

Pathogen Evolution and Vector-Borne Infection Emergence

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Recent years have seen vector-borne viral infections such as dengue, chikungunya and Zika become rising sources of global public health concern. The re-emergence of chikungunya in particular has been linked to pathogen mutation and a subsequent increase in efficiency of transmission via a secondary vector, such as *Ae. albopictus*. This change in vector brings about the possibility of spread of infection to areas where the population of the primary vector, *Ae. aegypti*, is either very low or absent – a phenomenon which was previously less likely. Prior work has looked at the effects of pathogen mutation on the probability of infection emergence and found that occasional mutation events can lead to infection emergence even when the average number of secondary infections (R_0) is less than the threshold value of 1. We applied this idea to vector-borne infections by incorporating their characteristic two-step transmission into a simulated branching process theory-based model and investigated the resulting impact on emergence probabilities. Our results suggest that there is a possibility of emergence even when the R_0 of only one step goes to zero (provided that the other step has a non-zero R_0) and indicate a dependence of emergence on the relative mutation probabilities of the two steps. We also compared the effect of host versus vector introduced infections to identify regions where introduction via one type of individual leads to a higher emergence probability than introduction via the other. Our stochastic model provides a framework to build upon for further analysis of mutation and infection emergence and has the benefit of successfully reflecting the inherently random nature of both mutation and transmission of infection through the population.