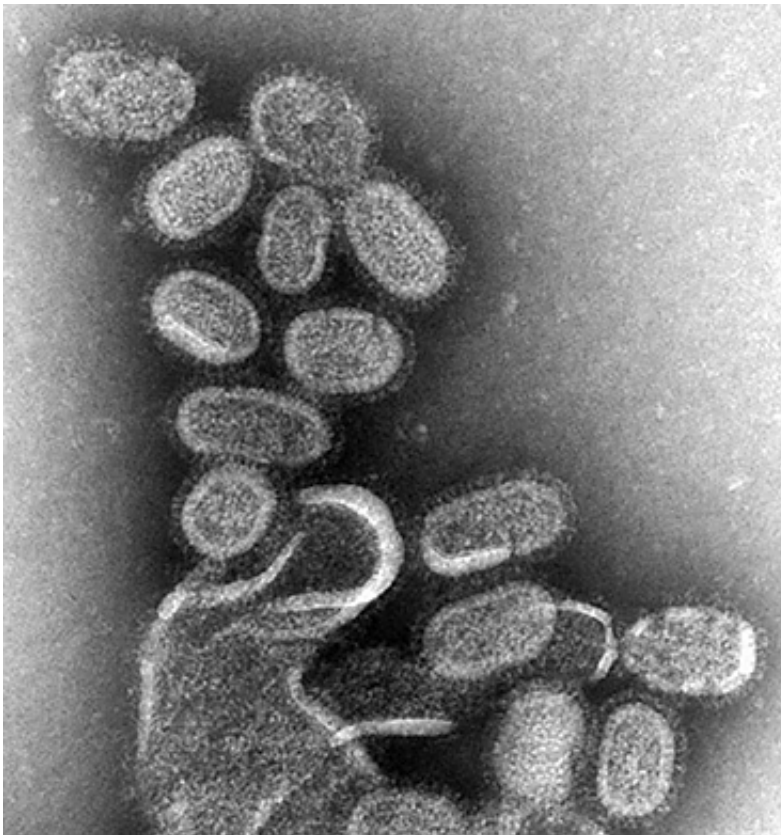


New analysis explores the geographical origins of the flu

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Electron microscopy of influenza virus. Credit: CDC

A computer model developed by scientists at the University of Chicago shows that small increases in transmission rates of the seasonal influenza A virus (H3N2) can lead to rapid evolution of new strains that spread globally through human populations. The results of this analysis,

published September 13, 2016 in the *Proceedings of the Royal Society B*, reinforce the idea that surveillance for developing new, seasonal vaccines should be focused on areas of east, south and southeast Asia where population size and community dynamics can increase transmission of endemic strains of the flu.

"The transmissibility is a feature of the pathogen, but it's also a feature of the host population," said Sarah Cobey, PhD, assistant professor of ecology and evolution at the University of Chicago and senior author of the study. "So a host population that potentially has more crowding, larger classroom sizes for children, or even certain types of social contact networks, potentially sustains higher [transmission rates](#) for the same virus or pathogen."

There are four [influenza strains](#) that circulate in the human population: A/H3N2, A/H1N1, and two B variants. These viruses spread seasonally each year because of a phenomenon known as antigenic drift: They evolve just enough to evade human immune systems, but not enough to develop into completely new versions of the virus.

The H3N2 subtype causes the most disease each year. Genetic sequencing shows that from 2000 to 2010, 87 percent of the most successful, globally-spreading strains of H3N2 originated in east, south and southeast Asia. Cobey and her colleagues, lead author Frank Wen from the University of Chicago and Trevor Bedford of the Fred Hutchinson Cancer Research Center, developed a computer model to simulate conditions in these areas.

The team used the model to test several hypotheses about why antigenically new, seasonal flu strains tend to emerge from this part of the world, including:

- Seasonality: 85 percent of Asia's population lives in tropical or

subtropical regions with no distinct winter, allowing continuous transmission of endemic flu strains and more opportunities for evolution of new strains.

- Host [population size](#): This area contains more than half of the world's population. The sheer number of people could contribute a larger fraction of strains that spread globally.
- Host population turnover: Birth rates have historically been higher in these areas than other temperate regions. This may contribute to a larger number of infants and young children who are more susceptible to the flu.
- Initial conditions: H3N2 first emerged in Hong Kong in 1968. One hypothesis states that this gives the viral population an evolutionary head start, thus new epidemics will almost always begin in the area.
- Transmission rates: Differences in the transmission rate of a given virus, or the expected number of secondary cases caused by a single infection, can affect the evolution of new strains.

Cobey and her colleagues simulated climate conditions, [population dynamics](#) and patterns of [flu epidemics](#) in these regions and found that only the transmission rate had a significant effect on the evolution of new strains that had the potential to spread globally. A transmission rate 17-28 percent higher in one region could explain historically observed patterns of flu epidemics.

"We basically find that increasing the transmission rate just a little bit greatly accelerates the rate at which antigenically novel strains can displace one another," Cobey said.

Understanding how and why seasonal flu tends to originate in these areas reinforces the need for surveillance to identify new strains, not just in the affected parts of Asia, but other parts of the world with high-density populations, like west Africa. It also highlights how public health efforts

to limit the spread of flu, namely widespread vaccination, can also limit the emergence of new [strains](#).

Cobey said that while the team's analysis focused initially on flu, it can also apply to any fast-evolving, human transmissible viruses like enteroviruses and colds.

"They spread from continent to continent over a pretty short time scale, so it will be exciting to see if we find similar patterns down the road once we have better surveillance of all these viruses," she said.

More information: Explaining the geographic origins of seasonal influenza A (H3N2), *Proceedings of the Royal Society B*, rspb.royalsocietypublishing.org/.../1098/rspb.2016.1312

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