Twitter Thread by Dog's Breakfast

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@breakfast_dogs

Evidence of Genetic Engineering of SARS-COV-2. Part 2 (thread).

The Outlandish Case of the Uncanny HIV Inserts.

Part 1 is below if you haven't yet read it:
https://t.co/CeztISvFQN

> Vincent Racaniello, a professor of microbiology and immunology at Columbia University, says such claims are not true. The coronavirus has no HIV-1 sequences, which can be seen by looking at the genome sequence, he said.
>
> "The spike glycoprotein of SARS-CoV-2 is just like the spike of every other CoV," Racaniello said in an email. "It is not from HIV-1. This post is pure nonsense, fake science, and not worth responding to."

Evidence of genetic engineering in SARS-COV- Thread

While the "lab leak" theory of SARS-COV-2 is now acceptable, many scientists still claim there's no evidence that SARS-COV-2 was genetically engineered.

These scientists either haven't looked, or need their eyes checked... pic.twitter.com/Bzz3XcW48t

— Dog's Breakfast (@breakfast_dogs) November 7, 2021

Early on in the pandemic a group of Indian HIV researchers announced they had found fragments of HIV in the SARS-COV-2 genome. While each fragment was small, they *rightly* stated that finding them all together was no coincidence.

https://t.co/vlAXv8UOKC

Although, the 4 inserts represent discontiguous short stretches of amino acids in spike glycoprotein of 2019-nCoV, the fact that all three of them share amino acid identity or similarity with HIV-1 gp120 and HIV-1 Gag (among all annotated virus proteins) suggests that this is not a random fortuitous finding. In other words, one may sporadically expect a fortuitous match for a stretch of 6-12 contiguous amino acid residues in an unrelated protein. However, it is unlikely that all 4 inserts in the 2019-nCoV spike glycoprotein fortuitously match with 2 key structural proteins of an unrelated virus (HIV-1).

For their efforts they were slammed by other scientists and media, and on Feb 2, 2019, the day after the Fauci teleconference with Holmes, Andersen, Farrar et al, they withdrew their pre-print.

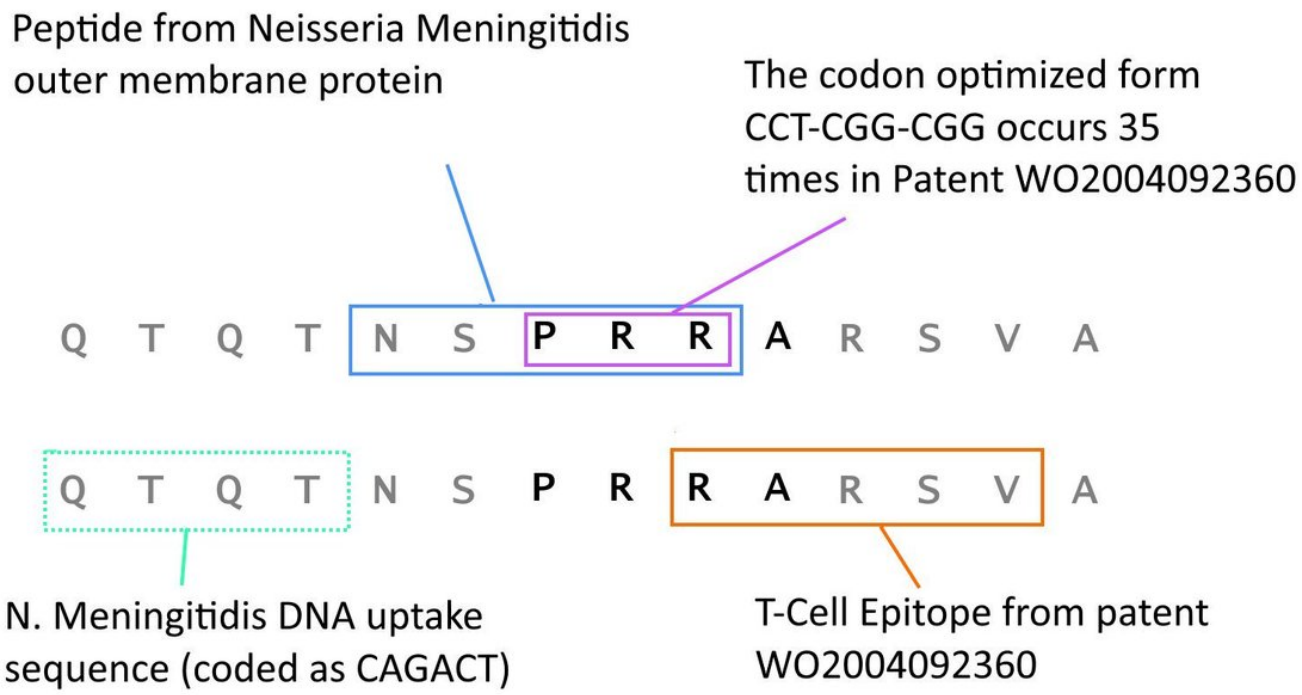
Multiple scientists, including Eric Feigl-Ding, a health economist at Harvard University's School of Public Health, and Shi Zhengli, a Chinese virologist at the Wuhan Institute of Virology and a member of a team that found the origin of the SARS virus in bats, have criticized the paper as lacking scientific merit and have called it misleading.

