Tropical areas aren't the only source of seasonal flu epidemics: study

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A commonly held theory says that flu virus originates every year in Southeast and Eastern Asia, making this region the source of seasonal flu epidemics in other parts of the world.

However, researchers at Duke-NUS Graduate Medical School in Singapore have found that influenza virus in tropical areas isn't the only global source of flu epidemics. The international team of scientists involved in the work found that any one of the urban centers they studied could act as a source for a flu epidemic in any other locality.

"We found that these regions are just one node in a network of urban centers connected by air travel, through which flu virus circulates and causes a series of local epidemics that overlap in time," said Gavin Smith, PhD, senior author and Associate Professor in the Program in Emerging Infectious Diseases at Duke-NUS.

The study was published the week of Nov. 14 in the online Early Edition of the Proceedings of the National Academy of Sciences.

The research team chose to study influenza A because it is much more prevalent than both influenza B and C. Influenza is a significant cause of human illness and death worldwide – the World Health Organization estimates that 250,000 to 500,000 influenza A related deaths occur per year worldwide, and about 49,000 deaths occur in the United States.

The team obtained RNA sequences of virus samples from 2003 to 2006

in Australia, Europe, Japan, New York, New Zealand and Southeast Asia, as well as some more recently sequenced viruses from Hong Kong. The virus populations from tropical Southeast Asia and Hong Kong showed relatively low levels of genetic diversity and no seasonal fluctuations in comparison with nnual temperate-area epidemics.

The analysis used time and space parameters to reveal high rates of viral migration among the urban centers tested. Although the virus population that migrated between Southeast Asia and Hong Kong persisted through time, the pattern of infections also depended on virus input from temperate regions that have distinct seasons. None of the temperate and tropical regions they examined was the source of all of the new flu strains in a given year.

The scientists showed that multiple lineages of a virus could seed annual flu epidemics, and that each region could function as a potential source population.

Current strategies for controlling flu virus through vaccination are based on biannual selection of vaccine candidates for the Northern and Southern hemispheres, and these plans require an understanding of circulating viruses.

"While current vaccine-strain selection strategies are generally effective, the results of our study could potentially be used to improve this process by incorporating knowledge of virus migration and connections between regions," said lead author Justin Bahl, Ph.D., Assistant Professor in the Duke-NUS Program in Emerging Infectious Diseases.

Many examples of the global movement of viruses facilitated by air travel exist, including the SARS epidemic and the H1N1 pandemic in 2009, Smith said. "Larger regions with greater connectedness may potentially contribute more to the global diversity of influenza viruses

circulating."

The researchers plan to build on this study by generating new data from areas where there is currently little or no genetic information available. This work forms part of a larger effort to understand the patterns and mechanisms of transmission of respiratory viruses in humans, using influenza as a model system, Bahl said.

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