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Beyond the biting: a comparative study of dengue modeling approaches

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Mathematical models play a crucial role in assisting public health authorities in disease control decision-making. For mosquito-borne diseases, integrating host and vector dynamics into models can be highly complex, particularly due to limited data availability, making system validation challenging.

In this study, extensions of SIR-type systems were proposed to model dengue fever transmission dynamics. The models differed in their treatment of mosquito dynamics: one incorporating it implicitly [1], while the other, explicitly modeling mosquito-host contact [2]. Both models considered temporary immunity after primary infection and disease enhancement in secondary infection, analogous to the temporary cross-immunity and the Antibody-dependent enhancement biological features observed in dengue epidemiology.

Qualitative analysis using bifurcation theory and numerical experiments revealed that the immunity period and disease enhancement outweighed the impact of explicit vector dynamics. Both models demonstrated similar bifurcation structures [3], that is, similar spread scenarios, indicating that explicit vector dynamics are only justified when assessing the effects of vector control methods. Otherwise, the additional complexity in the model is unnecessary, since both systems display similar dynamics.

The study underscores the importance of using simple models for mathematical analysis, initiating crucial discussions among the modeling community in vector-borne diseases.

Keywords: dengue fever, temporary cross-immunity protection, vector-host model, host-host model

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