BUZZ CHRONICLES > ALL
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Daoyu
@Daoyu15

https://t.co/SvP0tfbDki

https://t.co/k9mmL9e5kn

https://t.co/7fR13yb3qJ

https://t.co/EXerlaiG9u

> Interesting!
>
> NAHL Laos was built by USAID PREDICT to work with Metabiota. Daszak says Sep 2018 they were still not allowed to collect samples for Shi at WIV.
>
> Doesn't mean EcoHealth didn't get them before/after directly/indirectly. We know the Navy sampled bats there in 2017.\U0001f642 pic.twitter.com/mVp6dytD6X
>
> — Florin (@Florin_Uncovers) February 20, 2022

https://t.co/iNCdLY1Pzn

> EXCLUSIVE: Hunter Biden DID help secure millions in funding for US contractor in Ukraine specializing in deadly pathogen research https://t.co/fFBX7IFcKh
>
> — Daily Mail US (@DailyMail) March 25, 2022

https://t.co/F4Ktc27m4g

> PREDICT: Ecohealth; Metabiota; WIV; found every virus under the Sun in the bat caves in S.China in 2014, but "NONE" at any wet market where humans gather! What was their research really all about??
> \U0001f447https://t.co/Qun3IHsdUV pic.twitter.com/7Hb881BxyH
>
> — Keith Evans (@KeithEv84928885) April 29, 2022

https://t.co/3256saQ92M

> 24. DTRA Network for Collection of Viruses
> 7. DTRA - Metabiota - One Health - Ecohealth
> Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia
> pic.twitter.com/SOqSSXF3pa
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) January 9, 2021

https://t.co/Jdixf411T5

> 23. David Mustra can be seen at the 2:34 mark in the video, note: "Metabiota"
>
> Note: Martha Stokes from DTRA also appears in the video, who will be familiar to some of you from Cambodian Bat Research and BOHRN (with Dr. Jonathan Epstein (EHA).https://t.co/SSawjbdTcC pic.twitter.com/CG8sfoPz61
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) April 14, 2022

https://t.co/udOcFX8gf6

> Metabiota is getting funding from all the wrong placeshttps://t.co/BVs01rQCBr pic.twitter.com/3nuyz0FVaT
>
> — DIY (@mindnotforrent) March 26, 2022

https://t.co/qA4hINXL1e
Also see that “PREDICT-2”

https://t.co/ljSEOh77zN
Metabiota-GVP connection

https://t.co/VnUvdBmqRr

> https://t.co/QpHGiNN8Fg
> In the CAS implementation of DEFUSE, S.E. Asia is clearly in the scope. https://t.co/4th2qCSr3X
> Specifically, \u201csamples from surrounding areas of my country and the Belt and Road regions\u201d was set into the scope for the umbrella project where the two CAS
>
> — Daoyu (@Daoyu15) May 31, 2022

https://t.co/0qpvycEQ35

https://t.co/fv2UDYV39M

> Metabiota/USAID planned visit in Laos in Oct 18
> p. 39/41 of part 3.@garyruskin pic.twitter.com/NHwK5XXryg
>
> — Gilles Demaneuf (@gdemaneuf) January 11, 2022

https://t.co/MnFC5ooRO3

> A lot of the South-East Asia USAID/EHA/Metabiota work is coordinated via Bangkok, where Sudarat has been a key trusted partner for many years.
>
> The project umbrellas include PREDICT, the Global Virome Project, OneHealth, SEAOHUN and other initiatives. pic.twitter.com/vog2oLd5Vl
>
> — Gilles Demaneuf (@gdemaneuf) January 11, 2022

https://t.co/V3wrNOZSJ6

> #Metabiota were aligned to Government contracts, which in 2014, far out-weighed Commercial contracts. pic.twitter.com/s1oGQlCaNC
>
> — Fools Multiply (@FoolsMultiply) April 6, 2022

