



Climate-driven mathematical models to understand the spatio-temporal heterogeneity of a chikungunya outbreak in the presence of widespread asymptomatic infection

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The emergence and persistence of human pathogens in the environment represents a constant threat to society, with global implications for human health, economies and ecosystems. Of particular concern are vector-borne diseases, such as dengue, malaria and chikungunya, which are increasing across their traditional ranges and continuing to infiltrate new regions. This unprecedented situation has been partly attributed to the increase in global temperatures in recent decades which has allowed non-native mosquito species to invade and successfully colonise previously inhospitable environments. The spatio-temporal evolution of these diseases is determined by the interaction of the host and vector, which is strongly dependent on social structures and mobility patterns. In turn, vector populations are thought to be driven by external environmental variables, such as precipitation and temperature. Furthermore, the ability of asymptomatic individuals to successfully transmit the infection and evade control measures can undermine public health interventions. We employed a stochastic model, which explicitly included asymptomatic and undocumented laboratory confirmed cases, and applied it to a documented outbreak in Cambodia in 2012 (Trapeang Roka village, Kampong Speu Province). The resulting estimate of the reproduction number was considerably higher than values obtained for previous outbreaks and highlights the importance of asymptomatic transmission. Subsequently, we develop an agent-based model (ABM), in which each individual is explicitly represented and vector populations are linked to precipitation estimates in a tropical setting. The model is implemented on both scale-free and regular networks. The spatio-temporal transmission of chikungunya is analysed and the presence of asymptomatic silent spreaders within the population is investigated in the context of implementing travel restrictions during an outbreak. Preventing the movement of symptomatic individuals alone is found to be an insufficient mechanism to halt the spread of the disease, which can be readily carried to neighbouring nodes via sub-clinical individuals. Furthermore, the impact of topology structure versus precipitation levels is assessed and precipitation is found to be the dominant factor driving spatio-temporal transmission. Our results highlight the urgent need to establish adequate monitoring and mosquito control programs in vulnerable countries. These models can help to inform public health officials on both the impact and potential spatial expansion of vector-borne diseases through both urban and rural regions under the influence of dynamic climatic conditions. Given the climate sensitivity of vector-borne diseases, such as chikungunya, it is important to link the monitoring of meteorological conditions to public health surveillance and control.