

EVOLVING SURVEILLANCE

University of Pittsburgh assistant professor of medicine Elodie Ghedin works with a team at the J. Craig Venter Institute and the National Center for Biotechnology Information sequencing the complete genome of individual flu viruses. The team has completed more than 3,500 different samples of flu virus in the past five years, providing the raw data the scientific community uses to try to understand how this quick-change virus evolves. In the months since an unusual strain of H1N1 influenza virus (swine flu) emerged and became a pandemic, the team has sequenced about 50 individual samples each month.

In the chart Ghedin produced (above), amino acids that make up the viral genes are color coded. Note how different this outbreak (center) is from the typical seasonal flu from 2008 (left). And though it shares similarities with other swine flu samples (right), it is quite different from those as well. The newness of the virus explains why our immune systems seem unprepared for it. The fear, Ghedin says, is that it will combine with these other circulating flu viruses and suddenly become both unfamiliar and virulent.

"Some epidemiologists say that the 1918 Spanish flu was relatively mild initially," she points out. "Then a second wave became far more devastating." Ghedin and her colleagues plan to catch viral evolution in action—to better understand this outbreak and to better prepare for future ones. ***—Chuck Staresinic***

CHART BY ELODIE GHEDIN