Global risk of Zika virus depends critically on vector status of Aedes albopictus

Constância F J Ayres recently pointed out that Zika virus has been collected from several mosquito species including those from the genera, Anopheles, Culex, and Mansonia besides Aedes. Moreover, at least ten Aedes species are known to harbour Zika virus. However, the presence of the virus does not automatically make the species an efficient vector for the disease. It is, therefore, unfortunate that a recent risk map published in The Lancet considers Aedes aegypti and Aedes albopictus together. On the same basis, WHO has predicted that the virus will establish itself in all countries in the Americas except Canada and Chile.

However, while the vectorial competence of A aegypti is well established, that of A albopictus is not. Although there is evidence of the potential role of A albopictus, there is no quantitative estimate of its efficiency. It is, therefore, useful to conduct a risk analysis that considers two cases: spread driven by A aegypti presence alone and by both species.

In the context of dengue we have previously modelled the habitat suitability for both species globally and integrated the results with air transport data. We quantified the relative risk of Zika virus spread from infected travellers arriving at airports in new regions by aggregating incoming air travel from infected areas with vector habitat suitability at the destination. The habitat suitability models used a standard maximum entropy algorithm. Source airports were defined as those in areas with autochthonous Zika virus transmission as of Feb 15, 2016, according to the US Centers for Disease Control and Prevention and with vector suitability greater than 0·5 (on a 0–1 scale). Travel statistics from the International Air Transport Association were used to generate relative passenger travel volumes, which include direct and indirect routes (with stopovers). Habitat suitability at each airport was aggregated to circles with a radius of 50 km.

The following inferences can be drawn from the resulting relative risk map (figure). First, if A aegypti is the only competent Zika virus vector, then risk is geographically restricted; in North America to Florida, Louisiana, and Texas. Second, if A albopictus is a competent vector, then there is risk of autochthonous transmission cycles in Canada, Chile, much of western Europe, as well as south and east Asia. Third, for all these areas, the risk compounds that from flights originating in other areas historically endemic for Zika virus.

These results underscore Ayres’ point that the vector competence of the various potential mosquito species should be a matter of immediate quantitative assessment.

We declare no competing interests.

Lauren M Gardner, Nan Chen, Sahotra Sarkar
l.gardner@unsw.edu.au
University of New South Wales Australia, Sydney, NSW, Australia (LMG, NC); and Department of Integrative Biology, University of Texas, Austin, TX, USA (SS)


Figure: Risk map for spread of Zika virus
The circles depict the top 100 cities to which Zika virus might be imported from current infected regions of Latin America and which have suitable habitat for Aedes aegypti or Aedes albopictus in the surrounding region. The size of the circle is the estimated relative risk. Solid red indicates the risk from A aegypti alone. Open circles indicate total risk from both species. The inset shows the status of south Florida, the Caribbean, and nearby areas in more detail.


