

Maybe Scrolly?

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Clandestine

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1) This thread will breakdown source material between America's top scientists and health officials [@NIH](#), recently made available via FOIA.

Thanks to [@Jim_Jordan](#) and [@JamesComer](#), we have the emails sent to Fauci and Collins pertaining to C19 origin. republicans-oversight.house.gov/wp-content/upl...

2) Dr. Mike Farzan, Discoverer of SARS receptor, Harvard Medical, Immunology and Microbiology at University of Florida.

His initial assessment of C-19:

- furin site is unnatural and likely man made
- furin site manipulation enabled human adaption and transmission

From Mike Farzan (discoverer of SARS receptor):

1. The RBD didn't look 'engineered' to him – as in, no human would have selected the individual mutations and cloned them into the RBD (I think we all agree)
2. Tissue culture passage can often lead to gain of basic sites – including furin cleavage sites (this is stuff they have seen with human coronaviruses)
3. He is bothered by the furin site and has a hard time explain that as an event outside the lab (though, there are possible ways in nature, but highly unlikely)
4. Instead of directed engineering, changes in the RBD and acquisition of the furin site would be highly compatible with the idea of continued passage of virus in tissue culture
5. Acquisition of the furin site would likely destabilize the virus but would make it disseminate to new tissues.

So, given above, a likely explanation could be something as simple as passage SARS-live CoVs in tissue culture on human cell lines (under BSL-2) for an extended period of time, accidentally creating a virus that would be primed for rapid transmission between humans via gain of furin site (from tissue culture) and adaption to human ACE2 receptor via repeated passage.

...So, I think it becomes a question of how do you put all this together, whether you believe in this series of coincidences, what you know of the lab in Wuhan, how much could be in nature – accidental release or natural event? I am 70:30 or 60:40.



Michael Farzan

Chair

Professor

Department of Immunology and

Microbiology

Florida Campus

3) Dr. Bob Garry, Microbiology Professor for Biomedical at Tulane.

-“I really can’t think of a plausible natural scenario”

-I just can’t figure out how this gets accomplished in nature”

-introduction of the amino acids/ nucleotides introduction created GoF in humans

Robert Garry PhD



Robert F. Garry PhD is Professor of Microbiology and Immunology and Assistant Dean for Graduate Studies in Biomedical Sciences at Tulane University School of Medicine. Dr. Garry was involved in collaborative studies that lead to the determination that entry proteins of enveloped viruses form at least three distinct

structural classes. This work has been the foundation for the development of novel antiviral peptide drugs. He is currently managing the Viral Hemorrhagic Fever Consortium (VHFC), a public-private partnership that is developing countermeasures against Lassa virus, Ebola virus and other severe pathogens. The VHFC developed point-of-contact, point-of-care and confirmatory diagnostics for Lassa fever to commercial standards. The VHFC leveraged these advances to develop high sensitivity and specificity immunoassays for Ebola virus and other filoviruses, including an Ebola Rapid Diagnostic Test (Ebola RDT) that can be used in austere settings. RDTs using VHFC critical reagents have been the only immunodiagnostics to obtain FDA Emergency Use Authorization and WHO Listing for use in the current West African Ebola outbreak.

From Bob [Garry]:

Before I left the office for the ball, I aligned nCoV with the 96% bat CoV sequenced at WIV. Except for the RBD the S proteins are essentially identical at the amino acid level – well all but the perfect insertion of 12 nucleotides that adds the furin site. S2 is over its whole length essentially identical. I really can't think of a plausible natural scenario where you get from the bat virus or one very similar to it to nCoV where you insert exactly 4 amino acids 12 nucleotide that all have to be added at the exact same time to gain this function – that and you don't change any other amino acid in S2? I just can't figure out how this gets accomplished in nature. Do the alignment of the spikes at the amino acid level – its stunning. Of course, in the lab it would be easy to generate the perfect 12 base insert that you wanted. Another scenario is that the progenitor of nCoV was a bat virus with the perfect furin cleavage site generated over

2

evolutionary times. In this scenario RaTG13 the WIV virus was generated by a perfect deletion of 12 nucleotides while essentially not changing any other S2 amino acid. Even more implausible IMO.

That is the big if.

You were doing gain of function research you would NOT use an existing close of SARS or MERSv. These viruses are already human pathogens. What you would do is close a bat virus th[at] had not yet emerged. Maybe then pass it in human cells for a while to lock in the RBS, then you reclone and put in the mutations you are interested – one of the first a polybasic cleavage site.

4) In response to the experts above, Dr. Francis Collins, Director of @NIH, (government official) responded with:

-“I am coming around to the view that natural origin is more likely” despite the evidence

-We have to say it's natural or conspiracy theorists will harm science

5) Director of @NIH said we shouldn't admit the virus was man made or the conspiracists might think we are up to something.

When they were literally genetically modifying bat coronaviruses to gain lethality and transmissibility in humans. In China...



Opinion | How Fauci and Collins Shut Down Covid Debate

They worked with the media to trash the Great Barrington Declaration.

<https://www.google.com/amp/s/www.wsj.com/amp/articles/fauci-collins-emails-great-barrington-declaration-covid-pandemic-loc...>

6) Dr. Andrew Rambaut, Evolutionary Biologist and Professor of Molecular Evolution at University of Edinburgh.

