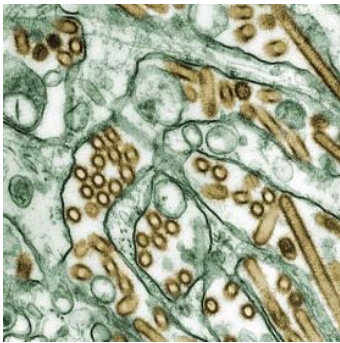


Contagion: Controversy Erupts over Man-Made Pandemic Avian Flu Virus

Two teams of scientists have independently constructed a deadly strain of flu. Some say the results should never be published

- By [Jeneen Interlandi](#) | December 9, 2011



Colorized transmission electron micrograph of Avian influenza A H5N1 viruses (seen in gold) grown in MDCK cells (seen in green). Avian influenza A viruses do not usually infect humans; however, several instances of human infections and outbreaks have been reported since 1997. When such infections occur, public health authorities monitor these situations closely. Image: Cynthia Goldsmith

It's a rare kind of research that incites a frenzied panic before it's even published. But it's flu season, and influenza science has a way of causing a stir this time of year.

Epidemiologists have long debated the pandemic potential of **H5N1, a.k.a. avian bird flu**. On one hand, the virus spreads too inefficiently between humans to seem like much of a threat: it has caused less than 600 known cases of human flu since **first emerging in 1997**. On the other hand, when it does spread, it can be pretty deadly: **nearly 60 percent of infected humans died from the virus**. For years now, the research has suggested that any mutations that enhanced the virus's ability to spread among humans, would simultaneously make it less deadly. But in a recent batch of as-yet-unpublished studies, two scientists - [Yoshihiro Kawaoka](#) from the University of Wisconsin, Madison and [Ron Fouchier](#) of Erasmus Medical Center, in the Netherlands – have shown otherwise.

Working separately, they each **hit on a combination of mutations** (**five**, in Dr. Fouchier's case) **that makes H5N1 airborne** (enabling it to spread readily between humans), without making it less deadly. In laboratory experiments, ferrets infected with this mutant strain passed it to other ferrets in nearby cages (ferrets are a common subject of flu studies

because they react to flu viruses in a similar way to humans). A significant proportion of infected subjects died.

Efforts to publish those findings have been fraught. Critics say that making the methodology or gene sequences widely available, amounts to giving would-be bioterrorists an easy recipe. They also worry that these manmade strains might escape from the lab.

Proponents counter that the threat of a global pandemic, were this mutated strain to arise in nature, is far greater than the threat of bioterrorism. Understanding what combination of mutations could transform H5N1 into a human pandemic virus, helps epidemiologists know what to watch out for in the wild, and gives them a leg up on preparing countermeasures; they can, for example, test existing H5N1 vaccines and antiviral drugs against the new strain in the lab, before it actually emerges in the natural world.

Both papers are being reviewed by the National Science Advisory Board for Biosecurity (NSABB), which will then advise researchers and journal editors how to proceed. In the meantime, most experts agree that we need a better way.

“This is not new for science,” says Michael Osterholm, director of the Center for Infectious Disease Research and Policy at the University of Minnesota, Twin Cities and a member of the NSABB. “Physicists have been doing sensitive, classified, and need-to-know work for 70 years, including academic researchers. We have to find a way to do the same in the health sciences, to work on agents that yield important information without compromising our safety and security.”