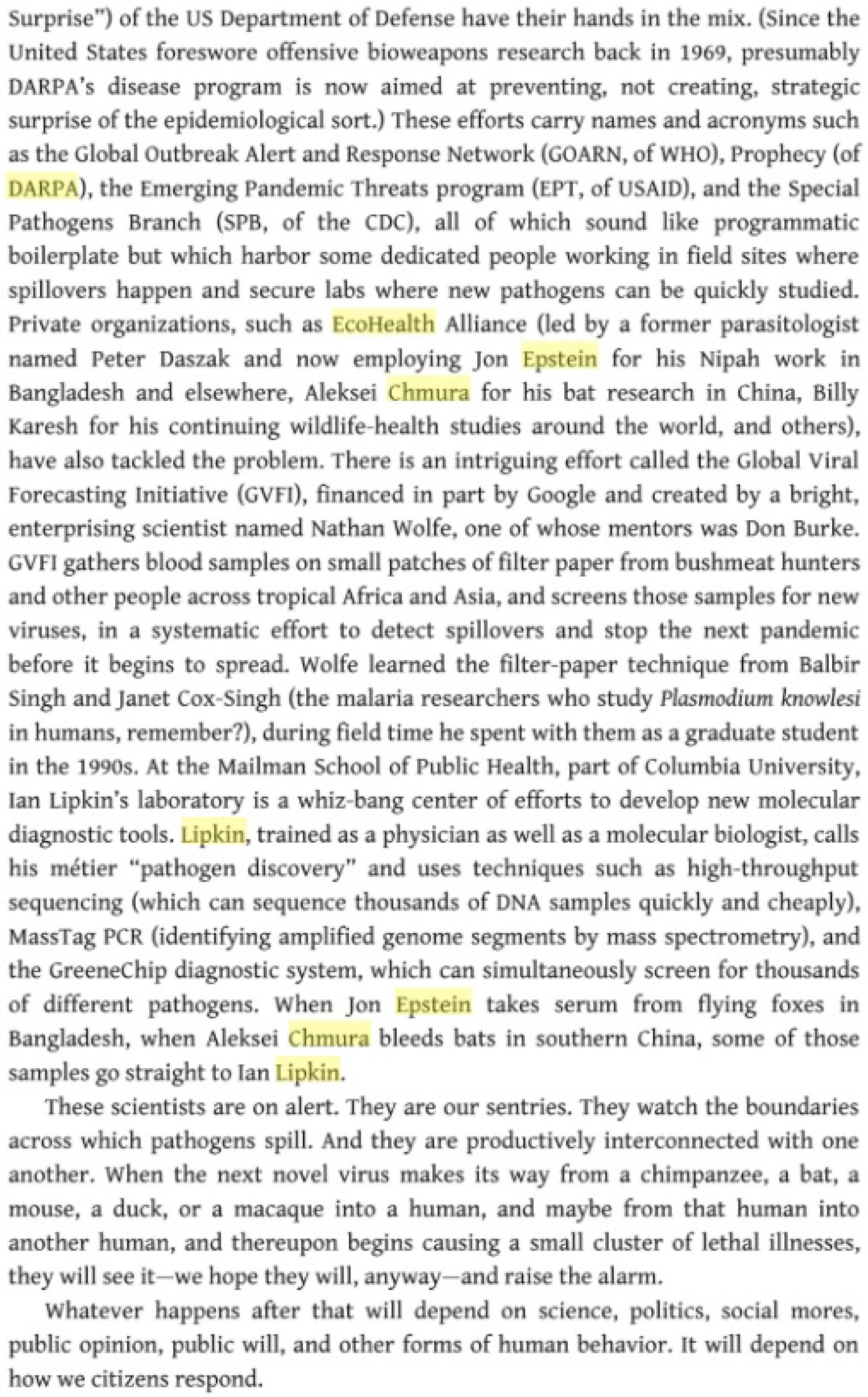
Twitter Thread by Billy Bostickson ■■&■ ■

Billy Bostickson ■■&■ ■
@BillyBostickson

1. Reading between the Lines - interview from Sept 2017
From wildlife to humans with the PREDICT project
– an interview with Tracey

2. First of all we need to take into account the EcoHealth/PREDICT - Lipkin connection
https://t.co/kKtDTYQD9D
Read it carefully...
Ecohealth/DARPA and PREDICT UC Davis smuggled viruses back to the US for GOF work by Lipkin and Atlanta CDC BSL4 (Dr. Stuart Nichol) and USAMRIID



