Twitter Thread by Dog's Breakfast

Dog's Breakfast
@breakfast_dogs

Evidence of Genetic Engineering in SARS-COV-2

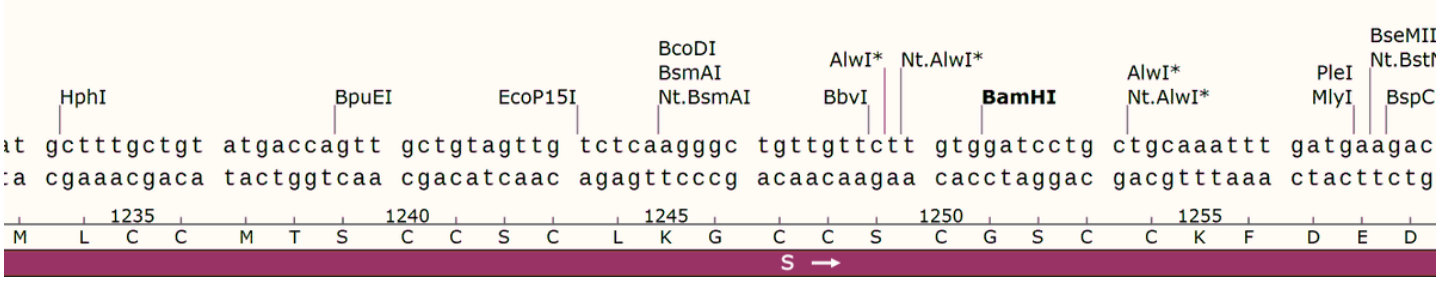
Part 4 A Sting in the Tale of Kristian Andersen

> **"The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered."**

When @K_G_Andersen "opened up" about the infamous email in which he stated "Eddie, Bob, Mike, and myself all find the [SARS-CoV2] genome inconsistent with expectations from evolutionary theory" he never quite told us exactly what he saw, but still he left a few clues.

In a response to questions from @nicholsonbaker8 he mentioned the FCS and the RBD, but also "a unique restriction enzyme site (BamHI) ...a higher level of conservation towards the end of the spike...other residues that had been observed to be important from research with SARS"

Since much of the focus to date has been on the FCS and RBD, let's instead take a look at a different region towards the end of the spike that had been of interest to SARS researchers - a "Cysteine-rich endo-domain" - Cysteine denoted by C:



In 2007, SARS researchers had tried exchanging some of these Cysteine (C) residues for Alanine (A) in parts of this region and discovered that cell fusion (merging and entry into the cell) was reduced by 50-60% when they did so.

https://t.co/iUEMYnldU3

The second half of the spike (S2) is far more conserved between coronaviruses than S1. On an amino acid basis there may be only a handful of mutations in several hundred bases. Looking at just the last 40, there's remarkable homology over time, species and geographic region.

