

# Probing Question: Can a pandemic be predicted?

June 4 2009, By Traci Thomas

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SARS. Ebola. West Nile. Avian flu. Over the past decade, the world has watched and waited to see if these viruses would develop into global health threats. In recent weeks, the World Health Organization (WHO) sent a shockwave through the public when it ranked the emergent influenza swine-A/H1N1 virus--better known as swine flu--at alert Phase 5, implying that an influenza pandemic is imminent.

Some have slammed the media and others for over-reacting to this latest outbreak. However, authorities have long been watching for the next pandemic, defined simply as an outbreak of disease spread by human-to-human transmission over a wide geographic area. Some predicted that it was only a matter of time before another global [influenza](#) threat occurred.

Is it possible to predict a pandemic?

“The answer to this question is a qualified no,” says Ottar Bjornstad. To be capable of creating a pandemic, “it is important that a virus transmits fairly easily from human to human,” notes Bjornstad, professor of biology and [entomology](#) at Penn State. For this to occur, “several key pieces must fall into place,” he explains. “And we cannot predict when and if this will happen.”

Essentially, the virus needs to be able to do two things, Bjornstad continues. First, it must be able to evade immune defenses. Human immune systems easily attack viruses that have been around for a while,

he notes. We have good immunity to the current seasonal flu strains simply because they have been circulating in human populations for decades.

A brand [new virus](#), on the other hand, is much harder for the [immune system](#) to detect, and therefore more likely both to cause illness and to transmit, explains Bjornstad. “This typically occurs in subtypes of influenza A viruses, which can cross over from animals such as pigs, ducks, chicks or gulls into humans.” One cause for optimism with regard to the current A/H1N1 swine flu, he says, is that this particular strain is genetically related to a strain that has been circulating seasonally since the late 1970s.

The second key challenge for an emerging influenza virus is that it needs to be able to replicate efficiently in its new human host, he adds. “Different animals provide different living conditions.” Avian influenza, for example, is well-suited to reproduce in a bird’s gut, while influenza in humans attacks the respiratory tract, a cooler environment populated with different cell types.

“The easiest way for an influenza virus to make this change is when a regular seasonal flu of humans exchanges genes with non-human-adapted strains of bird flu,” says Bjornstad. Viruses can rearrange their genes to make new viruses through a process called reassortment. If two different viruses exist in the same host, their genetic codes can mix through this process, creating a brand-new bug.

Reassortment, Bjornstad notes, “is an inherently random process.” Because we cannot predict when a particular combination of genes will turn up, we cannot reliably predict when a pandemic will occur or where an outbreak will begin.

Once this genetic roll of the dice has occurred, however, we have “robust

mathematical models that can accurately predict the overall size of the epidemic and the pattern of global spread,” he says.

In the case of the new A/H1N1 flu, the pieces created by reassortment are in place, but the world is still anxiously waiting to see how inherently virulent this particular strain might be.

Provided by By Traci Thomas, Research/Penn State

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