Surprise") of the US Department of Defense have their hands in the mix. (Since the United States foreswore offensive bioweapons research back in 1969, presumably DARPA's disease program is now aimed at preventing, not creating, strategic surprise of the epidemiological sort.) These efforts carry names and acronyms such as the Global Outbreak Alert and Response Network (GOARN, of WHO), Prophecy (of DARPA), the Emerging Pandemic Threats program (EPT, of USAID), and the Special Pathogens Branch (SPB, of the CDC), all of which sound like programmatic boilerplate but which harbor some dedicated people working in field sites where spillovers happen and secure labs where new pathogens can be quickly studied. Private organizations, such as EcoHealth Alliance (led by a former parasitologist named Peter Daszak and now employing Jon Epstein for his Nipah work in Bangladesh and elsewhere, Aleksei Chmura for his bat research in China, Billy Karesh for his continuing wildlife-health studies around the world, and others), have also tackled the problem. There is an intriguing effort called the Global Viral Forecasting Initiative (GVFI), financed in part by Google and created by a bright, enterprising scientist named Nathan Wolfe, one of whose mentors was Don Burke. GVFI gathers blood samples on small patches of filter paper from bushmeat hunters and other people across tropical Africa and Asia, and screens those samples for new viruses, in a systematic effort to detect spillovers and stop the next pandemic before it begins to spread. Wolfe learned the filter-paper technique from Balbir Singh and Janet Cox-Singh (the malaria researchers who study *Plasmodium knowlesi* in humans, remember?), during field time he spent with them as a graduate student in the 1990s. At the Mailman School of Public Health, part of Columbia University, Ian Lipkin's laboratory is a whiz-bang center of efforts to develop new molecular diagnostic tools. Lipkin, trained as a physician as well as a molecular biologist, calls his métier "pathogen discovery" and uses techniques such as high-throughput sequencing (which can sequence thousands of DNA samples quickly and cheaply), MassTag PCR (identifying amplified genome segments by mass spectrometry), and the GreeneChip diagnostic system, which can simultaneously screen for thousands of different pathogens. When Jon Epstein takes serum from flying foxes in Bangladesh, when Aleksei Chmura bleeds bats in southern China, some of those samples go straight to Ian Lipkin.

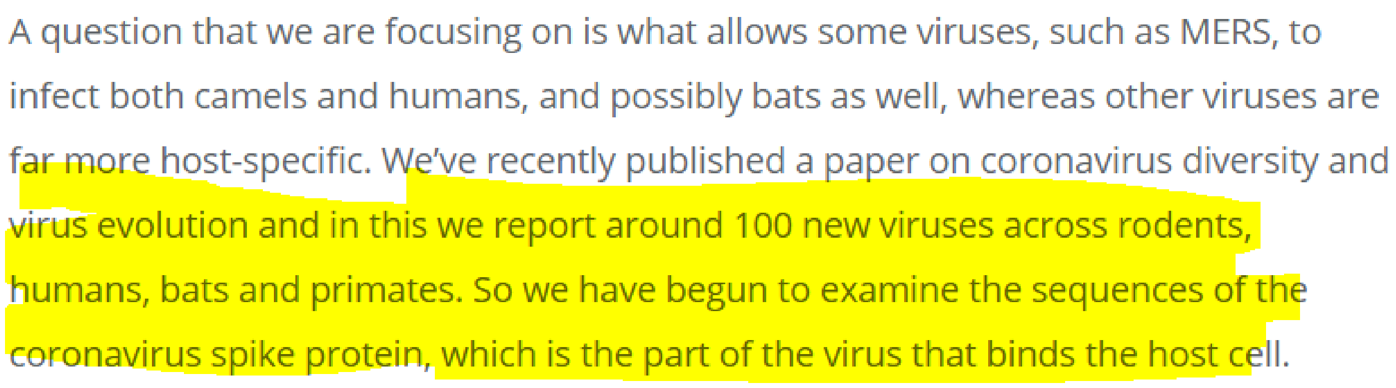
These scientists are on alert. They are our sentries. They watch the boundaries across which pathogens spill. And they are productively interconnected with one another. When the next novel virus makes its way from a chimpanzee, a bat, a mouse, a duck, or a macaque into a human, and maybe from that human into another human, and thereupon begins causing a small cluster of lethal illnesses, they will see it—we hope they will, anyway—and raise the alarm.

Whatever happens after that will depend on science, politics, social mores, public opinion, public will, and other forms of human behavior. It will depend on how we citizens respond.

Yes, he was included above in the last tweet.
Lipkin is a key player in this sordid saga, who received viruses via Predict/Prophecy/Ecohealth/Darpa for experiments in the mailman lab (according to our "friend" Quammen in his book Spillover) found by @gdemaneuf pic.twitter.com/1fq20TSR3A

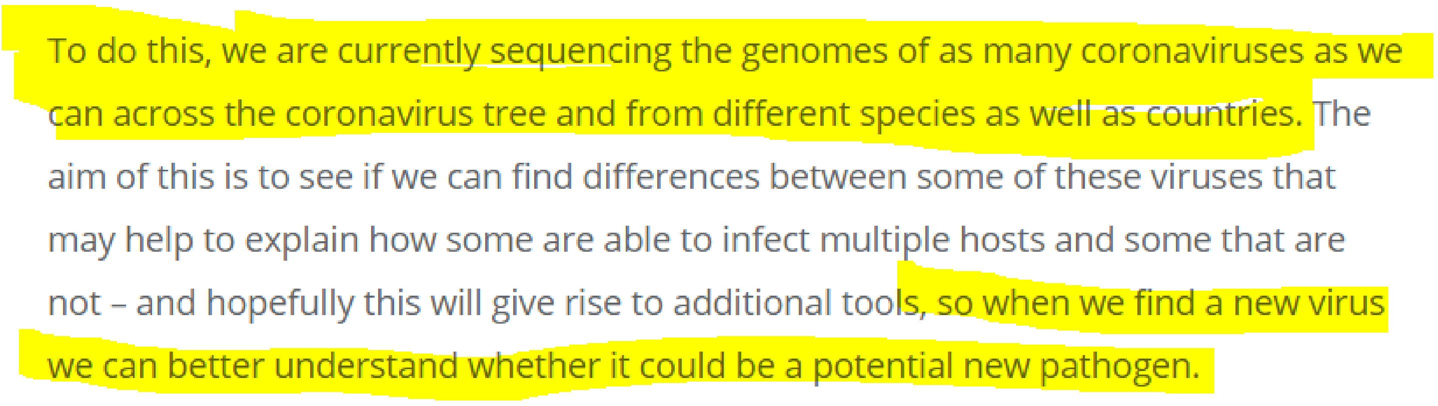
— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) September 26, 2020