IP was seen here too…… (2014) https://t.co/HqC1jMzzjk

> How much was passed to #Metabiota ? #InstitutPasteur #UCDavis #Ecohealth #Predict pic.twitter.com/Rrxm9b6gfX
>
> — Fools Multiply (@FoolsMultiply) April 6, 2022

https://t.co/TrZvLQCeyR…
An 2010 RacCS203-associated RdRp. Part of the PREDICT consortium samples. This is proof that IP/PREDICT are in possession of close SARS-CoV-2 relatives in their databanks at least since 2010. Also why this is published so late?

https://t.co/muLCPLRg0M

> All the diversity in the Shitou cave have been fully sampled, the ~9 Spike proteins and the ~5 representative (within 97% similarity) strains fully tested as by year 2017. A year before DEFUSE. The word \u201c6 asian countries\u201d appeared in the document for 2 times, where the data from
>
> — Daoyu (@Daoyu15) May 31, 2022

https://t.co/3asIgFJIZr

> In addition, the sequence acquisition step stated that consensus between strains are to be used\u2014in stead of a more highly accurate deep sequencing of (newly acquired) samples, with the workflow explicitly designed to remove sequencing errors by averaging assembled sequences in

> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/YPlJvozqrG

> Stead of sequencing each sample multiple times at a higher depth (which is how high accuracy error-free sequencing is performed by standard). This indicate that the scope of DEFUSE included \u201cQS strains\u201d where only a consensus sequence was available and of which re-sequencing
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/21sve6HegX

> is not possible, a scope that clearly included 1: non-newly-acquired samples. 2: samples that were already fully depleted (and where only sequencing data exists) at the time of the beginning of the program. 3:QS strains where deep sequencing is not conducted and only an assembled
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/tg9gf57nei

> sequence was available at the time of the beginning of the program.
> This represents a great deal of flexibility toward sampling protocol, condition of sample and original experimental protocol, indicating that the scope of the QS recovery operation is intended to span the entire
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/0eKI3FUu8g

> EHA database\u2014where the majority of the strains within contained only an assembly sequence but neither samples to deep resequenced nor sequencing data that may be used to make a non-multi-strain consensus. Only when the sampling is being done by multiple institutions with a wide
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/wWkqY8pkiM

> variety of protocol and sample condition at sequence release, will you need such a multi-strain consensus protocol, that even explicitly stated that \u201cwe will review past deep sequencing data\u201d, that is clearly designed for generalizability in stead of precision.
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/pai1fK7aFE

> The protocol for sequence acquisition and recovery is clearly intended for databases that contained a lot of different (un-controllable) experimental procedures in stead of those that contained only a single (specify-able from the project) experimental procedure.
>
> — Daoyu (@Daoyu15) June 4, 2022

https://t.co/ezJL10DjEi

> Now check this, #NIH's list of labs in low-resource countries. You not gonna believe this, check locations and then compare reported outbreaks past 2 decades \U0001f914\U0001f9d0#BioLabs #USA #NIH #CDC #USAID #DoD #WHO #PasteurInstitute #WorldBank #UNESCO #AFD #JICAhttps://t.co/fZ1Xktf7a1 https://t.co/42hwuNVKBP pic.twitter.com/Zoi4dcHMUr
>
> — Dieda (@DiedaExploring) June 14, 2022

About IP france and IP laos: https://t.co/Y3BeChiZqD

> https://t.co/o4QhOeAGDk
> IP collaboration with WIV\u2026\u2026(IP france. What was the \u201cSARS-like coronaviruses(unpublished data)\u201d? (Contained Yunnan bat samples)
>
> — Daoyu (@Daoyu15) May 20, 2022

https://t.co/G4xCnJ0Iqt

> https://t.co/0CMXHB2sKu
> Also BANAL caves were first sampled in 2017. https://t.co/9NFcvmc6gmhttps://t.co/G5nPPPen8v
> None of the reads from even the batflies, part from what that have been aligned to a single Orthoreovirus, have been released. https://t.co/BJx4j5Jq3L https://t.co/aOHh4ZSkfC
>
> — Daoyu (@Daoyu15) May 1, 2022