-“unusual furin cleavage site” suggesting C19 was created

-can't confirm natural occurrence without evidence

-should defer to experts working with the virus in Wuhan

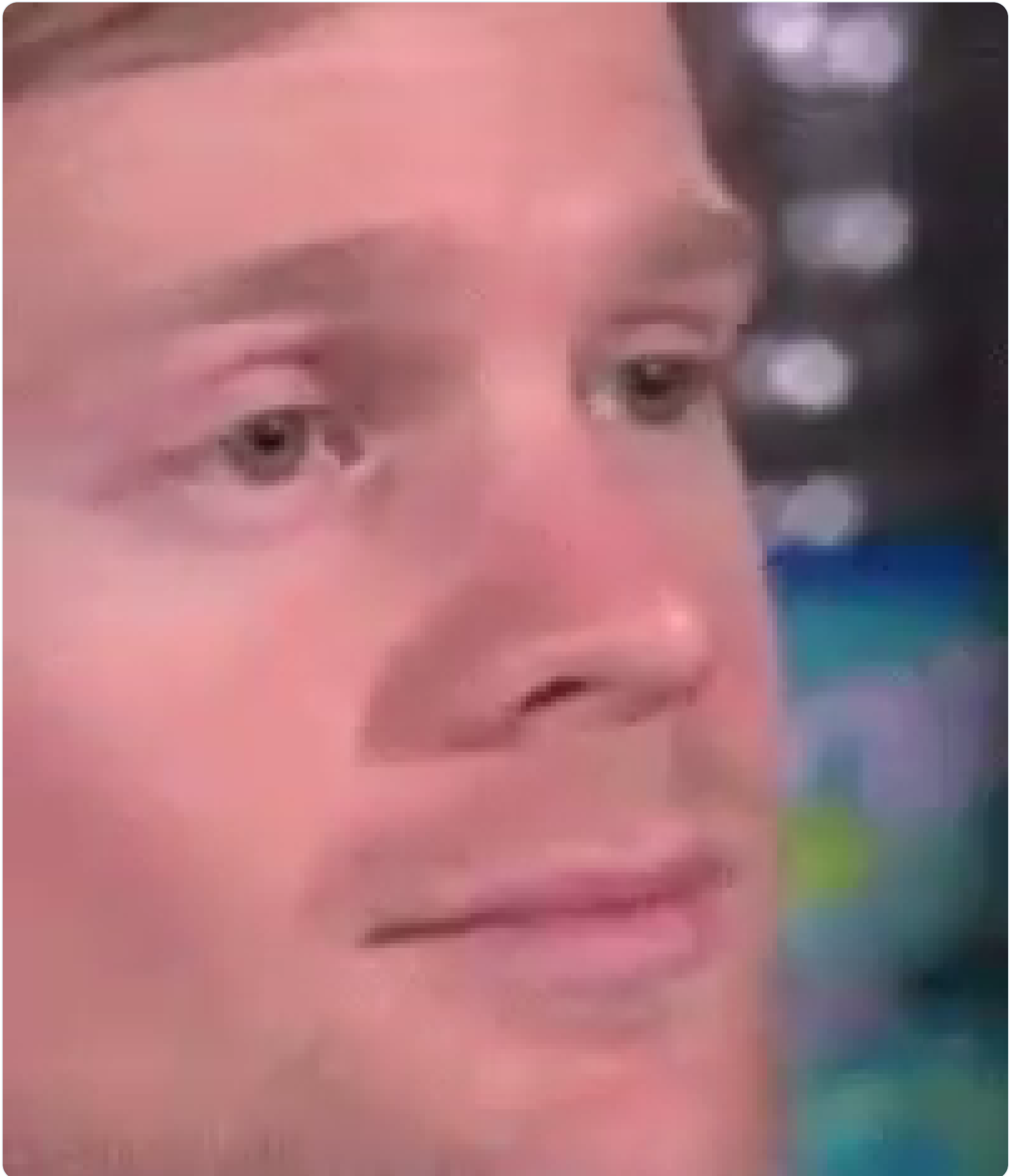
7) Dr. Ron Fouchier, Deputy Head of Viroscience at Erasmus MC.

-“discussion on possible origin of C19 would be of much interest”

-But we shouldn't worry about it because the scientific community has more important things going on and “WHO

8) Dr. Ron Fouchier says the quiet part out loud, and says we shouldn't have a discussion on the origin of covid, because the WHO and STAKEHOLDERS are present?!

Actively suppressed the origin of the virus to protect, their own asses and the confidence in science in CHINA?!



9) Dr. Edward Holmes, Evolutionary Biologist and Virologist Fudan University, Shanghai.

Dr. Jeremy Farrar, Professor of Tropical Medicine, Oxford.

- Holmes leaning on the lab leak origin "60-40" based on the evidence

-Farrar declares he is "50-50"

10) All of the communications shown above happened in Feb 2020. The following email from [@NIH](#) Director Collins 2 months later in April.

-the lab leak reality is harmful to our image, and it's growing in momentum due to the evidence
-how can we help make the truth go away?

11) And the final response from Fauci in regards to the growing theory that the virus came from the Wuhan Lab (which we now have proof that it did and Fauci knew about it.)

-this is a "shiny object" the sheep will forget in time. Just keep lying to them and they won't notice.

12) In summary:

World's top virologists and evolutionary biologists suggest lab leak due to molecular composition of C19 suggesting clear human modification.

The [@NIH](#) and Fauci ignored the world's top scientists in fear that if the public knew the truth, we wouldn't trust them.



13) Fauci claims he "represents science", but actively ignored and suppressed the assessments of the world's expert scientists to lie to the public, cover for the [@NIH](#) their stakeholders, and the [@WHO](#)

Those are the facts. Now it's time to act. [#ExposeFauci](#) [#Revolution](#)

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