3. In the interview, Tracy Goldstein does not specifically clarify or state this fact, we need to read between the lines/
"examine the sequences of the coronavirus spike protein"
"examine" refers to US Lab work by Lipkin and others



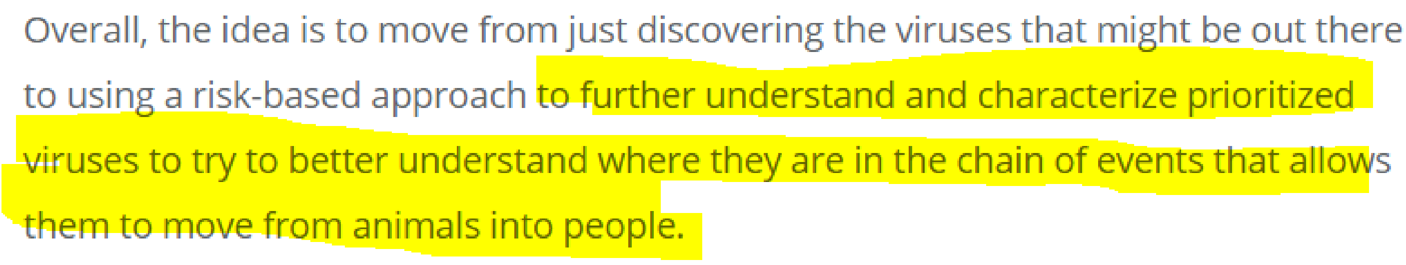
> A question that we are focusing on is what allows some viruses, such as MERS, to infect both camels and humans, and possibly bats as well, whereas other viruses are far more host-specific. We've recently published a paper on coronavirus diversity and virus evolution and in this we report around 100 new viruses across rodents, humans, bats and primates. So we have begun to examine the sequences of the coronavirus spike protein, which is the part of the virus that binds the host cell.

4. They were sequencing as many coronaviruses as they could and experimenting on them at US Labs, seeing if they could become more pathogenic or cross the species barrier



> To do this, we are currently sequencing the genomes of as many coronaviruses as we can across the coronavirus tree and from different species as well as countries. The aim of this is to see if we can find differences between some of these viruses that may help to explain how some are able to infect multiple hosts and some that are not – and hopefully this will give rise to additional tools, so when we find a new virus we can better understand whether it could be a potential new pathogen.

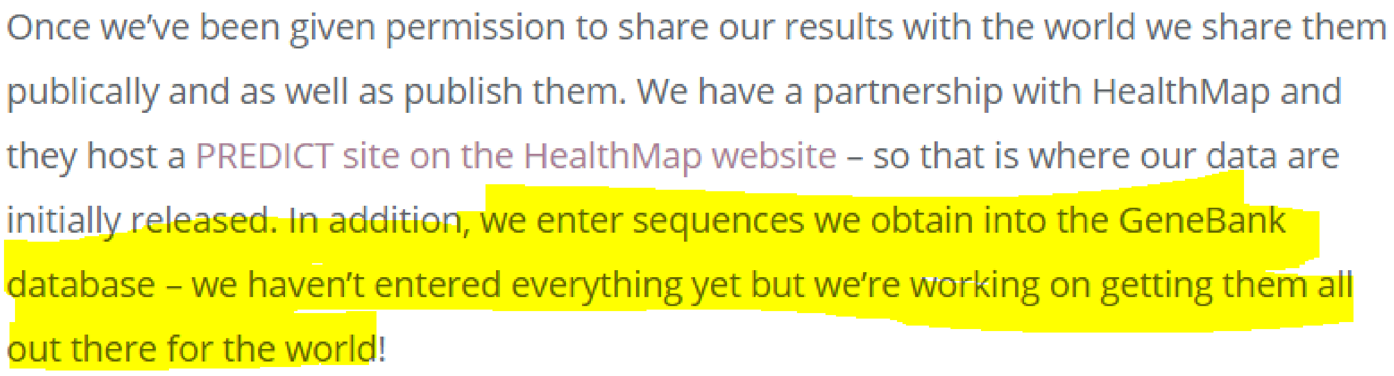
5. Goldstein says:
"to further "understand & characterise" "prioritised viruses" to see if they can jump to humans.
Only one way to do that, isn't there?
Shipping back the deadliest viruses to the US via US consulates as exposed via leaks from Georgia
https://t.co/va6Be7w2HL



> Overall, the idea is to move from just discovering the viruses that might be out there to using a risk-based approach to further understand and characterize prioritized viruses to try to better understand where they are in the chain of events that allows them to move from animals into people.

