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Estimating a feasible serial interval range for Zika fever

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Abstract

Objective: In this paper, we determine a feasible serial interval range for Zika fever.

Methods: Existing estimates of intrinsic and extrinsic incubation, as well as viraemic period, are used to develop a simple life cycle model of Zika fever to determine expected time between two consecutive infections in a chain of transmission. Case count alerts from the HealthMap digital surveillance system are then used to assess the feasibility of our estimated serial interval range.

Findings: Our model suggests that 10 to 23 days may be a feasible serial interval range for Zika fever. Though sparse, preliminary data from the Zapaca department of Guatemala and the Caribbean island of Martinique provide supporting evidence for this range.

Conclusion: Serial interval estimates from Zacapa (serial interval = 15 days) and Martinique (serial = 16 days) are reasonable when compared against estimates for similar arbovirus diseases, such as dengue [15, 17 days]. This suggests that our estimated serial interval range for Zika fever in Central and South America is likely feasible; moreover, it lends credibility to the recent practice of repackaging existing dengue models for predicting the forthcoming burden of Zika fever and potential Zika-related diseases (e.g. Guillain-Barré syndrome, microcephaly).
Objective. Growing concern over the potential relationship between Zika virus in pregnant women and microcephaly in newborn babies has brought global attention to an ongoing outbreak of the disease in Central and South America. Though evidence of vertical and sexual transmission exists, the virus is primarily transmitted via Aedes mosquitoes. It is possible that Zika fever was introduced to the Americas during the 2014 FIFA World Cup and has since been propagated by the density of competent vectors in the region.

Prior to 2015, events related to Zika virus were considered to be fairly rare; because of this, epidemiological research has been somewhat limited to date. Markedly, there currently exists no estimate for the serial interval (generation time) of Zika fever in the literature. The serial interval (SI) of a given disease may be defined as the average length of time between two consecutive infections in a chain of transmission. While largely context-driven and variable across both outbreaks and individuals, establishing mechanistically feasible upper and lower bounds is necessary for mathematical modeling and disease mitigation.

Methods. Since the discovery of Zika virus in 1947, estimates for intrinsic incubation in humans (three to 12 days) and extrinsic incubation in mosquitos (four to six days post-meal) – as well viraemic period in infected humans (between days three and five after symptom onset) – have been established. Using these parameter estimates, we developed a simple life cycle model for Zika fever to determine the expected time between two successive cases (figure). We then assessed the feasibility of our estimated serial interval range by examining Zika fever case count data over time from the HealthMap digital disease surveillance system.

Findings. Assuming that historical parameter estimates for intrinsic incubation, extrinsic incubation, and viraemic period remain accurate, our model suggests that 10 to 23 days may be a feasible serial interval range for Zika fever (figure).

After narrowing our search criteria to settings with minimal likelihood of reintroduction and confirmed autochthonous Zika virus transmission, we found case count data from two suitable locations in the HealthMap system: the Zacapa department of Guatemala and the small Caribbean island of Martinique. An index case was reported in Zacapa on 24-November-2015; then, 15 days later, 22 subsequent cases were reported on 9-December-2015. More recently, an index case was reported in Martinique on 23-December-2015; this was followed by a report of 11 subsequent cases 16 days later on 8-January-2016.

Conclusion. Properly estimating the serial interval of any given disease is essential for the assessment of real-time epidemic dynamics, in turn enabling more effective deployment and evaluation of interventions. Though sparse, preliminary digital surveillance data from the HealthMap system suggest that our estimated serial interval range of 10 to 23 days is likely feasible for Zika fever in the current context of Central and South America.
Notably, these data-driven serial interval estimates from Zacapa (SI = 15 days) and Martinique (SI = 16 days) are reasonable when compared against existing estimates for similar arbovirus diseases, such as dengue [15, 17 days]. This congruence lends credibility not only to our estimated serial interval range, but also to the ongoing repackaging of existing dengue models for predicting the forthcoming burden of Zika fever and potential Zika-related diseases (e.g. Guillain-Barré syndrome, microcephaly).

Continued collection and analysis of case count data over time, via both digital and traditional means, will allow us to further refine our understanding of Zika fever and its transmissibility. If data similar to what we acquired for Zacapa and Martinique become available for other locations, it may be possible to determine an empirical probability distribution for the serial interval associated with Zika fever – allowing us to build more accurate projection models in the months and years ahead.
Figure Legend. A simple life cycle model depicting a feasible serial interval range for Zika fever. Two examples are shown to demonstrate the lower (MIN = 10 days) and upper (MAX = 23 days) bounds of the range. *Time between viraemia (infectivity) and bite time is assumed to be negligible.
References