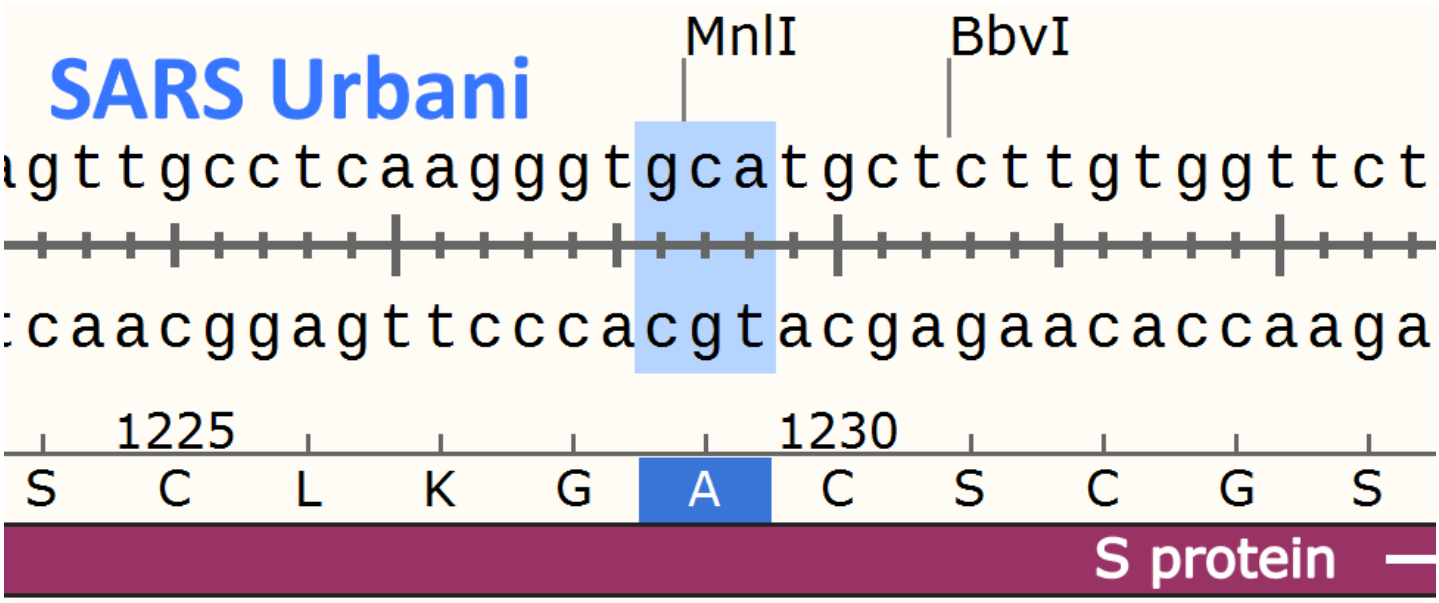
SARS (Urbani)	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
BtRs-BetaCoV/YN2018A	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rp/Shaanxi2011	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4247	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
YN2018B	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
As6526	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4237	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Longquan-140	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4081	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
BetaCoV/GX2013	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
HKU3	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
YN2013	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs806/2006	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Cp/Yunnan2011	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs3367	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
WIV1	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
YN2018D	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4255	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs_672/2006	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
WIV16	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
RsSHC014	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
SARS (Civet)	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT

One mutation stands out between SARS-COV-2 and others known previously. A single Ala is present in most viruses except SARS-COV-2 where it has been replaced by Cys.

Could this be a sign of engineering? If Cys->Ala reduces cell fusion, Ala->Cys might be expected to enhance it.