https://t.co/aOHh4ZSkfC

> "Bats for Peace"? Funded by DTRA...https://t.co/pmFrpgkQEC
>
> Links to archived documents of interesthttps://t.co/1X86x6sIl7 pic.twitter.com/9A9owXV3tj
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) March 15, 2022

https://t.co/y1DVwwl0QH
EHA is known to use funding intended for one project for other projects—including “unfunded projects”.

https://t.co/ljSEOh77zN
This connection between PREDICT, PREDICT-2, IP (Laos, Cambodge, France) and the EHA database (used for DEFUSE),

as well as the fact that the EHA splits funding amongst programs internally, is why it takes so long for them to release any data at all, and

Why most of this data was still partial. (The censored batflies……) https://t.co/P8pmPNzJ5i

> The initial expedition with Institut Pasteur du Laos was funded by US Naval MRC and DTRA in support of the US DoD's GEIS. Yes there is a story there, and what happened to the samples from that.https://t.co/2wL5EpSdlV
>
> — Dog's Breakfast (@breakfast_dogs) February 17, 2022

https://t.co/lzmjJCo158

Batflies: sent to IP france (Paris). Why no sequences other than the single Orthoreovirus was released?

(Not just assemblies. Even the raw reads were filtered such that only reads that aligned to the Orthoreovirus genome is released).
What was the “partners” of IP laos?

LOWMRU, which is a program operated under the Tropical Medical Network (Madihol Oxford Tropical Medicine Research Unit(MORU)), a close partner of the EHA.
https://t.co/kZQhJXH01e
https://t.co/fMNUoYNnoV
https://t.co/hcVNESCpes
https://t.co/GruWYr5F89

https://t.co/475S4bN3Jl

> Still seems odd Navy is overseer. Especially since a different DOD agency DTRA is EcoH's main funder at $37.86 million. Navy heavy into bat research, funding a Laos bat trip "U.S. Naval Medical Research Center-Asia (NMRC-A)" for "DoD-GEIS\u201d. DoD sure does like bat viruses & EcoH. pic.twitter.com/I0bAypew8H
>
> — sheila (@capitolsheila) November 4, 2021

The DOD also have the sample sequences—they funded the program. Material likely containing sequences of the closest relatives of SARS-CoV-2 is in possession of both the EHA and the DOD. https://t.co/2ix10Ls0tc

> This 2017 US Navy-funded study of Laos bats turned up lots of stuff the French group isn\u2019t allowed to publish, we hear. French go back in 2020 & now tell world \u201cHey guys, bat cave in Laos has really similar stuff to SARS2.\u201d
>
> Laos bat viruses? DOD?
> Secrets in a pandemic? Why? pic.twitter.com/1DXdlVykla
>
> — sheila (@capitolsheila) December 10, 2021

https://t.co/Uch7lZc0lk

https://t.co/AO1R4qtr19

> And that\u2019s not all\u2014the EcoHealth grant document also mentions plans for more sampling in SE Asia (including Laos) from Year 3 onwards, as part of their Specific Aims. pic.twitter.com/PUdEE1KZQA
>
> — The Seeker (@TheSeeker268) January 18, 2022

What was in these PREDICT sequences that they couldn’t submit to GenBank? See that RacCS203 related sample. Collected by IP Cambodge 2010 and placed under PREDICT. Still not full release. It is evident that at least some of this data were SARS-CoV-2 close relatives that were https://t.co/aBNNFqwhYc

> Peter Daszak asked for US-funded virus data to be withheld, FOIAed by @USRightToKnow
>
> "It's extremely important that we don't have these sequences as part of our PREDICT release.. Having them as part of PREDICT will being very unwelcome attention"https://t.co/yooVvKtkaJ pic.twitter.com/IVFJIZ9y1I
>
> — Alina Chan (@Ayjchan) January 11, 2022