One of those sequences will be very familiar to anyone who has been following the story carefully. Although there has been a deletion within, Insert 4 is an easily recognizable part of the sequence around the SARS-COV-2 S1/S2 junction - QTNSPRRA.

Motifs	Virus Glycoprotein	Motif Alignment	HIV protein and Variable region	HIV Genome Source Country/ subtype
Insert 1	2019- nCoV (GP) HIV1(GP120)	**71 76** **TNGTKR** **TNGTKR** **404 409**	gp120-V4	Thailand */ CRF01_AE
Insert 2	2019- nCoV (GP) HIV1(GP120)	**145 150** **HKNNKS** **HKNNKS** **462 467**	gp120-V5	Kenya*/ G
Insert 3	2019- nCoV (GP) HIV1(GP120)	**245 256** **RSYL- - - -TPGDSSSG** **RTYLFNETRGNSSSG** **136 150**	gp120-V1	India*/C
Insert 4	2019- nCoV (Poly P) HIV1(gag)	**676 684** **QTNS----------PRRA** **QTNSSILMQRSNFKG PRRA** **366 384**	Gag	India*/C

It seems that these sequences have been taken from HIV and inserted into SARS-COV-2 genome. But what are their purpose? And did they originate in HIV naturally, or are they also artificial origin?

The FCS sequence I said previously derives from N. Meningitidis. Was I wrong?



It turns out the other three HIV inserts originate in Cholera Toxin (CT). Cholera toxin (with uncanny taxid: 666) has been investigated as an adjuvant (vaccine enhancer) especially for a mucosal (i.e. administered nasally) vaccine for HIV.

