Spatial and temporal analysis of Zika and chikungunya epidemics in Colombia

Kelly Charniga, Imperial College London
Dr Zulma Cucunubá, Imperial College London
Dr Pierre Nouvellet, University of Sussex
Dr Christl A. Donnelly, Imperial College London & University of Oxford

What is the research?

In 2014-2017, Latin America experienced back-to-back outbreaks of chikungunya virus followed by Zika virus. Both viruses are transmitted by Aedes mosquitoes and had not been previously reported in the Americas. People with symptoms typically experience fever, rash and joint pain. Additionally, Zika virus infection during pregnancy increases the risk of severe birth defects in newborns and chikungunya fever can cause chronic joint pain that lasts weeks or months.

Colombia was one of the most affected countries during the recent outbreaks with over 100,000 Zika virus and 400,000 chikungunya virus suspected and laboratory-confirmed cases. Using surveillance data from Colombia's National Institute of Health, this study first estimated the week of invasion in each city (Figures 1-2). Next researchers fitted gravity models to study the invasion dynamics of both viruses between cities in Colombia. Gravity models describe movement from one location to another based on population size and distance.

Why is this research necessary?

There are currently no approved drugs to treat or prevent Zika virus disease or chikungunya fever and both diseases have the potential to cause further large epidemics in Latin America. Most spatiotemporal research has focused on studying these diseases separately. However, Zika virus and chikungunya virus share common vectors and were introduced into the same regions with large susceptible populations. Studying them together will improve understanding of disease spread at the subnational level, which is important for informing preparedness activities for future outbreaks.

What is the research impact?

This research found evidence that both viruses were introduced into Northern Colombia and intermediate levels of density dependence best described transmission. Although a small number of long-range transmission events were identified early in the outbreaks, invasion mainly occurred over short distances. Geographic distance fit the data better than estimated travel time to the nearest city. Both humans and vectors were likely responsible for disease spread across the country. However, the relative contribution of human versus vector movement on spatial transmission remains poorly understood. Future work on quantifying this relationship would have broad implications for surveillance and control for other vector-borne diseases such as dengue, Mayaro and yellow fever. The invasion dynamics of other epidemics could also be analysed using the approach from this study.
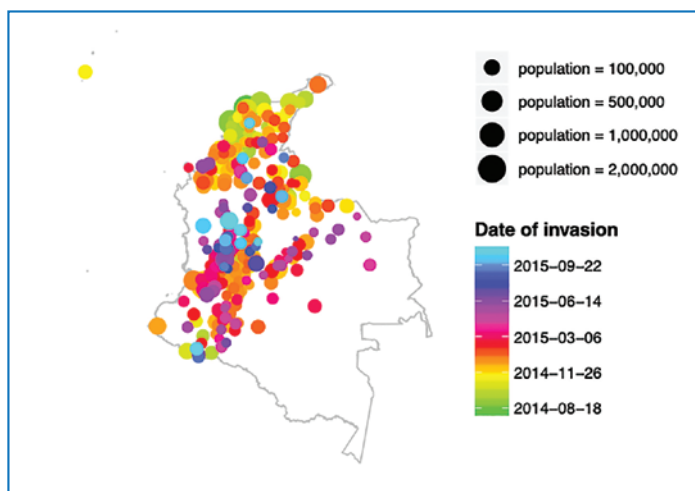
Figure 1. Date of invasion estimated from weekly times series of chikungunya virus. Each city is represented by an individual circle. Circle size is proportional to the size of the city's population and color reflects date of invasion (green areas have the earliest onsets and blue areas have the latest).
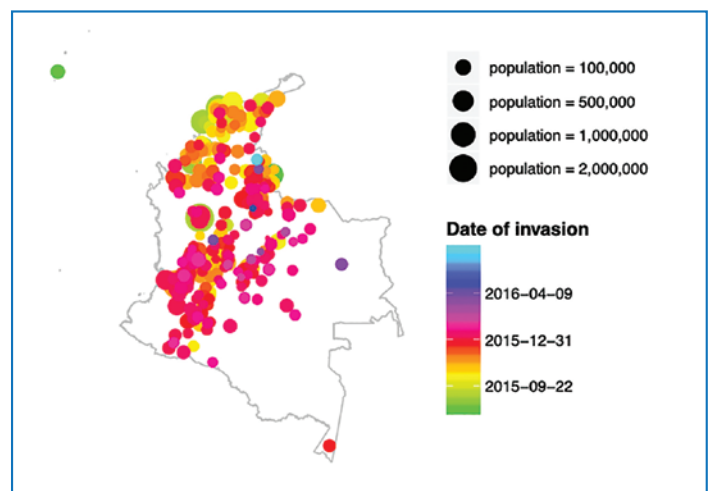
Figure 2. Date of invasion estimated from weekly times series of Zika virus. Each city is represented by an individual circle. Circle size is proportional to the size of the city's population and color reflects date of invasion (green areas have the earliest onsets and blue areas have the latest).