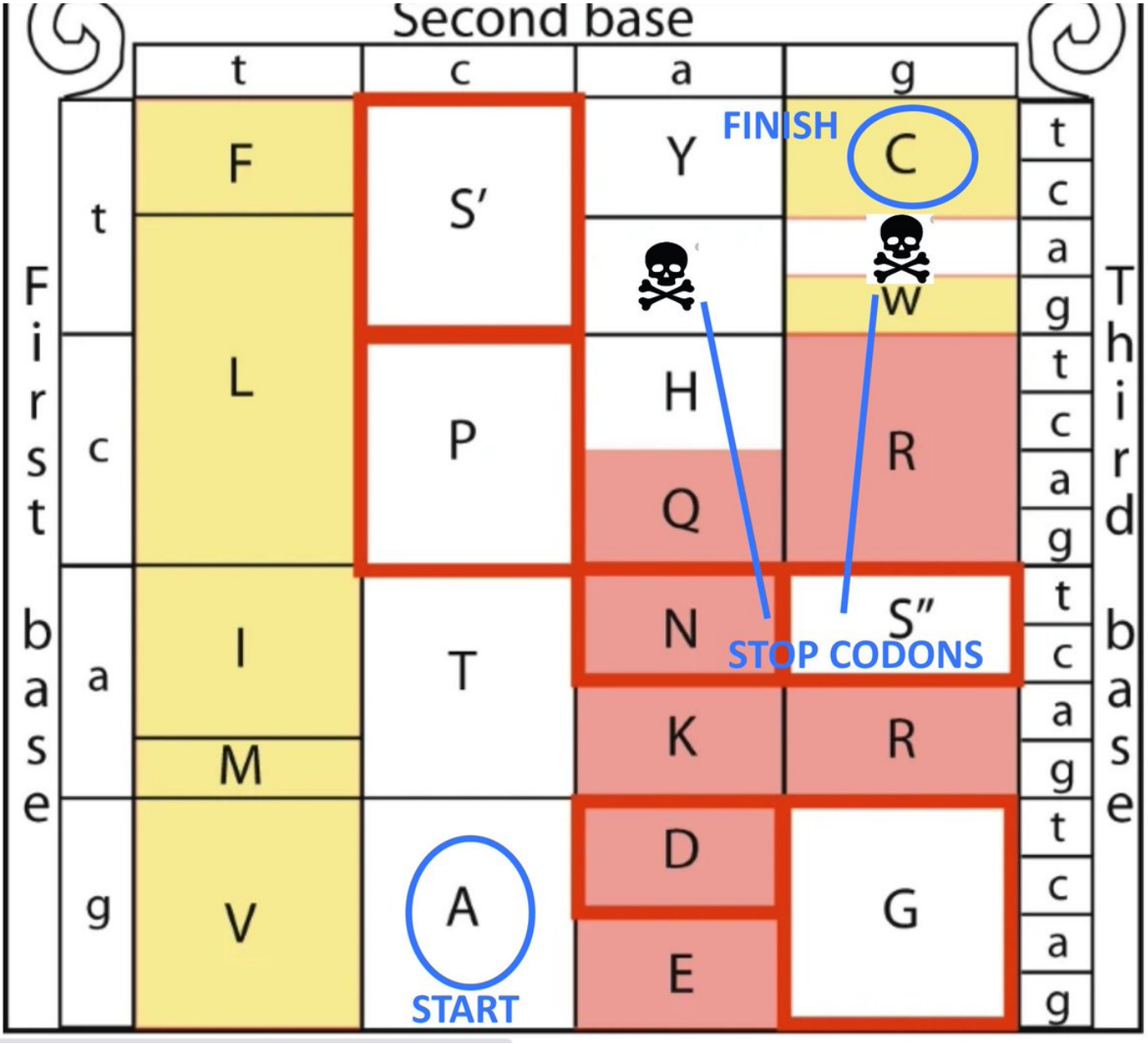
SARS-COV-2	LLCCMTSCCSCLKG**C**CSCGSCCKFDEDDSEPVLKGVKLHYT
SARS (Urbani)	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
BtRs-BetaCoV/YN2018A	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rp/Shaanxi2011	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4247	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
YN2018B	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
As6526	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4237	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Longquan-140	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
Rs4081	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
BetaCoV/GX2013	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
HKU3	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT
YN2013	LLCCMTSCCSCLKG**A**CSCGSCCKFDEDDSEPVLKGVKLHYT

Astonishingly, on a nucleotide basis all 3 codons have mutated between SARS and SARS-COV-2. GCA has become TGT. This is extremely improbable under natural evolution. Occasional single nt mutations are expected, but here are three in one base-in a region that is highly conserved.



For Ala to mutate to Cys via point mutations it must first mutate to intermediate residues in steps. We might expect to find some of these in nature. Some codon combinations near C are stop codons, dead ends.

The path from Ala to Cys seems "inconsistent with natural evolution".



But are there any other coronaviruses with Cysteine in this position? Prior to SARS-COV-2 there were only two - ZC45 and ZC21, viruses sequenced by PLA researchers. These were identified (for different reasons) as the potential backbone for an engineered virus by @drlimengyan1.

SARS-COV-2	LLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT
ZC45/ZC21	LLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT
SARS (Urbani)	LLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT
BtRs-BetaCoV/YN2018A	LLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT
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YN2013	LLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT
Rs806/2006	LLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT

Since the outbreak, new coronavirus discoveries have been springing up like weeds with features unseen prior to SARS-COV-2. Recently there's been a concerted effort to spam Genbank with fakes and frauds

Please check date added/modified if you find a CoV with similar mutations.

Link to earlier parts:

https://t.co/CeztISvFQN

> 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