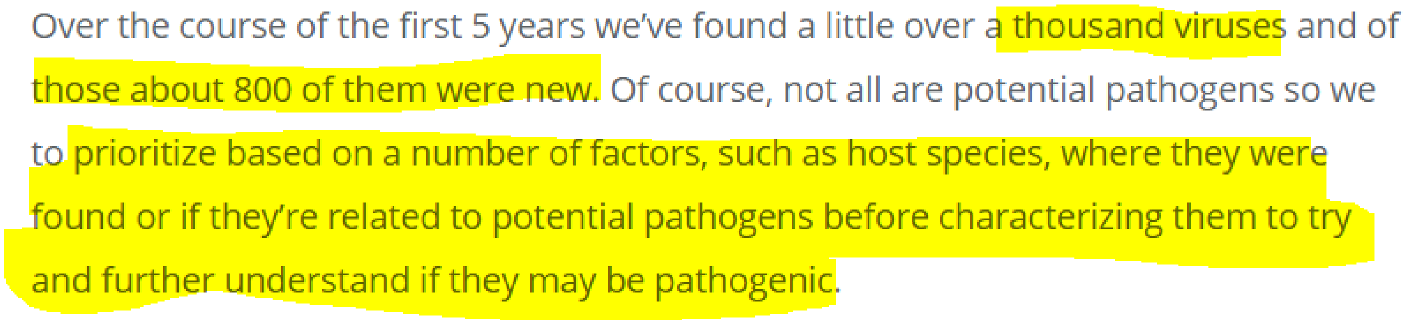
> Considering international transport of pathogens under PREDICT & DTRA rules, SCH014 & possibly other viruses from Yunnan must have been sent via a US Consulate, either Wuhan or Chengdu as hand-carry items to Dr. Stuart Nichol at Atlanta CDC exactly as was done in Georgia in 2012! pic.twitter.com/owU8BMZnaD
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) September 4, 2020

6. Many sequences were not entered into GENBANK, she admits



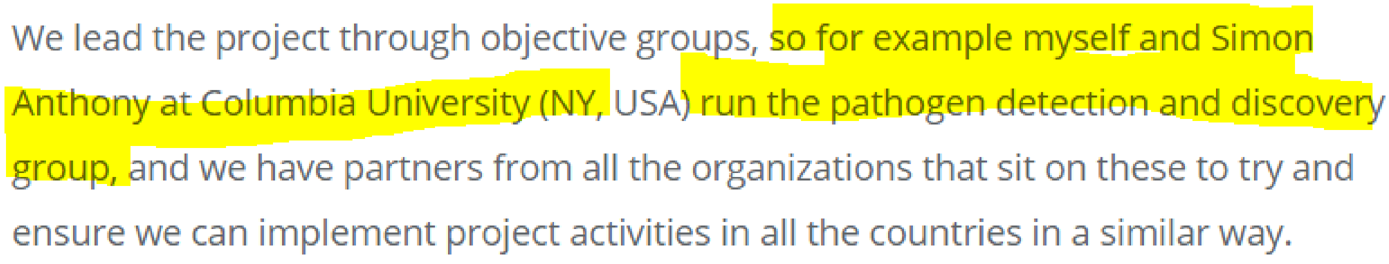
Once we've been given permission to share our results with the world we share them publically and as well as publish them. We have a partnership with HealthMap and they host a PREDICT site on the HealthMap website – so that is where our data are initially released. In addition, we enter sequences we obtain into the GeneBank database – we haven't entered everything yet but we're working on getting them all out there for the world!

7. "before characterising them to try and further understand if they may be pathogenic"
Again, only one way to do that, and it ain't exactly "characterising" them, is it?



Over the course of the first 5 years we've found a little over a thousand viruses and of those about 800 of them were new. Of course, not all are potential pathogens so we to prioritize based on a number of factors, such as host species, where they were found or if they're related to potential pathogens before characterizing them to try and further understand if they may be pathogenic.

8. Tracy Goldstein and Simon Anthony were in charge of the viral pathogen discovery group



We lead the project through objective groups, so for example myself and Simon Anthony at Columbia University (NY, USA) run the pathogen detection and discovery group, and we have partners from all the organizations that sit on these to try and ensure we can implement project activities in all the countries in a similar way.