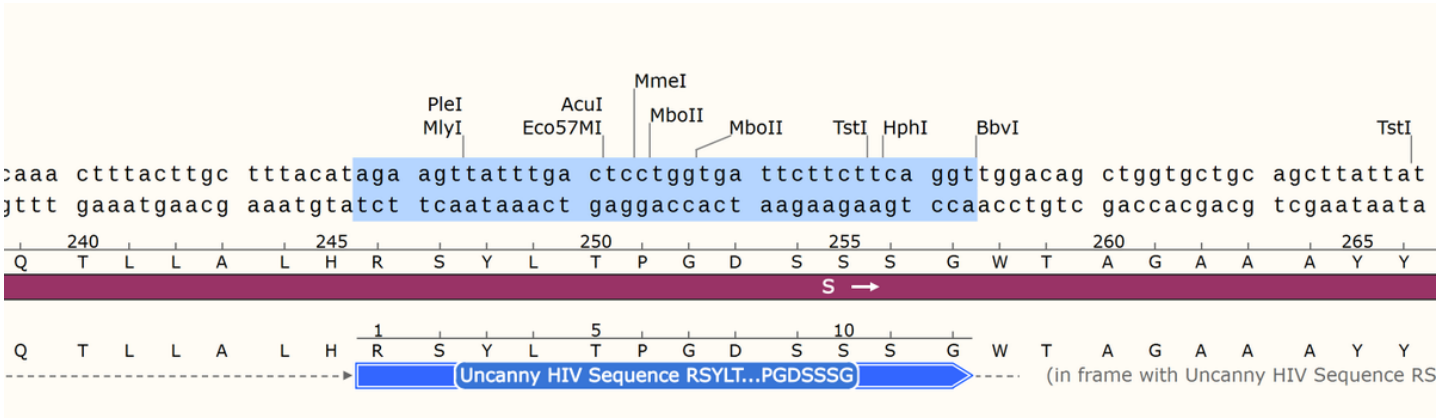
https://t.co/qERTHSD8tl

ADJUVANTS FOR MUCOSAL RESPONSES

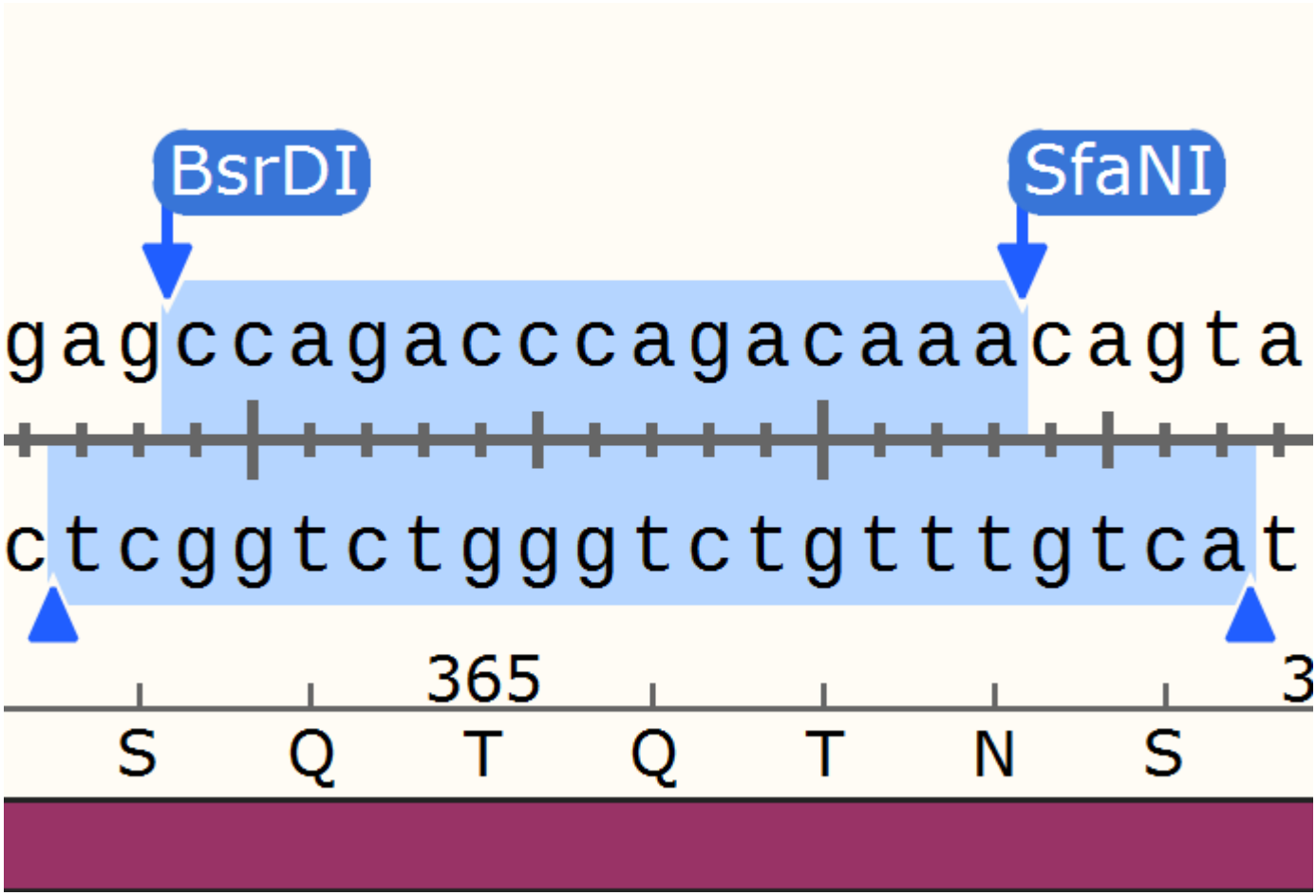
Go to:

For eliciting mucosal responses, cholera toxin (CT) and other bacterial products have been extensively tested in animal models. CT combined with Env gp120 elicited mucosal IgA in rhesus macaques [81]; other studies in rhesus (albeit with a different form of CT) have elicited more mixed responses [82]. CT has also been used to direct responses to the mucosa by combining it with agents that enhance retention at the mucosal surface, and has permitted dose sparing [83]. In addition, modified CT combined with cytokines were able to elicit mucosal antibodies to a peptide immunogen when given to cynomolgus monkeys [84], suggesting that promising combinations identified by other vaccine strategies (e.g., DNA vaccination) might be useful for mucosal immunization.

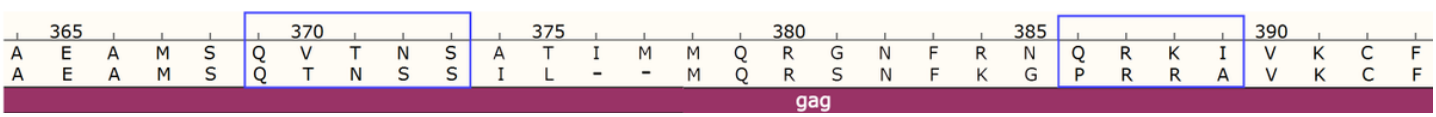
Here is "Uncanny HIV insert 3" within the SARS-COV-2 spike protein. The telltale signs of genetic engineering, Type IIS restriction sites abound. Note the SSS at end of sequence - it's significance is unknown but it is a recurrent motif around engineered sites.



In an HIV strain uploaded by USAMRIID in 2003 there is a different form of the Neisseria Meningitidis motif, flanked by Type IIS restriction sites and with an extra S residue. (Perhaps Serine is used simply as "padding"?)



In an alignment between an HIV sequence from 1998 and one from 2015, there is no recognizable PRRA in the earlier sequence. Uncanny.



In next thread let's look at some fake sequences from fake viruses. There's a growing pile of them each attempting to cover up the fake sequence that went before it. @nerdhaspower - and others - saw the problems with RaTG13 early on.

https://t.co/dJTOAFZ9AM

https://t.co/tl8Qh0ilOb

> Evidence of Genetic Engineering in SARS-COV-2
>
> Part 2 (continued) - The Hive of HIV. Mysteries of the Perez Codex...
>
> Previously...if you haven't already read, please catch up (10 min read).
>
> Part 1: https://t.co/CeztISvFQN
>
> Part 2:https://t.co/bHC8BsTfbJ
>
> — Dog's Breakfast (@breakfast_dogs) November 10, 2021