

Tracking influenza's every movement

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It's the case of the missing flu virus. When the flu isn't making people sick, it seems to just vanish. Yet, every year, everywhere on Earth, it reappears in the appropriate season and starts its attack. So where does it go when it disappears? Does it hibernate, lying dormant in a few people and preparing for its next onslaught? Does it bounce around from the Northern hemisphere to the Southern hemisphere and back, following the seasons?

Neither, it turns out. The virus's breeding grounds are in Asia, a crew of virus-hunters has found, and it then teems out to take over the world anew each year. New varieties almost always evolve in Asia and then hitch a ride with travelers, spreading to Europe, Australia and North America and finally to South America, where they die away.

The work may make the flu vaccine even better than it already is. Because the flu virus is constantly evolving, scientists meet at the World Health Organization twice a year to decide whether to update the vaccine. Their job is made harder because they have to decide on a formulation a year in advance of when the flu will actually hit, to allow time for the vaccine to be manufactured and administered. So they have to predict which of the strains of flu virus are going to be causing the most disease a year down the line.

“In order to try to predict how flu viruses might evolve, we have to understand how they're moving around the world and where they're evolving,” says Derek Smith, now of the University of Cambridge and formerly of the Santa Fe Institute, corresponding author of the research.

Asia, the study suggests, is the best place to look for up-and-coming strains.

The team published its findings April 18 in *Science* (<http://www.sciencemag.org/cgi/content/full/320/5874/340>).

The team traced the virus's steps by studying 13,000 flu samples from around the world. The World Health Organization Global Influenza Surveillance Network collected this data between 2002 and 2007, keeping track of when and where different strains of the virus popped up. They analyzed the shape differences between the proteins each virus uses to bind to human cells, along with the genetic makeup of each virus.

The team used this information to create an “antigenic map” which visually shows the relationships between all the different viruses. This map allowed them to determine the migration patterns of the virus around the world.

The work was funded by an NIH Director's Pioneer Award to Smith given for highly innovative research that has the potential for big impacts.

The roots of the project extend all the way back to when Smith was a graduate fellow at the Santa Fe Institute doing a PhD with Stephanie Forrest and Alan Perelson. He later began collaborating with Alan Lapedes, Robert Farber, and Terry Jones, all of whom were also affiliated with the Santa Fe Institute, to develop the methods and software to build antigenic maps.

“This work is highly multidisciplinary, with epidemiologists, computer scientists, computational biologists, mathematicians, virologists, immunologists, geneticists, veterinarians, and MDs,” Smith says. “It was made possible by collaborations with people from all of these

disciplines. The Santa Fe Institute is one of the few places that could have gestated such work and I am immensely grateful for the 5 years I spent at SFI.”

Source: Santa Fe Institute

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