

Mathematical models of disease transmission of Chikungunya: a report

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I. INTRODUCTION

Chikungunya is an infection caused by the chikungunya virus (CHIKV). This virus is a member of the genus Alphavirus, and family Togaviridae. The virus is vectored by *Aedes albopictus* or *Aedes aegypti* mosquitoes and is a deadly disease. The disease is a reemerging arboviral which is epidemic in Africa and Asia. A massive outbreak happened on Reunion Island in 2006. Chikungunya was detected in the first outbreak in 1952 in Tanzania and has continued increasing until now in many tropical and sub-tropical countries. While the disease typically occurs in Africa and Asia, outbreaks have been reported in Europe and the Americas since the 2000s. The incubation period of the Chikungunya virus ranges from one to twelve days, and is most typically three to seven. The disease may be asymptomatic, but generally is not, as 72% to 97% of those infected will develop symptoms. Characteristic symptoms include sudden onset with high fever, joint pain, and rash. Other symptoms may occur, including headache, fatigue, digestive complaints, and conjunctivitis. Chikungunya is generally transmitted from mosquitoes to humans. Less common modes of transmission include vertical transmission, which is transmission from mother to child during pregnancy or at birth. Transmission via infected blood products and through organ donation is also theoretically possible during times of outbreak, though no cases have yet been documented. The disease can be controlled by controlling the vector. Mosquito control focuses on eliminating the standing water where mosquitos lay eggs and develop as larva; if elimination of the standing water is not possible, insecticides or biological control agents can be added. It is challenging that the excessive use of chemical control leads to resistance in vectors.

II. LITERATURE REVIEW

Not many mathematical models have been developed and studied to explain a variety of features on the transmission of Chikungunya. Out of those, many models study Chikungunya and dengue together because both are vectored by the same mosquito, *aedes aegypti*. In this review, they basically report what existing studies have found and discussed.

In [1], a simple, deterministic mathematical model of the transmission of the virus between humans and mosquitoes was constructed and parameterized with the up-to-date literature on infection biology. The model is fitted to the large Reunion epidemic, resulting in an estimate of 4.1 for the type reproduction number of chikungunya. Although simplistic, the model provided a close approximation of both the peak incidence of the outbreak and the final epidemic size. Sensitivity analysis using Monte Carlo simulation demonstrated the strong influence that both the latent period of infection in humans and the pre-patent period have on these two epidemiological outcomes. They showed why separating these variables, which are epidemiologically distinct in chikungunya infections, is not only necessary for accurate model fitting but also important in informing control.

[2] proposed a model, including human and mosquito compartments, that is associated to the time course of the first epidemic of Chikungunya. They computed the basic reproduction number R_0 and showed that there exists a disease-free equilibrium that is locally asymptotically stable if $R_0 < 1$. They gave a necessary condition for global asymptotic stability of the disease-free equilibrium. They proposed a numerical scheme that is qualitatively stable and present several simulations as well as numerical estimates of the basic reproduction number for some cities of Reunion Island. For the episode of 2005, R_0 was less than one, which partly explains why no outbreak appeared. In [3], the authors proposed the first mathematical model to describe the

dynamic transmission of Dengue, Chikungunya, and Zika. They presented two SIR-like models for the human populations and for the vector to describe the single transmission dynamics of dengue, Chikungunya or Zika, and coinfection between two diseases in the same population. They studied analytically the system of 17 and 30 coupled ODEs for each model respectively. Using the signs of eigenvalues, they designed the numerical experiments.

[4] studied the infection of humans with chikungunya virus. Models describing the mosquito population dynamics and the virus transmission to the human population are discussed. The authors gave the

global analysis of equilibria, which used Lyapunov functions and the theory of competitive systems and stability of periodic orbits.

Use of chemical control tools such as adulticide and larvicide and mechanical control would have been useful to control the explosive 2006 epidemic in Reunion Island. Despite this, chemical control tools cannot be of long-time use, because they can induce mosquito resistance, and are detrimental to the biodiversity. It is therefore necessary to develop and test new control tools that are more sustainable, with the same efficacy (if possible). Mathematical models of sterile insect technique (SIT) to prevent, reduce, eliminate or stop an epidemic of Chikungunya are formulated and analysed. [5] proposed a new model that considers pulsed periodic releases, which leads to a hybrid dynamical system. This pulsed SIT model is coupled with the human population at different epidemiological states in order to assess its efficacy. Authors observed that pulsed SIT with small and frequent releases can be an alternative to chemical control tools, but only if it is used or applied early after the beginning of the epidemic or as a preventive tool.

It is reported that the transmission by *Aedes albopictus* (an *Aedes* genus specie) has been facilitated by genetic mutations of the virus and the vector capacity to adapt to non tropical regions. Authors in [6] proposed an optimal control problem, based on biological observations. Three main efforts are considered in order to limit the virus transmission. Noting that there is no vaccine nor specific treatment against chikungunya, the main measures to control the devastating effects are to be taken. The authors studied the time dependent breeding sites destruction, prevention and treatment efforts, for which optimal control theory is applied. They studied the problem analytically and numerically and showed that there exist cost effective control efforts.

In [7], the authors provided estimates of the transmission potential of the virus and assessed the efficacy of the measures undertaken by public health authorities to control the epidemic spread. They developed a model describing the temporal dynamics of *Aedes albopictus*, explicitly depending on climatic factors, coupled to an epidemic transmission model describing the spread of the epidemic in both humans and mosquitoes. The cumulative number of notified cases predicted by the model was 185 on average. This observation agreed with the available data. The probability of observing a major outbreak after the introduction of an infective human case was estimated to be in the range of 32%-76%. Their results confirmed the increasing risk of tropical vector-borne diseases in temperate climate countries, as a consequence of globalization. Their results showed that a timely intervention is extremely important even if the infestation of Chikungunya virus is very high.

The goal of authors in [9] is to understand (1) the differences in transient and endemic behavior of chikungunya and dengue (2) risk of emergence for different virus-vector assemblages, and (3) the role that virus evolution plays in disease dynamics and risk. To study this in depth, They authors proposed a mathematical model of chikungunya and dengue in *Aedes aegypti* and *Aedes albopictus* mosquitoes. They calculated critical conditions and important parameters for virus transmission. They also conducted sensitivity analysis of the model. It was found that chikungunya and dengue exhibit different transient dynamics and long-term endemic levels. While the order of most sensitive parameters is preserved across vector-virus combinations, the magnitude of sensitivity is different across scenarios, indicating that risk of invasion or an outbreak can change with vector-virus accumulation.

III. CONCLUSION

We simply report few studies that exist in literature. As already mentioned, as per our knowledge, there are no mathematical models that study Chikungunya by itself. We found and report models that study CHIKV in conjunction with Zika and/or dengue. It is difficult at this stage to suggest possible directions to study only CHIKV but this report will give a preliminary idea of literature which may guide future researches.

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