Competitive evolution of H1N1 and H3N2 influenza viruses in the United States: A mathematical modeling study

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Rationale and objective: The rationale of this study lies in the ongoing public health concern posed by seasonal influenza, which has considerable health and economic impacts globally. A key challenge in preventing and controlling influenza epidemics is the antigenic evolution of the viruses - they change over time, making it difficult to develop vaccines that are effective for a long duration.

The objective of this research was to create and use a novel modeling framework that accounts for these antigenic changes, to gain a better understanding of the evolution and transmission dynamics of H1N1 and H3N2 influenza viruses in the United States. This model was built on changes in the viruses' amino acid sequences and epidemiological data from October 2002 to April 2019. The researchers aimed to investigate how the antigenic changes influence disease transmission and how they can be incorporated into models for better predictive ability.

Summary: This study aimed to better understand and model the evolution and transmission of H1N1 and H3N2 influenza viruses, focusing on their antigenic changes. We developed a novel modeling framework based on changes in the viruses' amino acid sequences and relevant epidemiological data from the United States spanning October 2002 to April 2019.

We used this framework to calculate the time-varying disease transmission rate from reported influenza cases and the time-varying antigenic change rate from the changes in amino acid sequences. By incorporating the time-varying antigenic change rate into the transmission models, we were able to capture the evolutionary transmission dynamics of the influenza viruses more accurately.

The findings suggest that the antigenic change of the virus plays a crucial role in the dynamics of seasonal influenza. This research enhances our understanding of the factors influencing influenza transmission, which could inform future efforts to predict and control influenza outbreaks.

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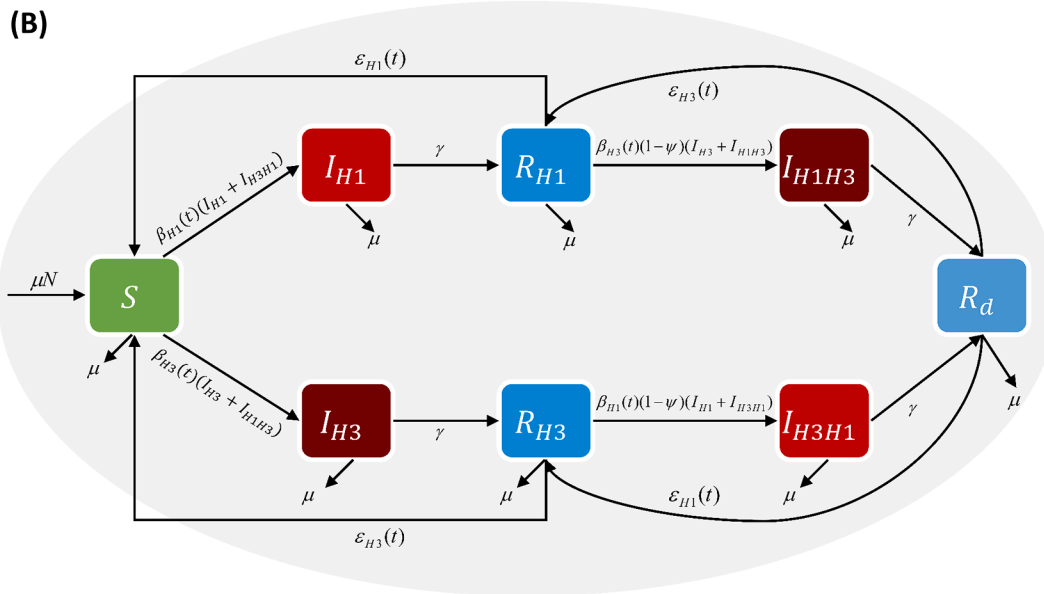
Graphical summary: Schematic of the evolutionary transmission model. The flow diagram of the evolutionary transmission model of the A(H1N1) and A(H3N2) influenza viruses with the selective competition.

Outcome: The key insight this research provides is the critical role of antigenic changes in the virus in influencing the dynamics of seasonal influenza. Understanding this could significantly improve our ability to predict and manage annual epidemics. The novel modeling framework that was developed could be used to predict the evolutionary dynamics and transmission patterns of the influenza virus based on its antigenic changes.

Related SDGs goal: 3. Good health and well-being.

Related publications:

Wilasang C., Suttirat P., Chadsuthi S., Wiratsudakul A., Modchang C. Competitive evolution of H1N1 and H3N2 influenza viruses in the United States: A mathematical modeling study. Journal of Theoretical Biology 555 (2022) 111292

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