pathog 3(12): e201. doi:10.1371/journal.ppat.0030201 (www.plospathogens.org)

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