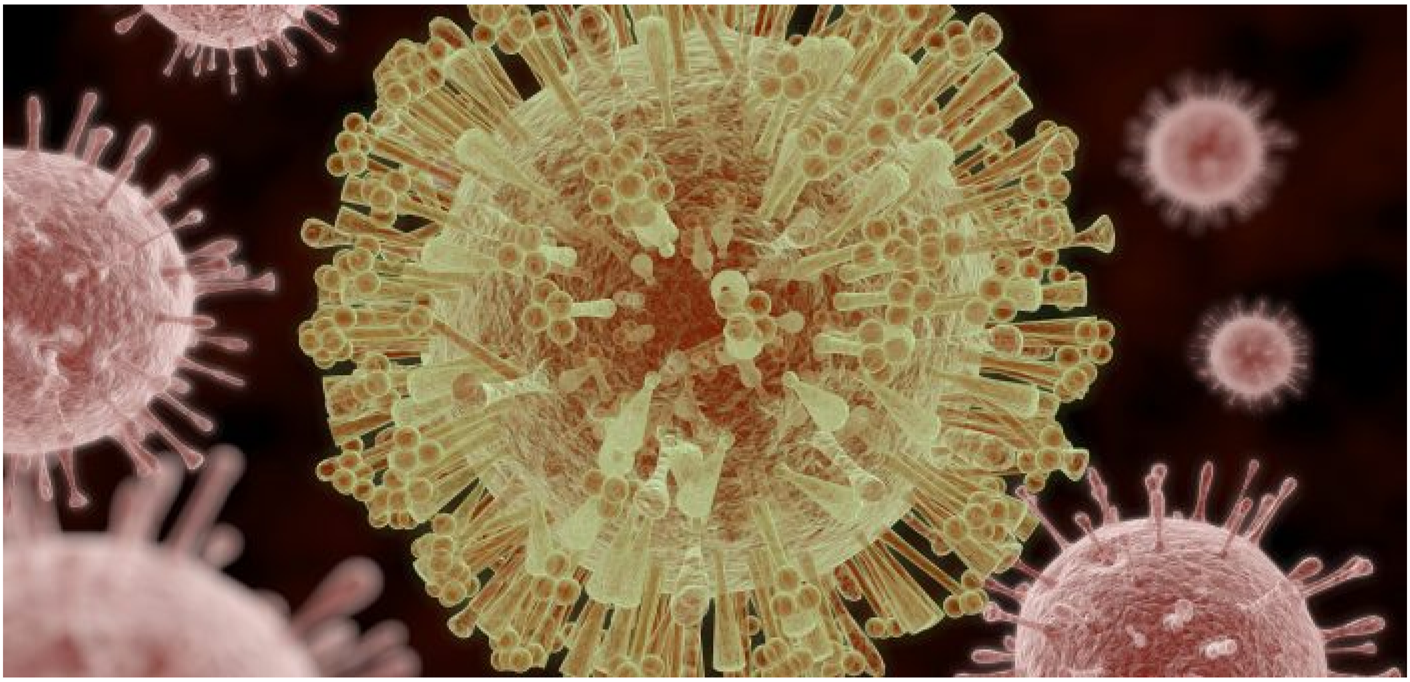
9. Notice some familiar names?
Yes, as Thick as Thieves....Virus Thieves!

Lipkin (Mailman), Daszak, Mazet, Karesh, Baric, Goldstein, Epstein, Olival, Wolfe (metabiota), Menachery, Scobey, Yount (USAMRIID)

Further Reading

1. Anthony SJ, Johnson CK, Greig DJ, Kramer S, Che X, Wells H, Hicks AL, Joly DO, Wolfe ND, Daszak P, Karesh W, Lipkin WI, Morse SS, PREDICT Consortium, Mazet JAK, Goldstein T. Global patterns in coronavirus diversity. *Virus Evol*, 3(1): vex012 (2017).
2. Anthony SJ, Gilardi K, Menachery VD, Goldstein T, Ssebide B, Mbabazi R, Navarrete-Macias I, Liang E, Wells H, Hicks A, Petrosov A, Byarugaba DK, Debbink K, Dinnon KH, Scobey T, Randell SH, Yount BL, Cranfield M, Johnson CK, Baric RS, Lipkin WI, Mazet JAK. Further Evidence for Bats as the Evolutionary Source of Middle East Respiratory Syndrome Coronavirus. *mBio*, 8(2): e00373-17 (2017).
3. Anthony SJ, Islam A, Johnson C, Navarrete-Macias I, Liang E, Jain K, Hitchens PL, Xiaoyu C, Soloyvov A, Hicks A, Ojeda-Flores R, Ulrich W, Rostal M, Epstein J, Petrosov A, Garcia J, Wolfe N, Goldstein T, Morse SS, Mazet J, Daszak P, Lipkin WI. Non-random patterns in viral diversity. *Nat Comms*, 6: 8147 (2015).
4. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, Daszak P, Lipkin WI. A strategy to estimate unknown viral diversity in mammals. *mBio*, 4(5): e00598-13 (2013).

10. Nice Image chosen back in Sept 2017 to illustrate?
https://t.co/lS4jwuP3E9
"This study was made possible by the generous support of the American people through the United States Agency for International Development (USAID) Emerging Pandemic Threats PREDICT project."



