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## Tracking a killer virus

### Computational biologist uses supercomputer, mapping software to follow swine flu's path

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**BY SPENCER HUNT**

#### THE COLUMBUS DISPATCH

A series of colorful dots and lines crisscross Daniel Janies' computer screen, tracing the history and path of a deadly virus.

Each dot and line symbolizes something dire, a change in the "novel H1N1 influenza virus," better known as swine flu. Armed with a supercomputer at Ohio State University, Google Earth and a network of scientists who share genetic data, Janies, a computational biologist who studies viruses that jump from animals to humans, can show how the virus mutates as it spreads and sickens people around the world.

Most people know that swine flu emerged in Mexico. Janies can trace its RNA ancestry and link it to viruses found in pigs, birds and people as far back as 1956.

"Here we are in Virginia in 1989, where it infected some pigs," Janies said as he used his mouse to spin the globe back in time to display a virus that held a segment of the current swine flu's genetic backbone.

But where swine flu was is not nearly as important as where it is going. And how it's changing.

"One mutation in one gene in this virus would render Tamiflu useless," said Janies, referring to the most commonly used flu treatment.

Janies created similar maps that tracked the evolution of the coronavirus known as SARS. He also produced a map that shows how standard influenza changed over time to become resistant to a class of flu-fighting drugs that were overused treating livestock in China.

Viruses are constantly evolving, capable of changing from host to host and from animal to human.

When a flu virus invades a host cell, it reproduces or replicates itself several times over. Most of the new viruses are exact copies, but the replication process also produces "mistakes" in the genetic code.



CHRIS RUSSELL | DISPATCH

**OSU computational biologist  
Daniel Janies with a large  
display of a map showing the  
worldwide spread of the H1N1  
virus**



"It's wonderfully sloppy in how it reproduces," Janies said of influenza. "That sloppiness is actually an advantage."

The mistakes create new flu viruses that can be either weaker or stronger than the original. They also can help the virus make the jump from animal to human.

Scientists believe the swine flu is a genetic combination of two influenza viruses that invaded the same cell, perhaps in a pig in Mexico. Two viruses replicating in one cell can trade whole segments of RNA and create a radically different disease.

Janies' research takes the work of scientists in the United States and other countries who record the RNA sequences -- the genetic fingerprints of swine-flu viruses from different patients -- and runs them through the state's Supercomputer Center at OSU.

A program he helped design looks for mutations.

When the computer finds a mutation, information about the virus -- location, date of discovery, etc. -- is added to Janies' map. The map also links back to the mutated virus' most likely genetic parents.

Janies said a growing network of scientists who share virus data makes the mapping possible.

A prime source is the Global Initiative on Sharing All Influenza Data, a public database created in August 2006. New sequences are constantly added.

Peter Bogner, the database's founder, said researchers used to hoard data until they could publish their own findings.

"The more data you have, the more accurate the picture becomes," Bogner said.

David Spiro, head of viral genomics at the J. Craig Venter Institute in Rockville, Md., said Janies' maps bridge a gulf of understanding between researchers, government officials and the public.

He said they show why health experts are so concerned about seasonal influenza and swine flu.

"It's really interesting to look at how this thing, in over the past few weeks to a month, has jumped across the globe," Spiro said. The disease was declared a pandemic late last week.

A "movie" that uses Janies' map and data and shows swine flu's spread from Mexico to other countries is part of a "biological update" on display at the American Museum of Natural History in New York.

Tracking a virus' genetic ancestry, Spiro said, can help researchers design drugs and vaccines. If the virus becomes more lethal or drug-resistant, the map would help officials justify, and more quickly order, quarantines and travel restrictions.

"The interconnectivity that's available now will hopefully help us keep a step ahead," Spiro said.

For now, Janies and fellow OSU researchers are downloading as many as 50 new swine flue sequences a week and running them through the supercomputer to update their Google Earth maps.

Janies said his prime concern is watching to see if the virus mutates again, either on its own or by combining with another flu virus, and becomes drug-resistant.

"Currently, it's not Tamiflu-resistant," Janies said. But, "Some of its cousins are."

To see Janies' work, go to <http://supramap.osu.edu/sm/supramap/home>.

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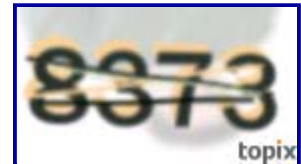
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