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Role of short-term dispersal on the dynamics of Zika virus in an extreme idealized environment

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ABSTRACT

In November 2015, El Salvador reported their first case of Zika virus (ZIKV) infection, an event followed by an explosive outbreak that generated over 6000 suspected cases in a period of two months. National agencies began implementing control measures that included vector control and recommending an increased use of repellents. Further, in response to the alarming and growing number of microcephaly cases in Brazil, the importance of avoiding pregnancies for two years was stressed. In this paper, we explore the role of mobility within communities characterized by extreme poverty, crime and violence. Specifically, the role of short term mobility between two idealized interconnected highly distinct communities is explored in the context of ZIKV outbreaks. We make use of a Lagrangian modeling approach within a two-patch setting in order to highlight the possible effects that short-term mobility, within *highly distinct* environments, may have on the dynamics of ZIKV outbreak when the overall goal is to reduce the number of cases not just in the most affluent areas but everywhere. Outcomes depend on existing mobility patterns, levels of disease risk, and the ability of federal or state public health services to invest in resource limited areas, particularly in those where violence is systemic. The results of simulations in highly polarized and simplified scenarios are used to assess the role of mobility. It quickly became evident that matching observed patterns of ZIKV outbreaks could not be captured without incorporating increasing levels of heterogeneity. The number of distinct patches and variations on patch connectivity structure required to match ZIKV patterns could not be met within the highly aggregated model that is used in the simulations.

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1. Introduction

Zika virus (ZIKV), an emerging mosquito-borne flavivirus related to yellow fever, dengue, West Nile and Japanese encephalitis (Hayes et al, 2009), has taken the Americas by storm. ZIKV is transmitted primarily by *Aedes aegypti* mosquitoes, which also transmit dengue and chikungunya. As of February 9, 2016, according to the CDC (CDC(a), 2016), ZIKV cases had been reported throughout the Caribbean, Mexico and South America with the exception of Chile, Uruguay, Argentina, Paraguay and Peru. Several states within the United States had also reported ZIKV cases (Petersen, 2016) and although it is expected that ZIKV will be managed effectively within the USA, the possibility of localized ZIKV outbreaks has yet to be ruled out.

Phylogenetic analyses have revealed the existence of two main virus lineages (African and Asian) (Faye et al., 2014; Haddow et al., 2012) albeit so far, no concise clinical differences have been identified between infections with strains from these lineages. Further, the reports are not surprising since most African samples come from a rhesus sentinel in Uganda, where ZIKV was first discovered, during primate and mosquito surveillance efforts aimed at assessing Yellow Fever trends in 1947 (Dick, Kitchen, & Haddow, 1952). The African lineage has circulated primarily in wild primates and arboreal mosquitoes such as *Aedes africanus* within a specific geographic habitat; a narrow equatorial belt running across Africa and into Asia. Spillover infections in humans have rarely occurred even in areas found to be highly enzootic (Fauci & Morens, 2016; Musso, Cao-Lormeau, & Gubler, 2015). The Asian lineage, which seems to have originated from the adaptation of the virus as it successfully invaded a different vector, *Aedes aegypti*, a variant capable of infecting human populations rather effectively, (Fauci & Morens, 2016; Haddow et al., 2012), is the dominant type in the Americas.

The first human infection was reported in Nigeria in 1954 (Macnamara, 1954). The evidence of when ZIKV moved out of Africa and Asia was provided by the 2007 outbreak in Yap Island in the Federated States of Micronesia (Duffy et al., 2009); an outbreak followed by larger outbreak in French Polynesia in 2013–2014 (Cao-Lormeau & Musso, 2014). The virus then appeared in New Caledonia, the Cook Islands and Eastern Islands (Musso, Nilles, & Cao-Lormeau, 2014). Decades old data from African researchers seem to support the possibility that ZIKV spread may have been facilitated by prior chikungunya epizootics (Fauci & Morens, 2016). If this is the case then the pattern seemed to have repeated itself in 2013 when chikungunya spread from west to east, a sequence of outbreaks followed by ZIKV outbreaks (Fauci & Morens, 2016).

In early 2015, ZIKV was detected in Brazil. Phylogenetic analyses of the virus isolated from patients, placed the Brazilian strains within the Asian lineage (Zanluca et al., 2015); that is, the one previously detected during the French Polynesian outbreak (Cao-Lormeau et al., 2014). Since the first detection of ZIKV in Brazil, we have seen its range to grow reaching rather quickly the nations of Bolivia, Brazil, Colombia, Ecuador, French Guyana, Guyana, Paraguay, Suriname and Venezuela (CDC(c), 2016). Furthermore, several Central America countries have now been invaded by the ZIKV, including Costa Rica, El Salvador, Guatemala, Honduras, Nicaragua and Panama (CDC(d), 2016). As of September 23, 2016, all of the nations in the Americas have experience active ZIKV outbreaks with the exception of Canada, Chile and Uruguay (CDC(f), 2016). The rapid geographic expansion of ZIKV has led the World Health Organization (WHO) to declare it an international public health emergency (W. H. O. (WHO), 2016).

It has been estimated that about 80% of people infected with ZIKV are asymptomatic (Zika virus, 2016; Duffy et al., 2009) in line with various vector born diseases spread by *Aedes aegypti* mosquitoes. ZIKV clinical manifestations include dengue-like symptoms, that is, arthralgia, particularly swelling, mild fever, lymphadenopathy, skin rash, headaches, retro orbital pain, and conjunctivitis, which normally last for 2–7 days (Zika virus, 2016; W. H. O. (WHO), 2016; Zanluca et al., 2015). The similarities in symptoms, sources of mis-identification, bring a high level of uncertainty in efforts to asses the number of patients infected with ZIKV. It is believe that it may be higher than what it has been reported (Fauci & Morens, 2016; Salvador & Fujita, 2015). Moreover, for example, co-infection with dengue and ZIKV is not uncommon and as a result ZIKV diagnosis is difficult (Dupont-Rouzeyrol et al., 2015).

At present, there is no ZIKV vaccine available. Further, ZIKV infections are being linked with neurological (microcephaly) and auto-immune (Guillain-Barré syndrome) complications. Evidence supports a troubling new transmission mode for a vector born disease, namely that of sexual transmission (CDC(b), 2016; W. H. O. (WHO), 2016). Education on ZIKV modes of transmission and ways of preventing transmission are essential to halt ZIKV spread at regional, national and global levels. Control measures are limited and include the use of insect repellents to the use of protection while engaged in sexual activity and sex abstinence (CDC(b), 2016). An inexpensive effective way to diagnose ZIKV seems to have been found. Scientists from Arizona State University and Harvard University have created a diagnostic tool, similar to a pregnancy test, capable of given a quick, effective, simple and inexpensive way of diagnosing ZIKV infections (Gazette, 2016; The Biodesign Institute, 2016).

Resource limited and poor nations face challenges that make the use of standard efforts and approaches aimed at controlling vector borne diseases ineffective due to extreme variations in the levels of public safety, gang violence and conflict. A lack of attention to the threats posed by the weakest links in the global spread of diseases poses a serious threat to global health policies (see (Castillo-Chavez et al., 2015; Chowell, Castillo-Chavez, Krishna, Qiu, & Anderson, 2015; Espinoza, Moreno, Bichara, & Castillo-Chavez, 2016, p. pp.123; Patterson-Lomba, Goldstein, Gómez-Liévano, Castillo-Chavez, & Towers, 2015, 2016, p. pp.1011; Perrings et al., 2014; Zhao, Feng, & Castillo-Chavez, 2014)). The