11. Maybe you are aware of the PREDICT sampling Map?
Here: https://t.co/T2lUWZf3HB
That is where "some" of their collected data goes

The local partners collect and enter the virus sampling data into a system called "EIDITH"
https://t.co/ezAdF1ROVB

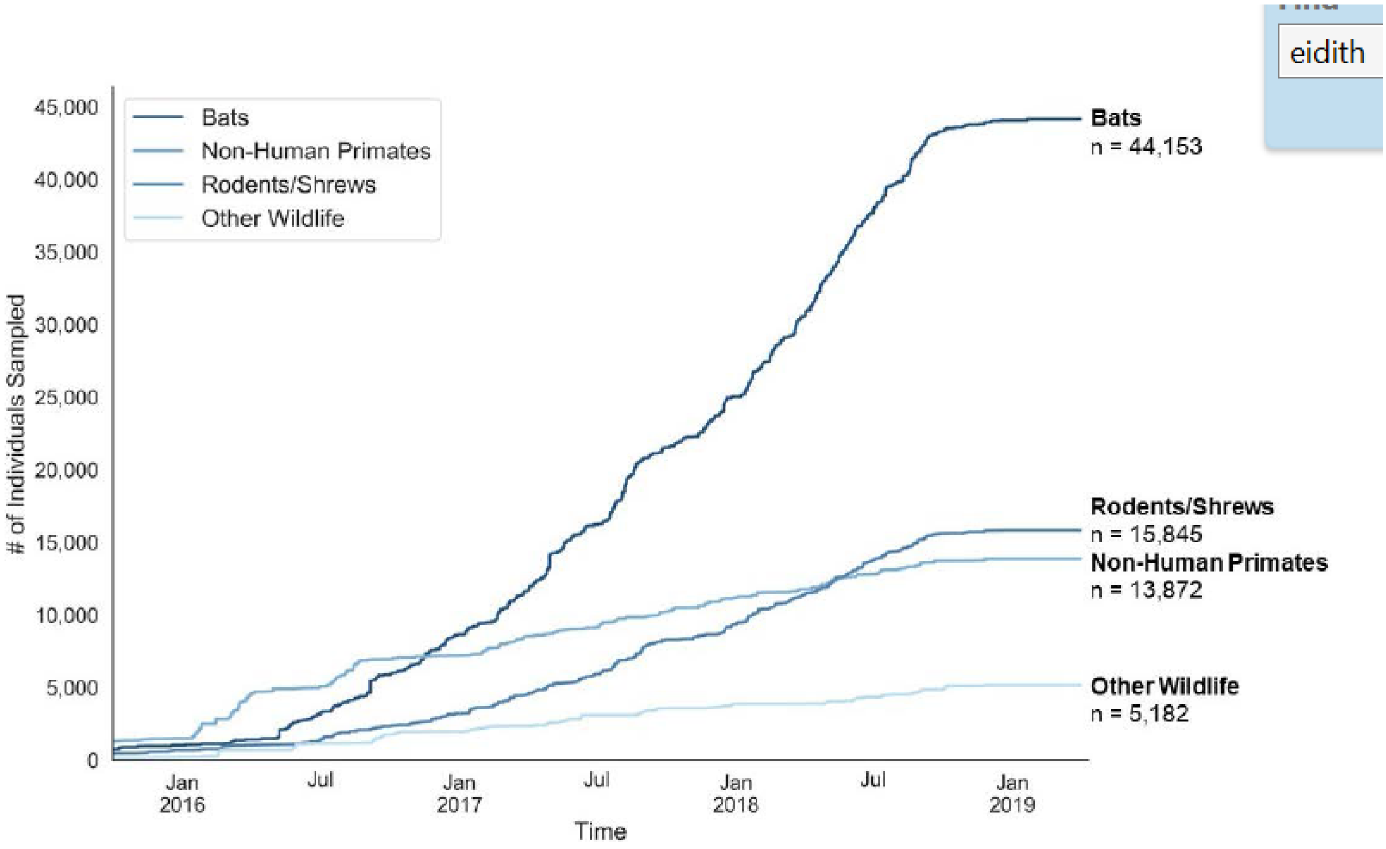


FIGURE 2. Number of individual wild animals sampled overall, by taxonomic group.*
**Depicts animals with data entered into the Emerging Infectious Disease Information Technology Hub (EIDITH), PREDICT's information and data management system.*

12. Not all viral data released onto their PREDICT Map
Here we have the Bangladesh & China Sections from the PREDICT 2019 report (pages 38, 39)
https://t.co/ezAdF1ROVB
The remaining data is kept secret on the EIDITH database....
(Page 44 - GVP and China Virome Project mentioned)

