Computer model developed to assess risk of a Zika epidemic in real-time

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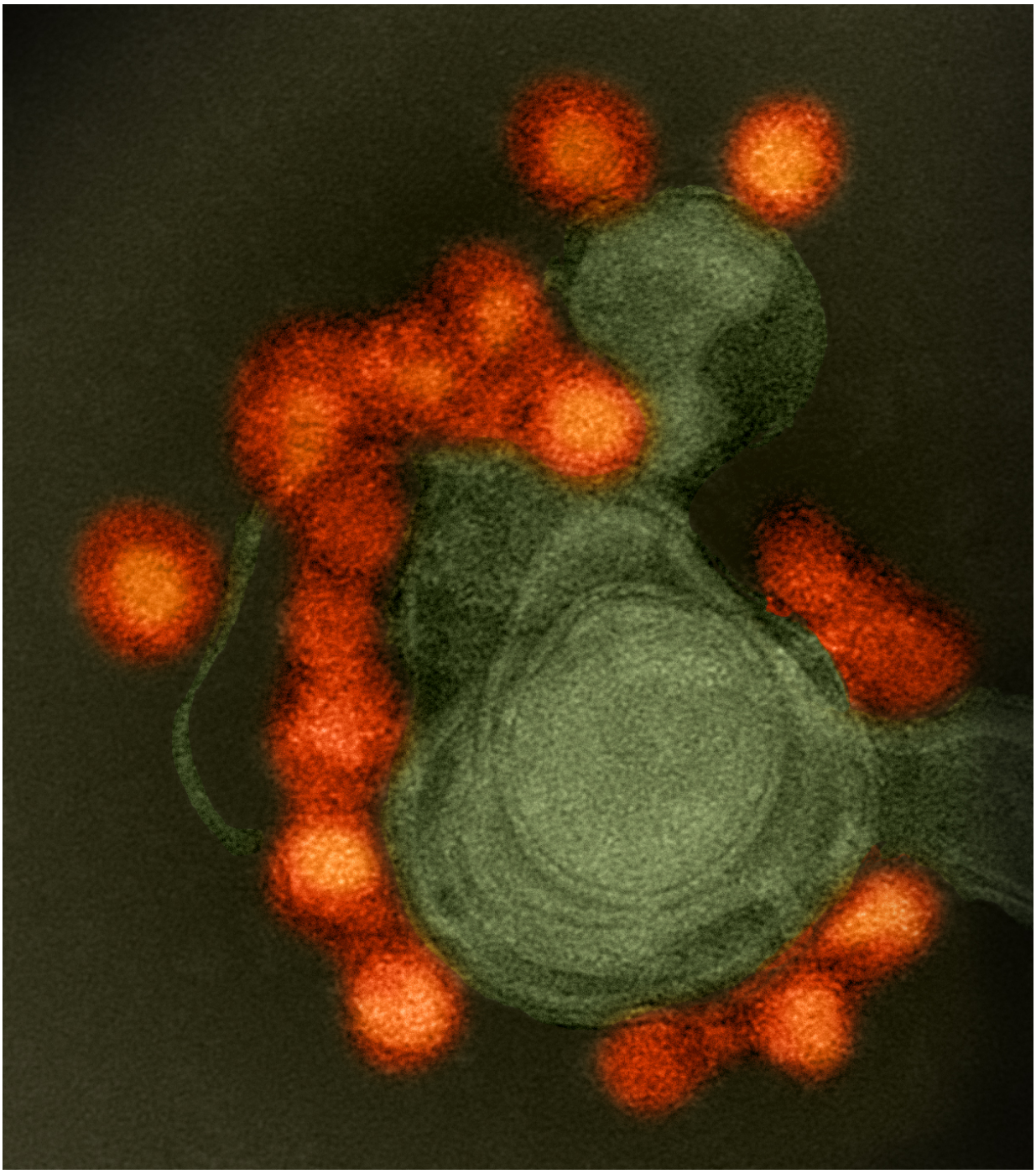

Transmission electron microscope image of negative-stained, Fortaleza-strain Zika virus (red), isolated from a microcephaly case in Brazil. The virus is associated with cellular membranes in the center. Credit: NIAID

A new model for assessing real-time risk of a Zika virus epidemic in the United States is described in research published in the open access journal *BMC Infectious Diseases*. The computer simulation, based on data from Texas including population dynamics, historical infection rates, socioeconomics, and mosquito density, is designed to help policymakers gauge the underlying epidemic threat as cases first appear in US cities.

In 2016, the US Centers for Disease Control and Prevention (CDC) recommended that public health officials trigger epidemic intervention when two non-familial locally-acquired cases of Zika are reported in an area. However, Zika importation and transmission rates vary widely, meaning that two such cases may pose very different threats in different locations. In this study, the authors describe a computer model that can be used to calculate the probability that the presence of two Zika cases in a given area will lead to an epidemic, based on real-time simulations of all the counties in the state of Texas.

Across the 254 counties in the state of Texas, the model predicted that Harris County, which includes the city of Houston, and Travis County, which includes the city of Austin, have the highest rates of Zika introductions by infected travellers. The counties located in the southeastern area of Texas were found to have the highest risk of Zika transmission from one person to another. The one Zika outbreak that occurred in Texas in Cameron County in November of 2016 falls within this region.

By combining all the data, the researchers found that the risk of a Zika epidemic varies widely across Texas counties. Even if two cases are reported locally, most Texas counties will have nearly no risk of an epidemic, while a few will have greater than 50% epidemic risk.

Spencer Fox, co-lead author and PhD Student at the University of Texas

at Austin, said: "Our model was designed to quantify the risk of local Zika outbreaks as cases accumulate across Texas, taking into account international travel patterns, mosquito habitat, and the low detection rate of Zika infections. Its flexible framework can be readily applied to other US states and adapted for risk assessments of other emerging arboviruses, including Chikungunya, Dengue, and Yellow fever."

Lauren Castro, co-lead author and PhD student at The University of Texas at Austin, said: "The CDC's recommendation to intervene following two reported Zika cases should ensure early action everywhere, even though Zika epidemic risk can vary enormously, even within a single state. Our model quantifies that variation in risk and can help officials prioritize high risk areas for monitoring and intervention resources."

Dr. Lauren Ancel Meyers, senior author and Professor at The University of Texas at Austin, added: "Zika outbreaks require the importation of the disease by infected travellers followed by local mosquito-borne transmission. Our model combines these processes to estimate local emergence risk. It enables policymakers to think carefully about risk tolerance—the certainty required before intervening and the potential consequences of premature or delayed interventions."

This is the first study to assess both the risk of Zika arrival to an area and the risk of local spread by mosquitoes. The flexibility of the model design means that as new information becomes available on Zika dynamics, epidemiology and biology it can be updated to help public health officials assess situational awareness, according to the researchers

More information: Lauren A. Castro et al, Assessing real-time Zika risk in the United States, *BMC Infectious Diseases* (2017). DOI: 10.1186/s12879-017-2394-9

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