

Flu Central

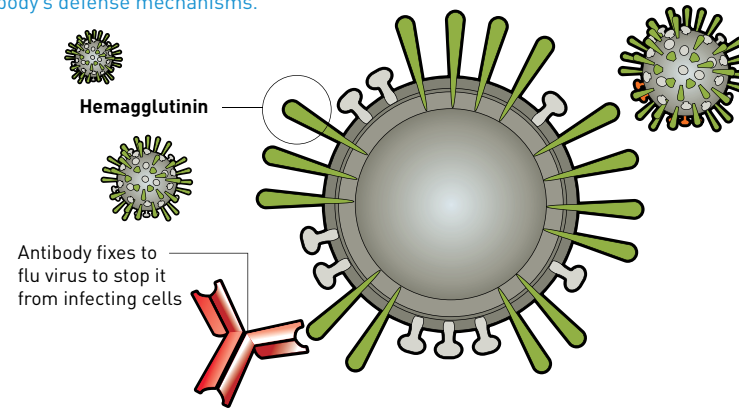
■ BY JENNIFER BAILS // INFOGRAPHIC BY FLYING CHILLI

Each February the World Health Organization announces the strains of influenza expected to circulate in the Northern Hemisphere the following winter—and thus identifies which should be targeted by the year’s flu vaccine. WHO’s projection requires calculated guesswork; the flu virus is constantly evolving, accumulating small mutations through a process called antigenic drift. What’s more, because it takes months to make, test and distribute the flu shot, the forecast must be made nearly a year in advance. The stakes of prediction are high; each year, seasonal flu sickens hundreds of millions of people and kills some 500,000.

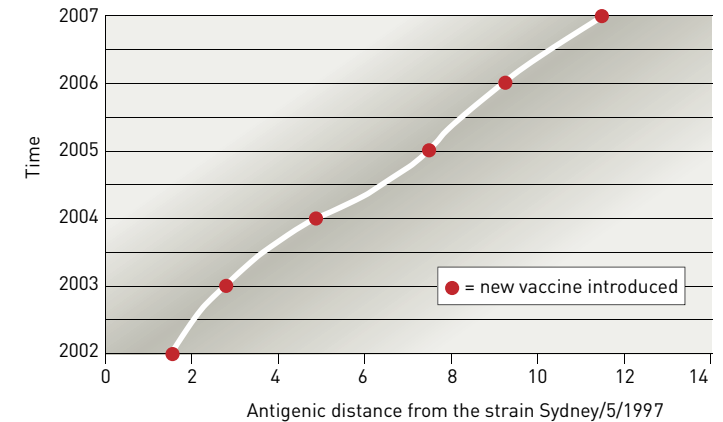
A recent study published in *Science* sheds new light on how flu viruses evolve and migrate around the world. Armed with this knowledge, scientists may be able to refine their forecasts of the flu strains most likely to cause epidemics and to better select viruses for the vaccine.

Have Drift, Will Travel

For the *Science* study, an international team led by Colin Russell and Derek Smith, both of the University of Cambridge, analyzed 13,000 samples of influenza A (H3N2) virus—the major cause of flu-related illness and death—that WHO’s Global Influenza Surveillance Network had collected across six continents from 2002 to 2007. Specifically, the team measured how well each sample bound to antibodies against a protein called hemagglutinin, which is found on the virus coat. Hemagglutinin triggers the body’s immune response to flu; changes in this antigen can allow the virus to escape the body’s defense mechanisms.



The scientists plotted their binding data on a new type of map that plots “antigenic distances,” tracing alterations to the hemagglutinin in their samples during the five-year study. They found that the samples changed by at least two units of antigenic distance per year, thus warranting modifications to the vaccine. These analyses also allowed the researchers to track the spread of flu strains around the globe.



From Asian Cradle to South American Grave

New flu strains generally emerge first in East and Southeast Asia. For reasons that aren’t well understood, the virus prefers the rainy season in the region’s tropical zones, while in temperate areas, such as Beijing, it thrives in winter. Overlap in the timing of these epidemics means the flu is always circulating somewhere in the densely populated region. Widespread travel and trade probably spread the virus from country to country, much like relay racers pass a baton.

Six to nine months after new flu strains appear in Asia, they surface in Australia, North America and Europe, a pattern likely resulting from heavy air traffic between these continents and Asia.

Several months later, the flu strains make their final stopover in South America, seeding epidemics in the Southern Hemisphere winter before mostly dying out for good. Even if viruses do manage to return to the Asian incubator, people there are probably immune to the old strains, and new ones would already be circulating.

Refining Prediction

When the viruses in the influenza vaccine are well matched to the predominant circulating strains, the flu shot is 70% to 90% effective, as has been the case in 16 of the last 20 U.S. influenza seasons. But last year, two of the three strains were not good matches, and the vaccine was only 44% effective.

Because the shape of the hemagglutinin molecule largely determines the corresponding antibody, it is the only portion of the virus WHO routinely sequences. Expanded sequencing of whole genomes could provide additional markers for tracking the flu. Researchers in the United States and England are now doing exactly that—and, crucially, stepping up surveillance in Asia.