Being used by the DEFUSE program.

https://t.co/jhChwjfnQ1

https://t.co/snWaM0M7T9

https://t.co/Qj4nIrEXBa
Ecohealth also “trained” (established moles inside) “students from the National university of Laos” for their own sampling purposes. PREDICT 2014.

https://t.co/XhtKjuXY5N
A collaboration was later established between the EHA and the National University of Laos, sacking 69 more bats at the end of 2019 in the PREDICT-2 program.

Note how the DARPA continued to fund the WIV in 2018. https://t.co/KQY7GOclwc

> Also notable is that Shi Zhengli was awarded nearly $1.5 million in January 2018 \u2013 a little more than what Peter Daszak had asked DARPA for WIV\u2019s part of the work (~$1.2 million).https://t.co/qYTWnm1ZVqhttps://t.co/xSpILJeY1Y pic.twitter.com/lHPXay7nW1
>
> — The Seeker (@TheSeeker268) March 13, 2022

And for the crowd saying that “GVP wasn’t funded”, here is the USAID funding “USAID GVP (Core)” in 2018.
https://t.co/2TGF078vBp

> \u25cf Sometime in 2018: A chart shows USAID provided $270,969 to Global Virome Project (GVP) pic.twitter.com/LWYhl61xJK
>
> — The Seeker (@TheSeeker268) February 23, 2022

https://t.co/tTdE8PVUXD

> From: Frieman, Matthew
> February 28, 2019
>
> "Inglesby is pushing on the fact that its not reported what it was that was discussed/changed/agreed to during this new approval process that allowed the Yoshi and Fouchier experiments/grants to be approved again." @T_Inglesby pic.twitter.com/PXepYik9xb
>
> — Jess (@uacjess) May 7, 2022

“no P3CO safety concerns” coincided with the DEFUSE documents’ explicit statement that the viruses they plan to resurrect would not constitute P3CO or GOF because they aren’t the exact SARS1 or MERS strain. https://t.co/Poddryx6fQ

> 2/28/2019
> Ralph Baric
> "Thanks for passing this on. It would be of value to hear about the additional safeguards, although I am overall uncertain as to what NIH is doing with SARS and MERS grants, beyond the "general" statement "no PC30 safety concerns". https://t.co/zSh3OHaa9X pic.twitter.com/g1aFRR2wUE
>
> — Jess (@uacjess) May 7, 2022

https://t.co/ypmrH9nEq3
A spike in readership of many articles related to CoVs and FCS happened in mid-late 2019. https://t.co/v1HEss37Ai

Another plausible vector for bringing DOD material to the WIV. (The collaboration behind him. Not that particular visit). https://t.co/05xRKv1o6t

> Pei-Yong Shi, who works at the University of Texas Medical Branch\u2019s biolab, has been at the DOD/NIH/CDC-funded Texas lab for over 5 yrs.
>
> In addition to visiting the WIV Oct. 19-20, 2019, he also was at China\u2019s newest BSL-4 lab, just as it was getting final certification to open. pic.twitter.com/mxgP0lbL8z
>
> — sheila (@capitolsheila) June 18, 2022

Why the Chinese BSL-3/BSL-4 need “confidentiality”? https://t.co/Qlz7j9fmkm

> There is plenty there that you may find interesting, especially related to Kunming ABSL-4, the 'old' new BSL-4 in China, compared to the WIV which was the \u2018only **publicly** known P4 lab\u2019 (all wordings from FOI'd emails). pic.twitter.com/KfqMAbPurt

> — Gilles Demaneuf (@gdemaneuf) June 19, 2022

(Note: this is the Kunming ABSL-4. Very little is know about what was being done there, other than that all CAS BSL-3/BSL-4 labs are intimately connected to each other).