Underlying Complexity in Dengue Reinfection Dynamics: Backward Bifurcation and Serotype Invasion in a Multi-Serotype Model

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Abstract

Reinfection plays a central role in dengue dynamics, as secondary infection with a different serotype may lead to severe forms such as Dengue Hemorrhagic Fever (DHF) through Antibody-Dependent Enhancement (ADE). We propose a multi-scale nested immuno-epidemiological model coupling within-host immune dynamics and between-host transmission. The model accounts for primary and secondary infections, capturing the interplay between immunity and epidemiological spread [1]. We show the occurrence of backward bifurcation, implying that the basic reproduction number alone does not ensure disease eradication. We also derive an invasion reproduction number characterizing the ability of a new serotype to invade a population where another is endemic. These results highlight the underlying complexity of dengue reinfection dynamics and the role of ADE in shaping transmission and disease severity.

References

[1] M. Adimy, C. Dugourd-Camus, and R. Taieb, *Multi-serotype nested immuno-epidemiological model for dengue hemorrhagic fever involving backward bifurcation and serotype invasion*, Discrete and Continuous Dynamical Systems - B, 2026 (Early access), doi: 10.3934/dcdsb.2026028.

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