Modelling and Analyzing Virus Mutation Dynamics of Chikungunya Outbreaks

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Chikungunya fever, caused by chikungunya virus (CHIKV) and transmitted to humans by infected *Aedes* mosquitoes, has posed a global threat in several countries in 2015. Recent outbreaks in La Réunion, Italy and China are related with a new variant of CHIKV with shorter extrinsic incubation period in contaminated mosquitoes, but the role of this new variant on the spread of chikungunya fever is unclear. We develop a mathematical model that incorporates the virus mutation dynamics in the transmission of CHIKV among mosquitoes and humans. Our numerical simulations show that a substantial virus mutation rate combined with high virus transmission probabilities from mosquito to human, could result in sustainable chikungunya fever outbreaks. Further, we apply Markov Chain Monte Carlo sampling method to fit our model to the 2007 chikungunya fever outbreak data in North-Eastern Italy where the mutant strain was detected. We conclude that the basic reproduction number might be underestimated without considering the mutation dynamics, and our estimation shows that the basic reproduction number of the 2007 Italy outbreak was $\mathcal{R}_0 = 2.035\,[95\%\mathrm{CI}: 1.9424 - 2.1366]$. Sensitivity analysis shows that the transmission rate of the mutant strain from mosquitoes to human is more influential on $\mathcal{R}_0$ than the shortened extrinsic incubation period. We conclude that the virus mutation dynamics could play an important role in the transmission of CHIKV, and there is a crucial need to better understand the mutation mechanism.(Based on a joint paper with Xi Huo, Sanyi Tang, Biao Tang, Kai Wang and Jianhong Wu)

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