

Lack of worldwide infrastructure to monitor flu variants leaves researchers in the dark

March 29 2012, by Bob Yirka

(Medical Xpress) -- Most people know that one of the greatest threats to mankind is a pandemic. As the human population has grown over the years, so too has the threat from diseases that are capable of wiping out huge numbers of people in one fell stroke. And of the types of pandemics that are most likely to occur, most would agree that it would likely be tied to influenza. Yet, despite the very real possibility that a strain could develop almost anywhere in the world at any time; one that could spread very quickly across the planet due to international travel, relatively little is being done to prevent it from happening. Right now today, we are all at risk due to the possibility of a strain developing that would be as lethal as the variant that killed so many during the first World War, and that could spread just as quickly, or worse. Because of this, scientists from across the globe have contributed to commentaries and editorials describing the current state of flu data collection efforts and how the process might be improved. All of which have been published in the journal *Nature*.

New strains of flu develop due to two main factors: The first is the intermingling of pigs, humans and fowl, primarily chickens. The second is natural evolution as [flu strains](#) change to meet new conditions, such as adapting to thwart [antibiotics](#). And because new strains are developing all the time, the best way researchers have of keeping ahead of them is by finding them as soon as possible after they develop and then adding them to a database. Ideally, every strain of flu, and every variant would wind up in the database shortly after being created. Unfortunately, as those writing for *Nature* point out, this is simply not happening.

The reasons for this are varied. One of the main ones is that there is no global central body in a position to take on such a task. Thus, there doesn't exist a worldwide central database for depositing flu related information and using it for research. Another, perhaps stronger reason is because of the way people live. Many hotbeds of flu evolution exist worldwide in backyard farms where the conditions are ripe for the development of new strains; pigs, humans and fowl, all living in close proximity. Most such farmers depend on their animals for survival and thus aren't likely to sound the alarm if they suspect a flu virus has hit struck. They'd likely find all of their animals being killed by authorities leaving them with no means of support. And governments in such countries have little reason to cooperate with global organizations that would insist on widespread culling with no compensation, which would add credence to many third world policymakers belief that data retrieved from such countries would only go towards vaccinations that would be manufactured and distributed in richer countries.

The end result is just a handful of countries sampling and maintaining databases containing vital flu data, a situation that leaves us all vulnerable to a truly terrifying worldwide [pandemic](#) of unheralded proportions.

The fix of course, as those commenting in *Nature* point out, is relatively easy. Create a central worldwide body responsible for building a global database and obtaining data on new strains or variants, that has not just the authority to test for flu in any country, but the financial resources to do so. Also, to get everyone to work together, put in place incentives for farmers and governments to report [flu](#) outbreaks, so that everyone has a reason to cooperate. And finally, make tracking [influenza](#) a worldwide cooperative effort by getting governments all over the world to add financial backing to support such an effort.

More information: Flu surveillance lacking, *Nature* 483, 520–522 (29

March 2012) [doi:10.1038/483520a](https://doi.org/10.1038/483520a)

Editorial: Under surveillance, *Nature* 483, 509–510 (29 March 2012)
[doi:10.1038/483509b](https://doi.org/10.1038/483509b)

Comments:

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