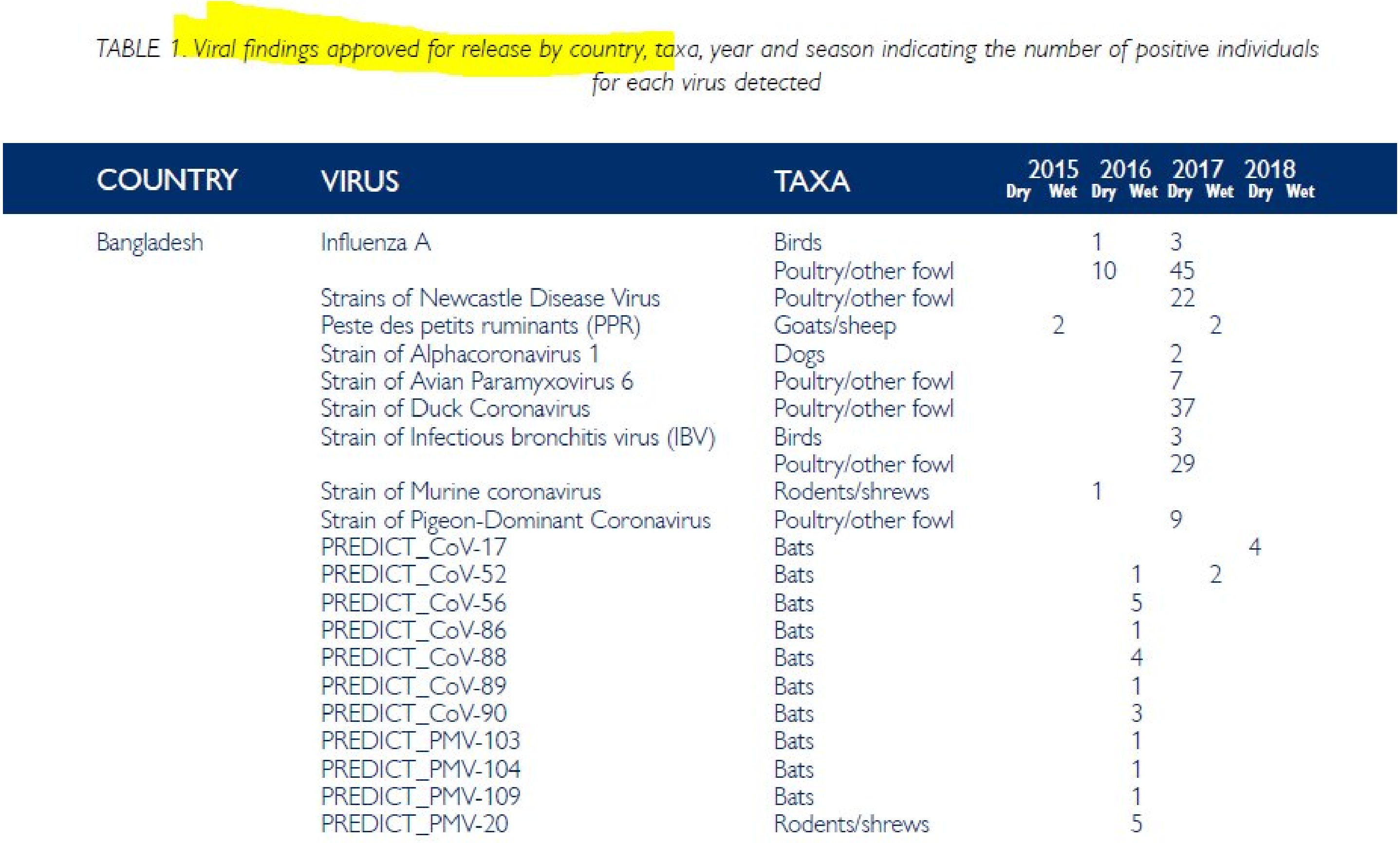


TABLE 1. Viral findings approved for release by country, taxa, year and season indicating the number of positive individuals for each virus detected

COUNTRY	VIRUS	TAXA	2015		2016		2017		2018	
			Dry	Wet	Dry	Wet	Dry	Wet	Dry	Wet
Bangladesh	Influenza A	Birds			1		3			
		Poultry/other fowl			10		45			
	Strains of Newcastle Disease Virus	Poultry/other fowl					22			
	Peste des petits ruminants (PPR)	Goats/sheep		2				2		
	Strain of Alphacoronavirus 1	Dogs					2			
	Strain of Avian Paramyxovirus 6	Poultry/other fowl					7			
	Strain of Duck Coronavirus	Poultry/other fowl					37			
	Strain of Infectious bronchitis virus (IBV)	Birds					3			
		Poultry/other fowl					29			
	Strain of Murine coronavirus	Rodents/shrews			1					
	Strain of Pigeon-Dominant Coronavirus	Poultry/other fowl					9			
	PREDICT_CoV-17	Bats							4	
	PREDICT_CoV-52	Bats				1		2		
	PREDICT_CoV-56	Bats				5				
	PREDICT_CoV-86	Bats				1				
	PREDICT_CoV-88	Bats				4				
	PREDICT_CoV-89	Bats				1				
	PREDICT_CoV-90	Bats				3				
	PREDICT_PMV-103	Bats				1				
	PREDICT_PMV-104	Bats				1				
	PREDICT_PMV-109	Bats				1				
	PREDICT_PMV-20	Rodents/shrews				5				

13. So, where is EIDITH when we need her?
Guess what? You were right again, it has been scrubbed!
Guess who scrubbed it? Right again, EcoHealth!
Oh what a wonderfully clean world we live in lately
Proof:
Website: https://t.co/dy37Y81DoN
Ecohealth Github:
https://t.co/D0YOvULn5v

