

## SME\_and\_PR Material for TETRADYN and CADS Use

### ***H1N1 and Pigs***

**Topic:**

The implications of H1N1 going to real swine, finally, and what that can mean this season and in terms of a pandemic, present vaccine plans, and our economic stability.

**Article:**

Humans and pigs have lived together for a long, long time. There are many affinities also in the transmission of disease including different strains of influenza virus. In several investigations of the origin of the 1918 pandemic, pigs have been implicated as the cross-over species from which the human-to-human killer virus made its emergence. In any case there is no doubt that pigs can provide a good melting pot and mixing ground for mutations and development of virulent strains of influenza and other microorganisms that can affect the human population. We have seen that the original H1N1 virus emerging in Mexico during April and May of 2009 may have – and this is not definitive – links to pig-farming communities in Mexico, and now we are seeing evidence for possible transmission of H1N1-related strains from humans to pigs, in Argentina and Canada.

Among the articles that address these developments are the following:

<http://www.pigprogress.net/news/argentina-h1n1-pigs-possibly-infected-by-humans-3157.html>

Argentinean farm workers are thought to have infected pigs with the new H1N1 flu strain, only the second suspected case of humans passing the deadly virus to swine, a government spokesman has said.

The Argentine case adds weight to the theory that pigs can be infected by humans, although people are catching it from other people and not from animals.

<http://www.bloomberg.com/apps/news?pid=20601124&sid=aUAzwSOYmR3g>

A new strain of H1N1 flu sickened at least two workers at a pig farm in Saskatchewan, Canadian health officials said. Tests found the strain is different from the pandemic swine flu circulating the globe.

The two people recovered from mild illness, and a third case is under investigation, according to a government statement. Pigs from the farm tested positive for a common version of swine flu and didn't carry the new human version found in the workers. ...

The new Canada strain is made up of genes from human seasonal flu and genes from swine flu viruses, according to the statement from the Public Health Agency of Canada.

There is an observation to be made here, one that goes beyond the farm and beyond the particular incidents. This is an observation that should be used to move forward, to accelerate rapidly, such programs and projects that are able to deliver rapid diagnostics and accurate identification and classification of viral strains, directly from the point of origin (the infected person or animal) to both public health authorities and medical researchers. Such projects include CUBIT (Coordinated Biothreat Intervention and Treatment), for instance, and within it, CRAIDO (Community Rapid Response Diagnostics for Infectious Disease Outbreaks) and VSRB (Virtual Sample repository Bank). Here is why these implementations of today's latest technologies of instrumentation, analytical testing, and biomedical informatics are needed now, more than ever, and faster than ever.

Consider the mix of human seasonal flu and various H1N1-class swine flu viruses. Consider also the mix of both of the above, in particular a mixtures of H1N1 and seasonal influenza, with H5N1 bird flu. You have a perfect melting pot and mixer bowl – the friendly, ubiquitous pig. You have variations now that are different also from those being used, very slowly (due to the microbiological nature of the H1N1 in general and the constraints of vaccine development today, a simple fact of biology) to manufacture vaccines for mass-population administration. These variations may be themselves immune to the vaccine that is still in production, based upon a prior known and perhaps now diminished strain of H1N1. We may be preparing a mass vaccination program in schools, workplaces, and community centers that will have only limited and questionable effectiveness against new strain(s) of virus that are emerging into the public world as we speak.

We need to disperse, almost like viral outbreaks, the resources and tools that are going to be most effective and efficient, in the hands of general medical practitioners and healthcare providers, at detecting where are there new strains, of what types, and of what mutational dispositions and characters, genetically speaking, that can have the most impact upon our populations. We have such resources and tools, we have the know-how, and we have the means to connect all the dots and have a powerful network in place, soon, to aid in our public health protection and in disease management on a widespread public scale.

Time's a-wastin' and these solutions, like CRAIDO and VSRB, and the full CUBIT Suite, are neither expensive nor particularly complicated. If we wait for the slow-mo grinding-forward of the wheels of Corporate and Financial America and the standard competitive procurement process of government grants, we will be in so deep in a public health problem that it will surely have grave effects upon our economy and also our national security. We don't need forty-plus percent of our work force out sick all at once – this is a realistic possibility. We don't need massive quarantines and shut-downs of businesses, malls, hotels, offices, factories, and transit systems. And we certainly don't need five to ten percent of our population in different sections of the country or different demographic groups dying from something that can be avoided or better treated with some common-sense and here-now-today available bright answers and working medical technology.

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