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Modelling Zika Virus, Dengue Fever and Chikungunya Virus: Gaining Insights into the Co-Dynamics of the Three Diseases

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Abstract The recent spike in the concurrent circulation of Zika, Dengue fever, and the Chikungunya virus poses a severe threat to public health, both at home and in the diaspora. This study dives into the interplay of these three diseases, applying mathematical analysis to explain their co-dynamics within a population where they coexist. A comprehensive investigation of the model indicates that the sub-models experience backward bifurcation when the relevant reproduction numbers for each disease fall below unity. To gain insights, real-life data from Espirito Sant o State in Brazil, where both diseases are co-circulating and endemic, was gathered and incorporated into our model. This allowed us to estimate important parameter values that were embedded in the model. Through uncertainty and sensitivity analysis, we identified the top-ranked parameters that drive the spread of these three diseases, which are, effective contact rate of infected mosquitoes with susceptible humans, infected humans interacting with susceptible mosquitoes, and sexual transmission (specifically for the Zika virus). Simulations of the comprehensive Zika-Dengue-Chikungunya model revealed that minimizing the biting and contact rates of mosquitoes with humans decreases the disease load. Conversely, the absence of pesticide spraying and failure to utilize treated nets, together with unprotected sexual intercourse with sick individuals, result in the co-circulation of the three diseases, considerably aggravating the overall disease burden.

Keywords Modeling, Zika virus, Dengue fever, Chikungunya, co-infection, stability analysis

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1. Introduction

Zika virus was first found in Africa [1] and subsequently migrated to Yap [2] and French Polynesia, where it caused outbreaks in 2007 and 2013–2014 [3], respectively.

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It also spread to neighboring Pacific countries and later to South American countries, including Brazil and Colombia [4, 5]. In 2015, the virus was commonly transmitted via mosquitoes, but it was discovered that it may also be transferred through sexual contact with an infected individual and also through blood transfusions [4]. The principal way in which the Zika virus is transmitted is by the Aedes species mosquito [9]. Furthermore, it serves as a vector for the dengue virus. Research has suggested that the Zika virus can remain in tropical places outside of Africa and South America, continuing its transmission [10]. The indications of a Zika virus infection consist of fever, skin rashes, and neurological abnormalities, such as microcephaly, in babies born to moms who have been infected [11–13]. The World Health Organization declared a public health emergency of international concern because of the higher prevalence of microcephaly and other neurological abnormalities during the current Zika virus outbreaks in Brazil and French Polynesia [14]. However, the outbreak in French Polynesia witnessed 42 instances of Guillain-Barré syndrome [11, 15]. A previous investigation identified ten occurrences of microcephaly, each linked to severe brain malformations [12]. Given its global potential for dispersion, it is crucial to understand the disease's transmission patterns. On the other hand, dengue fever is an infection transmitted by vectors and largely caused by the dengue virus. This virus comprises multiple serotypes, notably DENV 1 to DENV 4, which are members of the Flavivirus family. This illness poses a severe threat to many countries globally, with the most heavily hit regions being the Americas, subtropical climates, the Eastern Mediterranean, Africa, and particularly the Western Pacific region and Southeast Asia. [16–18]. After malaria, dengue fever emerges as one of the most lethal diseases carried by mosquitoes or other vectors, resulting in thousands of fatalities and impacting over 390 million individuals globally [16, 17]. A 2012 analysis underlines that more than 100 countries globally face the risk of dengue fever infection [19]. This illness is spread by numerous mosquito species, with Aedes, notably Aedes aegypti, functioning as the predominant carriers. Classical dengue fever, commonly known as "break bone fever," typically leads to both modest morbidity and mortality, with patients usually recuperating within one to two weeks from the onset of fever [20]. However, certain individuals may develop severe illnesses such as dengue shock syndrome (DSS) or hemorrhagic fever (DHF) [21]. Every year, the World Health Organization (WHO) registers a substantial number of cases of dengue hemorrhagic fever (DHF) internationally [22]. The principal mechanism of transmission to humans is through bites from mosquitoes infected with the dengue virus [23]. These mosquitoes acquire the virus by feeding on an infected person and subsequently transferring it to others. It is important to emphasize that recovery from one specific DENV serotype gives only partial or transitory immunity against other serotypes [21]. Presently, there is no effective treatment available for dengue virus infection other than fluid replacement therapy, which is most beneficial when begun early. Some traditional medicines are also in existence [24]. Furthermore, there is currently no effective vaccine on the market for preventing dengue virus infection in vulnerable individuals. Although the World Health Organization (WHO) has advocated the development of a dengue vaccine, none has thus far proven effective and accessible on the market. A 2015 report mentioned the creation of the first dengue vaccine in Mexico [25].

Chikungunya, a viral disease carried by mosquitoes, was originally detected in Tanzania in 1952 [26]. In 1964, an epidemic of Chikungunya raged in the Vellore, Calcutta, and Maharashtra regions of India [27]. Another outbreak occurred in 1969