

- [ScienceWatch Home](#)
- [Inside This Month...](#)
- [Interviews](#)

- Featured Interviews
- Author Commentaries
- Institutional Interviews
- Journal Interviews
- Podcasts

Analyses

- Featured Analyses
- What's Hot In...
- Special Topics

Data & Rankings

- Sci-Bytes
- Fast Breaking Papers
- New Hot Papers
- Emerging Research Fronts
- Fast Moving Fronts
- Corporate Research Fronts
- Research Front Maps
- Current Classics
- Top Topics
- Rising Stars
- New Entrants
- Country Profiles

About Science Watch

- Methodology
- Archives
- Contact Us
- RSS Feeds



Interviews

Analyses

Data & Rankings

2010 : February 2010 - Fast Breaking Papers : Yi Guan on H1N1 - the First Human Influenza Pandemic of the 21st Century

fast breaking papers - 2010

February 2010



Yi Guan talks with *ScienceWatch.com* and answers a few questions about this month's Fast Breaking Paper Paper in the field of Clinical Medicine.



Article Title: Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic

Authors: Smith, GJD;Vijaykrishna, D;Bahl, J;Lycett, SJ;Worobey, M; Pybus, OG;Ma, SK;Cheung, CL;Raghwani, J;Bhatt, S;Peiris, JSM; Guan, Y;Rambaut, A

Journal: NATURE, Volume: 459, Issue: 7250, Page: 1122-U107, Year: JUN 25 2009

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(addresses have been truncated.)

SW: Why do you think your paper is highly cited? Does it describe a new discovery, methodology, or synthesis of knowledge?

H1N1 is the first human influenza pandemic of the 21st century. Obviously, our paper has been highly cited due to the fact that the 2009 pandemic influenza virus is still an ongoing concern. Our paper answered the question of how and where the H1N1 pandemic virus was generated. These are new findings which convey a detailed understanding of the 2009 H1N1 pandemic.

SW: Would you summarize the significance of your paper in layman's terms?

Our findings demonstrated the evolutionary pathway of the 2009 H1N1 virus and described, step by step, how it was generated.

SW: How did you become involved in this research, and were there any problems along the way?

All findings generated by this project were based on our long-term influenza surveillance in Hong Kong. Our lab is the only lab in the world to have more than 10 years of continuing influenza surveillance data on pigs. This offers an ideal opportunity to answer where and how the pandemic influenza virus emerged.

"Pandemic influenza outbreaks pose a significant threat to public health worldwide"

As the PI for the influenza surveillance program, it is my duty to get the data interpreted properly. In this regard, my colleague Dr. Andrew Rambaut of the University of Edinburgh's Institute of Evolutionary Biology Ashworth Lab used his ample experience in the usage of modern bioinformatic knowledge in order to obtain insights into the evolution of the H1N1 virus.

SW: Where do you see your research leading in the future?

I am going to continue our surveillance study. This is essential to understanding the viruses which possess human infectious potential, with the precondition being to outline the steps of a basic preparedness for pandemic influenza and other emerging infectious diseases.

SW: Do you foresee any social or political implications for your research?

Pandemic influenza outbreaks pose a significant threat to public health worldwide. Certainly, at least, people do understand and believe that pandemic influenza virus is derived from those viruses residential in animals and that the pandemicity of an influenza virus may, in fact, take many years to dissipate.

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KEYWORDS: MULTIPLE SEQUENCE ALIGNMENT; UNITED-STATES; GENETIC REASSORTMENT; VIRUSES; PIGS; INFECTION; TRANSMISSION.



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[back to top](#)

2010 : [February 2010 - Fast Breaking Papers](#) : Yi Guan on H1N1 - the First Human Influenza Pandemic of the 21st Century