

From: [Peter Daszak](#)
To: [Morens, David \(NIH/NIAID\) \[E\]](#)
Cc: [Stemmy, Erik \(NIH/NIAID\) \[E\]](#); [Alison Andre](#)
Subject: More on Wuhan novel coronavirus - NIAID's role in bat-origin CoVs
Date: Monday, January 27, 2020 5:49:34 PM
Importance: High

Great to hear back, and of course this is all confidential. Erik – hope you don't mind this communication, and please share with your Head of Dept if you like

Re. the likely final size of this outbreak – here are the key metrics I'm looking at:

1. Mortality rate – Currently around 2-3%, which is not bad compared with the 7+% of SARS
2. Secondary outbreaks: So far, no evidence that international travelers have seeded de novo transmission within destination countries. In the richer countries, USA, Canada, Europe, Japan, Australia, I expect that Port Authority surveillance will catch most with symptoms and follow up will mop up secondary cases for the few that get through. My concern is for SE Asian and African countries that our Flight Risk Tracker predicted arrivals earlier in the outbreak (see figure attached) – <https://flirt.aha.io> (funded by DHS and DoD DTRA).
3. Transparency from China: Good rapid response, open sharing of information (albeit that this was once they'd all got their initial high-impact papers accepted). They're working with WHO, and WHO is holding regular meetings on sharing samples/reagents/viruses (organized via WHO R&D Blueprint group that I'm part of), as well as PHEIC meetings.
4. Travel ban: This is a significant difference to SARS, and although the virus had already traveled, the lockdown of Wuhan and many other places/sites during the New Year festivities is a remarkable move that has to have had a big impact on reducing spread.

So, for those reasons I'm cautiously optimistic that this will end up with a max of around 15-20,000 total cases identified (most mild), only a couple of examples of secondary transmission, and a lower mortality rate once all the cases are accounted for (1-2%). There'll still be a temporary shock to the global economy, and this is already similar to SARS (10% hit on airline stocks etc), but that's prob due to massive increase in travel from China to most other destinations since SARS, and to increase in social media and hype. Should settle down once we're over the peak of the epidemic curve.

Cheers,

Peter

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

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Sent: Monday, January 27, 2020 4:54 PM
To: Peter Daszak
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Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Great info, thanks. Tony doesn't maintain awareness of these things and doesn't know unless program officers tell him, which they rarely do, since they are across town and may not see him more than once a year, or less....

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Interested in your feeling about where this is going. The experts buzzing around us are all over the map, between doomsday and not that big a deal, with everything in between.



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From: Peter Daszak (b) (6)
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Subject: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Importance: High

Hi David – Happy to have a phone call re. the Wuhan CoV, but just wanted to mentioned a few things for your information and hopefully to pass on to Tony Fauci for when he's being interviewed re. the new CoV:

NIAID has been funding coronavirus work in China for the past 5 years through an R01 to me (1R01AI110964: "Understanding the Risk of Bat Coronavirus Emergence"). That's now been renewed, with a specific focus that we identify cohorts of people highly exposed to bats in China, and work out if they're getting sick from CoVs. Erik Stemmy is the Program Officer (cc'd here). Collaborators include Wuhan Institute of Virology (currently working on the nCoV), and Ralph Baric. The results of our work to date include:

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- Discovered Swine Acute Diarrheal Syndrome Virus (SADS-CoV) killing >25,000 pigs in Guangdong Province (Published in Nature)
- Found SARS-related CoVs that can bind to human cells (Published in Nature), and that cause SARS-like disease in humanized mouse models.

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Also – FYI, prior to the R01, we worked under an R01 with Eun-Chung Park as Program Officer on viral discovery in bats, where originally identified SARS-CoV as having a likely origin in bats (published in Science)

As I mentioned, I'm now part of a group that's meeting by phone weekly with CEIRS to discuss the nCoV and Erik's part of that.