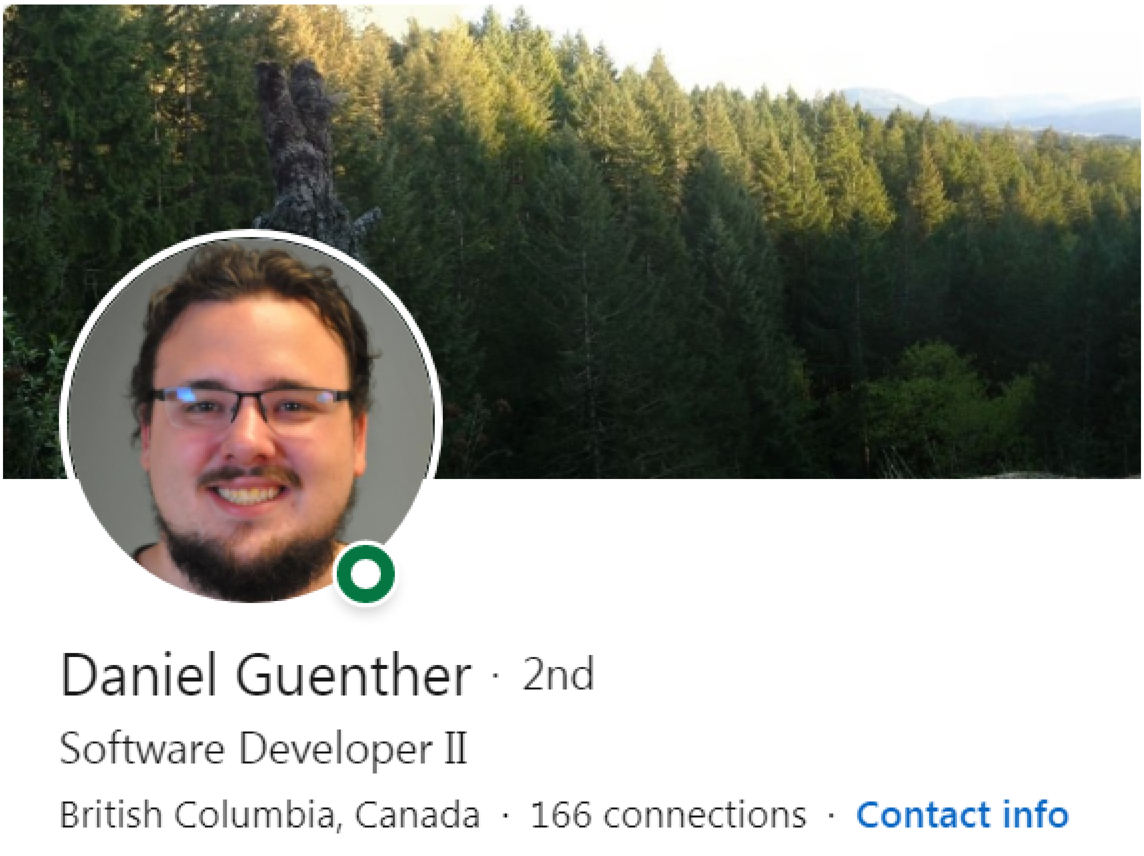
PREDICT Program

PREDICT is enabling global surveillance for pathogens that can spillover from animal hosts to people by building capacities to detect and discover viruses of pandemic potential. The project is part of USAID's Emerging Pandemic Threats program and is led by the UC Davis One Health Institute. The core partners are USAID, EcoHealth Alliance, Metabiota, Wildlife Conservation Society, and Smithsonian Institution.

14. Goodbye, Dear Eidith, we will miss you!
I tried to send her an email but it bounced

Try for yourself:
technology@eidith.org
Maybe that horrid man, Dr. Daszak is keeping her locked up in his basement full of nasty viruses, poor dear Eidith, we do hope he doesn't abuse you...

15. Maybe Mr. Guenther from Metabiota knows where she is?
https://t.co/dAY7Tfj9k2
"Creating new features for "Connect" web-application, a data collector for EIDITH (Emerging Infectious Disease Information Technology Hub) as part of USAID & UC Davis's PREDICT initiative"



Daniel Guenther · 2nd
Software Developer II
British Columbia, Canada · 166 connections · Contact info

16. What could EIDITH show us?
Quite a lot actually, we would be able to see ALL viruses collected in Yunnan in 2012-2013, not just those on the PREDICT Map.
We can see an EIDITH generated csv file for Vietnam:
https://t.co/dZEnEOADIf
used in this paper:
https://t.co/dwFewxxIls

17. Summary:
EIDITH is a database of virus sampling activities by local partners which (If "governments" agree) are reflected in the PREDICT map.
Ecohealth removed that data from the net so we cannot check the viral pathogens they found in Yunnan in 2012.

Welcome to the EIDITH website, an internal site used for the USAID funded PREDICT project

18. Ecohealth deleted the Github project as well.
This project is funded by the long suffering US Taxpayers (poor sods) thanks to Fauci & NIH via USAID.
Why is the data not publicly available?
Why has the website been taken down?
Why have the media not even investigated this?

19. We can't access deleted Chinese virus databases that we have been demanding to see since February
But, this is a taxpayer funded US NGO, so if you are Americans, demand answers from UC Davis, from Lipkin, Goldstein, write to your congressmen or whatever,
Make a Bloody Fuss!