

Scientists decoding genomic sequences of H1N1 using isolates from outbreak in Argentina

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Researchers at the Center for Infection and Immunity (CII) at Columbia University Mailman School of Public Health are working with Argentina's National Institute of Infectious Diseases, the National Administration of Laboratories and Health Institutes (ANLIS), and Roche 454 Life Sciences to decode the complete genomic sequences of influenza pandemic (H1N1) 2009 virus from patients with severe respiratory disease. The scientists will be comparing sequences of viruses associated with the current outbreak in Argentina with those found in other locations to determine if there are differences that may be linked to higher mortality rates or provide insights into virus evolution.

The Mailman School of Public Health researchers, led by Gustavo Palacios, PhD, assistant professor of Epidemiology and CII Director W. Ian Lipkin, MD, John Snow Professor of Epidemiology, and professor of Neurology and Pathology at Columbia University, plan to completely sequence up to 150 virus specimens from nasopharyngeal swabs and cultures over the next 10 days, and will share their findings with the larger scientific community. The complete sequencing of these virus specimens will allow the team to both characterize severe versus mild cases, as well as determine how the virus evolved at different points in time. [Swine flu](#) has killed 165 people in Argentina, more than any nation with the exception of the U.S. Any significant changes in the virus might influence the effectiveness of vaccines or drugs used to fight the pandemic.

"No one knows how this pandemic will evolve. Continuous surveillance will be essential to focusing both research and public health response. We are analyzing these isolates in New York and Argentina; nonetheless, we expect that members of the broader scientific community will bring new insights. Thus, our plan is to release sequences in draft form so that the vetting process can begin as soon as possible," said Dr. Lipkin.

"While there is no evidence so far to indicate the emergence of resistance to the oseltamivir vaccine, the antiviral drug that blocks the influenza virus from spreading between cells in the body, we are cautious about the findings until we have more sequences," said Gustavo Palacios, PhD. "The changes already noted in comparing the outbreak in Argentina to the U.S. haven't previously been associated with greater virulence."

Source: Columbia University's Mailman School of [Public Health](#) ([news : web](#))

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