Math models analyze the evolution of epidemics during air travel

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Philadelphia, PA—Air travel connects distant worldwide territories like never before. The benefits of high-connectedness are numerous, but epidemic outbreaks in recent decades highlight one pitfall of the global air travel network. Commercial flights remain a leading factor in the spread of commonly-known infectious diseases like tuberculosis, measles, and seasonal influenza.

In a paper published this fall in the *SIAM Journal on Applied Dynamical Systems,* Diána H. Knipl, Gergely Röst, and Jianhong Wu formulate a model to describe the evolution of an epidemic in regions connected by international flights. Using the 2009 influenza A(H1N1) epidemic in Mexico and Canada as an example, the model describes the spread of disease within and between two regions.

“Studying the role that the global air transportation network plays in the worldwide spread of infectious diseases has been in the focus of mathematical epidemiology for a while, especially since the 2002-03 SARS outbreak,” says lead author Diána Knipl. “Previous works were mostly concerned with the structure of the network and the volume of travel between connected airports. However, as highlighted in the risk assessment guideline of the European CDC, on-board transmission is a real threat for many infectious diseases, even during flights with a duration of less than eight hours.”

“Our aim was to incorporate into the model the consideration that infected travelers not only carry the disease from one place to another, but also infect some of their fellow passengers,” Knipl continues. “Our results demonstrate that taking into account the dynamics of on-board infections can give a more accurate estimation of the peak time of an invading epidemic.” This allows more time for a region to prepare for the pending epidemic.

Existing epidemic models assume that the speed of disease spread between regions decreases as the distance between those regions increases. By contrast, the Knipl- Röst-Wu SEAIR model accounts for the notion that in cases of air travel, the speed at which a disease spreads in relation to distance undergoes opposite behavior.

“The connectedness of two regions is determined by cultural, economical and touristic factors rather than distance, and since a crowded plane is a good platform for disease transmission, longer flights provide more opportunity for infection than shorter ones. Thus, somewhat paradoxically, farther cities

can be at more risk, as we have seen in the case of SARS hitting Toronto," author Gergely Röst explains. "Thus we use the phrase 'anti-gravity model' to express this special feature of our model that accounts for on-board transmissions as well. The expression originates from the fact that usually the closer two regions are, the more connected they are; and thus the infection spreads more readily from one to another, and this inverse relationship with distance shows some analogy to physical gravity."

The model distinguishes local residents from visitors to account for differences in mixing patterns—tourists staying in a hotel may interact with more individuals than a resident of the region, for example. Disease behavior during travel is then modeled using a time-structured framework based on susceptible, exposed, asymptomatic infected, symptomatic infected, and recovered groups within populations of the two regions.

The model is a delay differential system made up of a series of differential equations. Ordinary differential equations state how a rate of change in one variable is related to other variables. The delay system indicates that variables at the current time depend on the solution at previous times.

"We used the SEAIR model as a basic building block to describe transmission dynamics in specific regions and coupled it to a similar SEAIR-type model to describe evolution during travel. The major mathematical challenge was to find the basic reproduction number for such systems," Knipl says.

The reproduction number is the expected number of secondary infections caused as a result of a single infection in a susceptible population. The authors show that the disease transmission rate during travel can significantly affect this number. The highly elevated transmission potential of an infectious disease in a crowded airplane cabin can greatly increase the basic reproduction number. This figure can be used to find the final size of the epidemic and assess its severity.

Using real demographic and air travel data for three hypothetical situations where travelers from Mexico, the U.K., and China travel into Canada, the model demonstrates the effect of varying values for trip duration and traveler numbers on epidemic peak times in both origin and destination. Application of the model to the 2009 A(H1N1) influenza pandemic in Canada and Mexico shows that it correlates with real data.

The study reinforces the importance of considering disease transmission during travel to analyze the spread of disease. Unlike older simpler models, the SEAIR model takes into account onboard infections, suggesting that infection is greatly expedited by elevated potential for disease transmission during travel.

Future work will likely look at more general settings for emerging breakouts. "It is both exciting and natural to see how delay differential equations provide the appropriate setting to model the interaction of disease transmission during an inter- or intra-continental flight and within the populations residing in the regions. Much remains to be done in terms of mathematics for global dynamics, including the calculation of the basic reproduction number in a more general setting; and in terms of applications to real-time risk prediction of emerging outbreaks," author Jianhong Wu says.