Imported Infections’ Importance: Global Change Driving Dengue Dynamics

Mikkel B. Quam

Akademisk avhandling

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Fakultetsopponent: Professor Dave D. Chadee
Department of Life Sciences, The University of The West Indies
St. Augustine, Trinidad and Tobago
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Abstract

Background Dengue is a significant problem of international health concern. According to the World Health Organization in 2012, globally, dengue is “the most important mosquito borne viral disease” with incidence 30 higher than it had been 50 years ago. While most of the burden of disease associated with dengue is located in areas with a tropical and sub-tropical climate, increasing evidence suggests temperate areas are also at risk. Considering the recent introduction of relevant mosquito vectors into Southern Europe, and increasing numbers of imported dengue via travelers, Europe and other temperate areas may be increasingly at risk for dengue emergence, establishment and local transmission in the foreseeable future.

Methods Recent dengue emergence in Madeira and reemergence in Tokyo underline the hypothesis that passenger air-travel can be an important conduit for the importation of vector-borne disease leading to emergence in naïve areas climatically suitable for dengue transmission, including parts of Europe. Combining information on travel with virus genetic similarity was useful in discerning likely pathways of for the importation of infections. Generalizing information learned from outbreaks in Tokyo and Madeira with global epidemic intelligence, global travel networks, and climate change projections, leads to more refined understanding of the magnitude of dengue infectious imported into temperate areas and these virus introduction events’ potential implications for seeding epidemics in the 21st century.

Results While compared to total travel, imported dengue events and epidemics of dengue outside the tropics are rare, our combined evidence and modeled estimations suggest strongly that epidemic dengue emergence in temperate areas is possible and will continue to increase. We found that global change dynamics including warming temperatures in the much of the northern hemisphere and increasing passenger interconnectivity between areas endemic for dengue and dengue free areas are key mechanisms partly explaining these unprecedented epidemiological transitions.

Conclusion While we calibrated our models on information known about dengue, many elements of the methods and conclusions may increase understanding of the potentially global implications for imported infections of other climate-sensitive infectious diseases that may have similar parameters. During 2016 and the years to come, techniques developed in this doctoral research will contribute to models used in risk analysis for vector-borne diseases of interest, including the increasing important potential for imported Chikungunya and Zika viruses into a variety of unexposed areas.

Keywords
Dengue, Zika, Vector-borne Disease, Aedes, Global Change, Climate Change, Viral Evolution, Phylogenetics, Travel, Interconnectivity, Disease Modeling, Madeira, Italy, Japan, Europe

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