

Scientists put interactive flu tracking at public's fingertips

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The green lines on this interactive map represent how pandemic influenza (H1N1) has moved from points in the United States to geographic locations across the globe. Screenshot taken using Google Earth. Credit: Ohio State University

New methods of studying avian influenza strains and visually mapping their movement around the world will help scientists more quickly learn the behavior of the pandemic H1N1 flu virus, Ohio State University researchers say.

The researchers linked many [powerful computer](#) systems together to analyze enormous amounts of [genetic data](#) collected from all publicly available isolated strains of the H5N1 virus - the cause of [avian flu](#). They then developed a new Web-based application that will allow health officials and the public visualize how the virus moved across the globe

using Google Earth.

The resulting visualizations, based on results of the data analysis, represent the most comprehensive map to date of how avian flu has been transmitted among sites in Asia, Africa and Europe.

But underlying those findings is a new way of analyzing genetic data that generates more complete information about the flu's spread. The method, combined with the increasing availability of sequenced genomes of isolated flu strains, is expected to help [public health officials](#) make more knowledgeable predictions about how the H1N1 [flu pandemic](#) will evolve.

"We are taking into account more data but at the same time, we're making simpler visualizations, allowing users to choose what they want to see," said Daniel Janies, associate professor of biomedical informatics at Ohio State and senior author of the study.

"We've created an environment where people can avail themselves of flu information specific to their region of the world or their area of interest. We waded through all of the complexities so people in the public health realm who want to determine how a flu virus got from point A to point B can find that out, and we'll have better public health outcomes as a result."

The visualizations and application are available online at <http://routemap.osu.edu>.

The research appears online in the journal *Cladistics*.

The research environment has changed dramatically since 1997, when an avian flu outbreak in Hong Kong alerted health officials to its dangers to humans, Janies noted. The technology behind the Human [Genome](#)

Project has improved to enable the rapid sequencing of numerous genomes, and avian flu's broad transmission has encouraged scientists to place viral sequence data into the public domain. At the same time, computational power has continued to expand.

Janies and colleagues obtained high-quality avian flu sequences contained in the repositories at the National Institutes of Health's GenBank and the Global Initiative on Sharing Avian Influenza Data (GISAID). They then focused on studying two genes within the virus whose mutations are believed to have the most impact on H5N1 behavior: hemagglutinin, which produces the protein that recognizes the host cell receptor, and neuraminidase, an enzyme that helps the virus escape one cell so it can enter other cells.

The researchers used 1,646 sequences of hemagglutinin and 1,335 of neuraminidase in this study.

Biologists construct what are called phylogenetic trees to trace evolutionary relationships among species or strains believed to share a common ancestor. These trees' branching diagrams can be designed to track similarities in physical characteristics, for example, in the study of dinosaurs, for which genetic data cannot be easily recovered. Or, in the study of influenza, the trees can show how viral strains are related based on shared mutations.

In the past, scientists - including Janies - have selected a single phylogenetic tree to represent related viruses that share mutations. But in this paper, the researchers used the power of supercomputers to generate millions of trees representing relationships among these thousands of viruses. They then picked a pool of thousands of high-quality trees based on a scoring system in the bioinformatics field to use in their analysis of disease transmission.

The scientists then asked of these trees - what are the geographic connections between the isolated viral strains?

These resulting diagrams were then used as the basis for an interactive map that traces the genetic, geographic and evolutionary history of avian [influenza](#) over 12 years. The highly pathogenic lineage of avian flu that crossed Asia and Africa can be traced to an isolate taken from a goose in 1996. Little genetic data is available for H5N1 viruses isolated before that.

To avoid creating a complex map that looks like "spaghetti thrown on the screen," Janies and colleagues also simplified the map's design. Green lines represent transmission pathways most strongly supported by the research findings. Yellow lines indicate less certainty. Lines also are colored differently depending on whether they indicate an incoming or outgoing virus from a specific location. And users can search for specific transmission routes rather than seeing all transmission events on the map at once.

The maps represent scientists' best approximation of avian flu transmission based on the information available, Janies explained. Without access to every complete genome of every flu virus that ever infected a bird or human, researchers can never fully track evolutionary relationships, genetic histories and specific locations of each outgoing and incoming viral transmission.

"Collect and share as much data as possible and let the data tell the story," he said. "We're honest about the uncertainty our results may have - but even with partial data, we can infer much about a virus in an area based on its sources."

The method has already been applied to studies of the H1N1 flu currently infecting millions of people in the United States. International

cooperation spearheaded by the NIH, GISAID and the Centers for Disease Control and Prevention has resulted in ready availability of H1N1 sequences for study.

"With what we have so far, we can see the spread of H1N1 out of the United States and all over the world. There is a different dynamic, in that this is a virus carried by humans, who are cosmopolitan and moving both ways," Janies said. "It's also a [virus](#) that has been transmitted all over the world in a matter of months, and it's still similar to its ancestors."

H5N1, on the other hand, has been creeping across Asia and into Europe and Africa for more than a decade and picked up mutations along the way, he noted. While H1N1 has spread more quickly, it is far less deadly to humans than [H5N1](#) - meaning it is still useful for the world to keep an eye on avian flu, Janies said.

His group's visualizations will help make that possible.

Source: The Ohio State University ([news](#) : [web](#))

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